wwPDB EM Validation Summary Report (i)

Mar 20, 2025 – 01:21 pm GMT

PDB ID	:	9HNY
EMDB ID	:	EMD-10180
Title	:	Mitoribosomal small subunit in complex with Mettl15 and Mettl17
Authors	:	Zgadzay, Y.; Aibara, S.; Gahura, O.; Amunts, A.
Deposited on	:	2024-12-11
Resolution	:	3.30 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

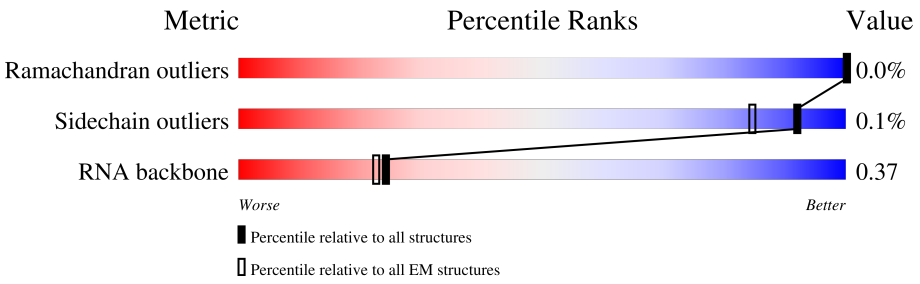
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.5

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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 <=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	620	20% 49% 32% 19%
2	CC	74	32% 91% 9%
3	CE	435	8% 85% 15%
4	CF	160	• 99% •
5	CH	282	• 76% 24%
6	CI	443	13% 94% 6%
7	CJ	817	21% 85% 15%
8	CK	326	11% 63% 37%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	CN	158	70% 94% 6%
10	CO	429	5% 83% 17%
11	CP	188	96%
12	CQ	336	15% 70% 30%
13	CR	320	7% 42% 58%
14	CS	244	34% 35% 65%
15	Ca	602	11% 82% 18%
16	Cb	311	11% 48% 51%
17	Cd	440	42% 58%
18	Cg	490	13% 99%
19	Ci	181	30% 81% 19%
20	Cj	257	88% 12%
21	Ck	874	12% 60% 39%
22	Cn	250	10% 90%
23	Cp	187	91% 9%
24	DB	1181	23% 50% 50%
25	DC	1165	48% 88% 12%
26	DD	812	5% 96%
27	DE	747	61% 78% 22%
28	DF	666	21% 73% 27%
29	DG	631	16% 89% 11%
30	DH	581	23% 86% 14%
31	DI	407	96%
32	DJ	396	16% 79% 21%
33	DK	324	29% 70% 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	DL	307	6% 65% 35%
35	DO	282	11% 68% 32%
36	DP	274	77% 23%
37	DR	270	93% 7%
38	DT	247	14% 89% 11%
39	DU	228	17% 96%
40	DV	183	20% 79% 21%
41	DW	179	22% 73% 26%
42	DX	169	42% 52% 48%
43	DY	163	36% 94% 6%
44	DZ	94	6% 30% 70%
45	F1	1041	15% 82% 17%
46	F2	1024	87% 13%
47	F3	966	11% 91% 8%
48	F4	811	31% 64% 36%
49	F5	754	38% 69% 31%
50	F6	676	13% 67% 33%
51	F7	679	95% 5%
52	F8	726	6% 65% 35%
53	F9	608	5% 35% 65%
54	FA	642	25% 90% 10%
55	FB	588	65% 35%
55	FC	588	10% 59% 41%
56	FD	579	26% 77% 23%
57	FE	553	8% 78% 22%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	FF	474	15% 85% 15%
59	FG	463	6% 37% 62%
60	FH	457	14% 67% 33%
61	FI	445	22% 79% 21%
62	FJ	362	19% 98%
63	FK	372	15% 56% 44%
64	FL	353	10% 89% 11%
65	FM	370	87% 13%
65	FN	370	20% 85% 14%
66	FO	334	93% 7%
67	FP	349	93% 7%
68	FQ	307	5% 74% 25%
68	FR	307	5% 70% 30%
68	FS	307	22% 83% 17%
68	FT	307	8% 70% 30%
68	FU	307	13% 76% 24%
69	FV	264	12% 79% 21%
70	FW	263	92% 8%
71	FX	239	88% 12%
72	FY	189	29% 81% 19%
73	FZ	178	69% 72% 28%
74	Fa	171	16% 94% 6%
75	Fb	151	20% 82% 17%
76	Fc	148	13% 57% 43%
77	Fd	143	64% 36%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
78	Fe	123	24% 97%
79	Fi	629	65% 66% 34%
80	UA	27	70% 100%
81	UB	6	33% 100%
82	UC	10	100%
83	UF	11	27% 100%
84	UG	16	12% 100%
84	UJ	16	38% 100%
85	UI	8	100%
86	UK	24	67% 100%
87	UL	22	18% 100%
88	UM	9	11% 100%
88	UQ	9	22% 100%
89	UN	7	14% 100%
90	UO	30	37% 100%
91	UP	45	64% 100%
92	UY	85	98% 98%
93	Ud	59	64% 100%
94	Ug	167	42% 100%
95	Uh	263	99% 100%
96	Uk	31	55% 100%
97	Ul	14	86% 100%

2 Entry composition (i)

There are 104 unique types of molecules in this entry. The entry contains 454141 atoms, of which 221033 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 RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	CA	502	15241	4551	5079	1648	3461	502	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	614	U	A	conflict	GB X02547.1
CA	615	U	G	conflict	GB X02547.1
CA	616	U	C	conflict	GB X02547.1
CA	618	U	A	conflict	GB X02547.1
CA	619	U	A	conflict	GB X02547.1
CA	620	U	A	conflict	GB X02547.1

- Molecule 2 is a protein called uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
2	CC	67	1195	410	610	87	88	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein uS5 C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	CE	370	5998	1916	2979	553	535	15	0	0

- Molecule 4 is a protein called bS6m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	CF	159	2626	835	1309	234	242	6	0	0

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	CH	214	3495	1105	1737	337	307	9	0	0

- Molecule 6 is a protein called Ribosomal protein S9/S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	CI	418	6606	2087	3283	596	623	17	0	0

- Molecule 7 is a protein called LysM domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	CJ	691	11059	3556	5432	1001	1048	22	0	0

- Molecule 8 is a protein called uS11m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	CK	205	3335	1063	1652	306	304	10	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 9 is a protein called uS14m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	CN	148	2483	799	1233	236	208	7	0	0

- Molecule 10 is a protein called Mitochondrial ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	CO	356	5926	1883	2960	555	512	16	0	0

- Molecule 11 is a protein called bS16m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	CP	180	2999	956	1510	274	250	9	0	0

- Molecule 12 is a protein called uS17m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	CQ	236	3857	1230	1927	360	331	9	0	0

- Molecule 13 is a protein called Mitochondrial ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	CR	134	2280	746	1127	210	195	2	0	0

- Molecule 14 is a protein called uS19m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	CS	85	1396	463	688	121	121	3	0	0

- Molecule 15 is a protein called Chromosome passenger complex (CPC) protein INCENP N terminal.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	Ca	494	8283	2705	4061	750	746	21	0	0

- Molecule 16 is a protein called mS23.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	Cb	152	2550	816	1283	230	215	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cb	6	VAL	GLU	conflict	UNP A0A3L6L708

- Molecule 17 is a protein called mS26.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	Cd	186	3199	1037	1574	298	282	8	0	0

- Molecule 18 is a protein called Mitochondrial SSU ribosomal protein 29.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	Cg	483	7704	2503	3793	686	702	20	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 19 is a protein called mS33.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	Ci	147	2414	770	1192	226	218	8	0	0

- Molecule 20 is a protein called mS34.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	Cj	225	3522	1133	1737	309	339	4	0	0

- Molecule 21 is a protein called mS35.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
21	Ck	529	8539	2688	4281	764	788	18	0	0

There are 4 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	339	GLU	VAL	conflict	UNP Q387C7
Ck	871	GLY	GLU	conflict	UNP Q387C7

- Molecule 22 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
22	Cn	25	408	143	196	36	33	0	0

- Molecule 23 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
23	Cp	171	2859	919	1408	262	265	5	0	0

- Molecule 24 is a protein called mS49.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
24	DB	588	9775	3118	4798	941	900	18	0	0

- Molecule 25 is a protein called mS50.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
25	DC	1021	16155	5161	7983	1445	1536	30	0	0

- Molecule 26 is a protein called mS51.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
26	DD	780	12633	4076	6198	1155	1164	40	0	0

- Molecule 27 is a protein called Mitochondrial SSU ribosomal protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
27	DE	581	8987	2930	4393	823	825	16	0	0

- Molecule 28 is a protein called mS53.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
28	DF	487	7877	2487	3932	732	702	24	0	0

- Molecule 29 is a protein called mS54.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
29	DG	560	8989	2853	4455	826	824	31	0	0

- Molecule 30 is a protein called mS55.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
30	DH	501	8098	2567	4021	754	738	18	0	0

- Molecule 31 is a protein called mS56.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
31	DI	390	6330	2018	3152	554	592	14	0	0

- Molecule 32 is a protein called mS57.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
32	DJ	311	5012	1615	2481	450	452	14	0	0

- Molecule 33 is a protein called mS58.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
33	DK	227	3589	1134	1797	321	332	5	0	0

- Molecule 34 is a protein called mS59.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
34	DL	199	3211	1038	1590	286	287	10	0	0

- Molecule 35 is a protein called mS62.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
35	DO	192	3067	972	1521	277	287	10	0	0

- Molecule 36 is a protein called mS63.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
36	DP	212	3562	1155	1765	321	312	9	0	0

- Molecule 37 is a protein called mS65.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
37	DR	251	4056	1305	2027	367	347	10	0	0

- Molecule 38 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
38	DT	221	3704	1232	1792	334	336	10	0	0

- Molecule 39 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
39	DU	218	3373	1093	1638	307	331	4	0	0

- Molecule 40 is a protein called mS69.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
40	DV	144	2398	771	1185	222	216	4	0	0

- Molecule 41 is a protein called mS70.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
41	DW	132	2236	725	1106	212	188	5	0	0

- Molecule 42 is a protein called mS71.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
42	DX	88	1493	479	749	136	123	6	0	0

- Molecule 43 is a protein called mS72.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
43	DY	154	2580	827	1287	245	216	5	0	0

- Molecule 44 is a protein called mS73.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
44	DZ	28	451	157	213	38	42	1	0	0

- Molecule 45 is a protein called Mitochondrial small ribosomal subunit Rsm22.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
45	F1	860	14086	4376	7088	1342	1240	40	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F1	695	ARG	CYS	conflict	UNP D0A703
F1	707	SER	GLY	conflict	UNP D0A703

- Molecule 46 is a protein called Pentacotripeptide-repeat region of PRORP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	F2	888	14071	4470	6971	1247	1344	39	0	0

- Molecule 47 is a protein called mt-SAF3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
47	F3	886	13695	4291	6834	1217	1301	52	0	0

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 48 is a protein called Methyltranfer_dom domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
48	F4	522	8425	2717	4169	743	775	21	0	0

- Molecule 49 is a protein called Kinteoplast poly(A) polymerase complex 1 subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
49	F5	517	7167	2348	3398	709	697	15	0	0

- Molecule 50 is a protein called DUF4460 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
50	F6	456	7255	2311	3609	635	686	14	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F6	88	VAL	ALA	conflict	UNP A0A3L6L7Z3
F6	192	VAL	LEU	conflict	UNP A0A3L6L7Z3
F6	246	VAL	LEU	conflict	UNP A0A3L6L7Z3
F6	291	ILE	THR	conflict	UNP A0A3L6L7Z3

- Molecule 51 is a protein called mt-SAF7 (KRIPP10).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
51	F7	645	10208	3254	5096	896	928	34	0	0

- Molecule 52 is a protein called Cupin type-1 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
52	F8	475	7316	2327	3651	668	655	15	0	0

- Molecule 53 is a protein called Trichohyalin.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
53	F9	211	3379	1056	1671	322	325	5	0	0

- Molecule 54 is a protein called mt-SAF10.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
54	FA	580	8975	2806	4550	787	810	22	0	0

- Molecule 55 is a protein called tRNA pseudouridine synthase A-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
55	FB	383	6160	1967	3051	580	552	10	0	0
			Total	C	H	N	O	S		
55	FC	344	5623	1781	2801	538	495	8	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FB	385	THR	ALA	conflict	UNP A0A1G4II72
FC	375	THR	ALA	conflict	UNP A0A1G4II72

- Molecule 56 is a protein called PPR_long domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
56	FD	448	6998	2229	3482	626	639	22	0	0

- Molecule 57 is a protein called mt-SAF13.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
57	FE	430	6905	2241	3425	600	621	18	0	0

- Molecule 58 is a protein called S-adenosyl-methyltransferase mraW-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
58	FF	405	6416	2036	3179	580	597	24	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FF	106	GLY	CYS	conflict	UNP A0A3L6L433
FF	259	ALA	VAL	conflict	UNP A0A3L6L433

- Molecule 59 is a protein called mt-SAF15.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
59	FG	174	2828	878	1426	269	246	9	0	0

- Molecule 60 is a protein called mt-SAF16 (P32).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
60	FH	305	4734	1500	2338	424	453	19	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FH	169	ASP	HIS	conflict	UNP D0A6K1
FH	260	MET	ARG	conflict	UNP D0A6K1

- Molecule 61 is a protein called mt-SAF17.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
61	FI	350	5514	1731	2716	511	543	13	0	0

- Molecule 62 is a protein called mt-SAF18 (RbfA).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
62	FJ	353	5886	1844	2968	550	515	9	0	0

- Molecule 63 is a protein called Mitochondrial glycoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
63	FK	209	3303	1089	1595	285	328	6	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 64 is a protein called Metallo-beta-lactamase domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
64	FL	314	4986	1586	2478	455	450	17	0	0

- Molecule 65 is a protein called mt-SAF21.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
65	FM	323	4839	1498	2415	444	462	20	0	0
			Total	C	H	N	O	S		
65	FN	317	4742	1471	2363	434	454	20	0	0

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 66 is a protein called mt-SAF22.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
66	FO	312	5145	1623	2560	495	454	13	0	0

- Molecule 67 is a protein called ADP-ribosylglycohydrolase.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
67	FP	326	5001	1609	2474	444	464	10	0	0

- Molecule 68 is a protein called Potassium voltage-gated channel, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
68	FQ	229	3661	1173	1817	330	334	7	0	0
			Total	C	H	N	O	S		
68	FR	216	3495	1120	1736	317	315	7	0	0
			Total	C	H	N	O	S		
68	FS	254	4088	1306	2027	374	373	8	0	0
			Total	C	H	N	O	S		
68	FT	215	3469	1112	1720	316	314	7	0	0
			Total	C	H	N	O	S		
68	FU	234	3766	1204	1871	344	339	8	0	0

- Molecule 69 is a protein called mt-SAF25.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
69	FV	209	3185	1033	1561	281	299	11	0	0

- Molecule 70 is a protein called Low molecular weight protein tyrosine phosphatase.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
70	FW	242	3985	1245	1991	379	364	6	0	0

- Molecule 71 is a protein called PPR_long domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
71	FX	211	3272	1037	1616	305	300	14	0	0

- Molecule 72 is a protein called mt-SAF28.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
72	FY	154	2480	784	1243	221	226	6	0	0

- Molecule 73 is a protein called mt-SAF29.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
73	FZ	128	1804	592	854	176	180	2	0	0

- Molecule 74 is a protein called mt-SAF30.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
74	Fa	161	2635	853	1324	234	220	4	0	0

- Molecule 75 is a protein called Complex 1 protein (LYR family).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
75	Fb	126	2140	691	1068	195	179	7	0	0

- Molecule 76 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
76	Fc	84	1333	427	664	106	135	1	0	0

- Molecule 77 is a protein called Probable Zinc-ribbon domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
77	Fd	91	1444	459	722	138	117	8	0	0

- Molecule 78 is a protein called mt-SAF34.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
78	Fe	119	1997	631	985	196	179	6	0	0

- Molecule 79 is a protein called mt-SAF38.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
79	Fi	417	6663	2132	3315	605	589	22	0	0

- Molecule 80 is a protein called UNK-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
80	UA	27	164	81	29	27	27	0	0

- Molecule 81 is a protein called UNK-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
81	UB	6	38	18	8	6	6	0	0

- Molecule 82 is a protein called UNK-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
82	UC	10	65	30	15	10	10	0	0

- Molecule 83 is a protein called UNK-F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
83	UF	11	72	33	17	11	11	0	0

- Molecule 84 is a protein called UNK-G,J.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
84	UG	16	100	48	20	16	16	0	0
84	UJ	16	102	48	22	16	16	0	0

- Molecule 85 is a protein called UNK-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
85	UI	8	52	24	12	8	8	0	0

- Molecule 86 is a protein called UNK-K.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
86	UK	24	149	72	29	24	24	0	0

- Molecule 87 is a protein called UNK-L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
87	UL	22	135	66	25	22	22	0	0

- Molecule 88 is a protein called UNK-M,Q.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
88	UM	9	59	27	14	9	9	0	0
88	UQ	9	56	27	11	9	9	0	0

- Molecule 89 is a protein called UNK-N.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
89	UN	7	45	21	10	7	7	0	0

- Molecule 90 is a protein called UNK-O.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
90	UO	30	183	90	33	30	30	0	0

- Molecule 91 is a protein called UNK-P.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
91	UP	45	278	135	53	45	45	0	0

- Molecule 92 is a protein called UNK-Y.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
92	UY	83	507	249	92	83	83	0	0

- Molecule 93 is a protein called UNK-d.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
93	Ud	59	357	177	62	59	59	0	0

- Molecule 94 is a protein called UNK-g.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
94	Ug	167	1023	501	188	167	167	0	0

- Molecule 95 is a protein called UNK-h.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
95	Uh	263	1619	789	304	263	263	0	0

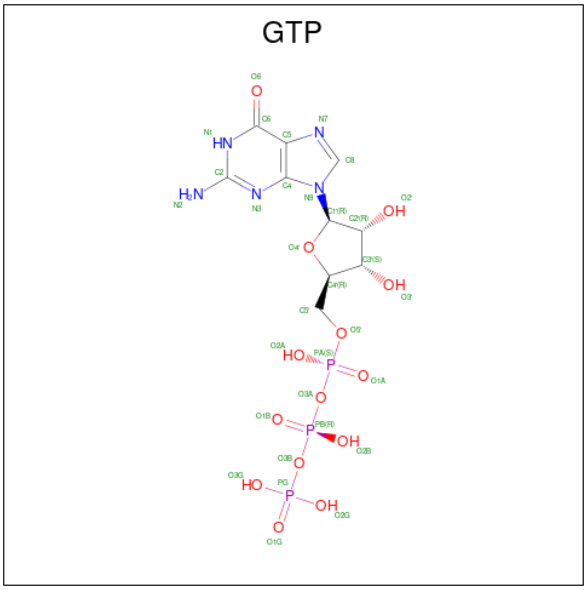
- Molecule 96 is a protein called UNK-k.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
96	Uk	31	188	93	33	31	31	0	0

- Molecule 97 is a protein called UNK-l.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
97	Ul	14	86	42	16	14	14	0	0

- Molecule 98 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

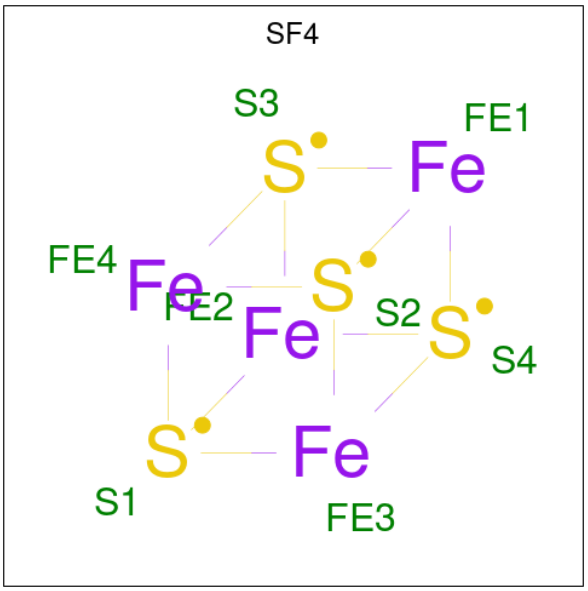


Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
98	Cg	1	44	10	12	5	14	3	0

- Molecule 99 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

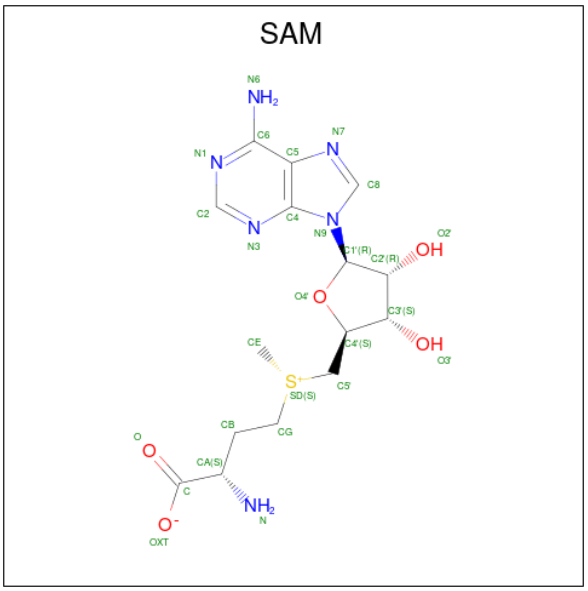
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
99	Cg	1	1	1	0

- Molecule 100 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



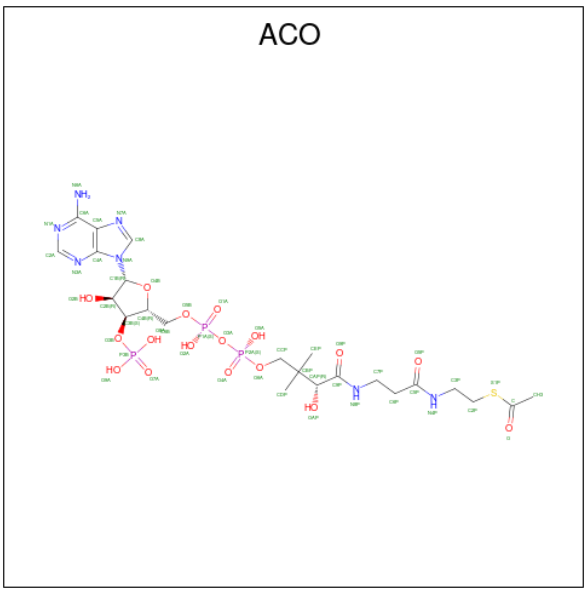
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
100	F1	1	8	4	4	0

- Molecule 101 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	S	
101	F1	1	46	15	19	6	5	1	0
			Total	C	H	N	O	S	
101	FF	1	46	15	19	6	5	1	0

- Molecule 102 is ACETYL COENZYME *A (three-letter code: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$).

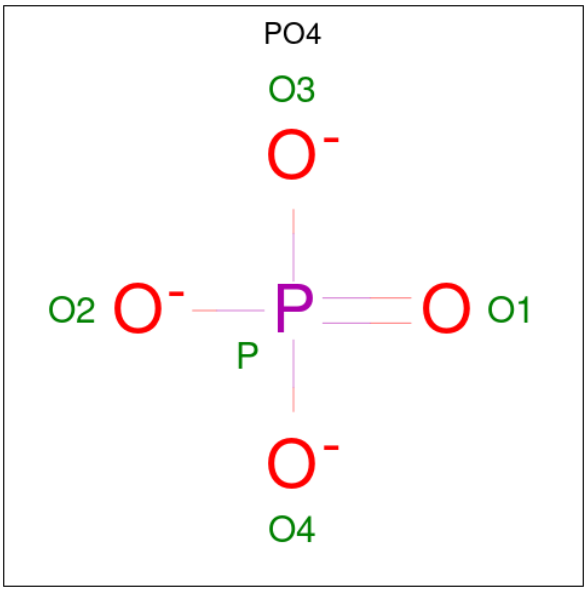


Mol	Chain	Residues	Atoms							AltConf
			Total	C	H	N	O	P	S	
102	F3	1	85	23	34	7	17	3	1	0

- Molecule 103 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
103	FG	1	1	1	0
103	FL	1	1	1	0
103	Fd	1	1	1	0
103	Fe	1	1	1	0

- Molecule 104 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



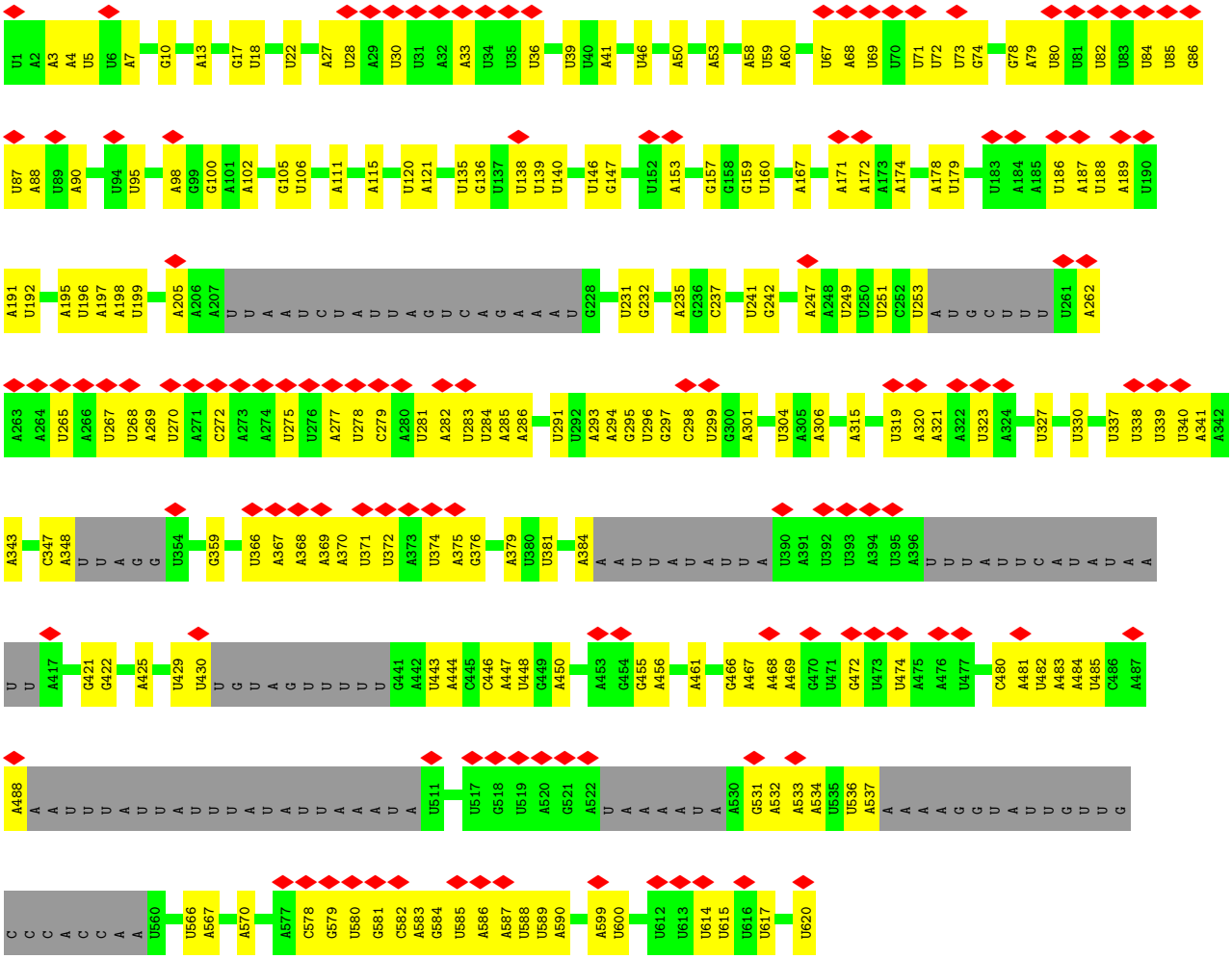
Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
104	FW	1	5	4	1	0

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.

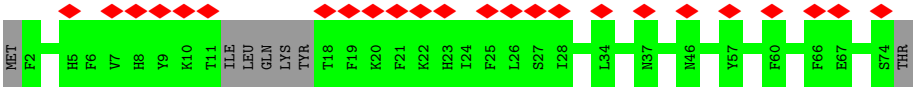
- Molecule 1: 9S RNA

Chain CA: 20% 49% 32% 19%



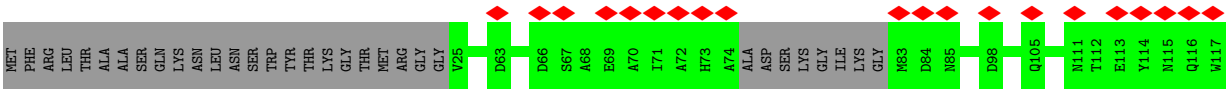
- Molecule 2: uS3m

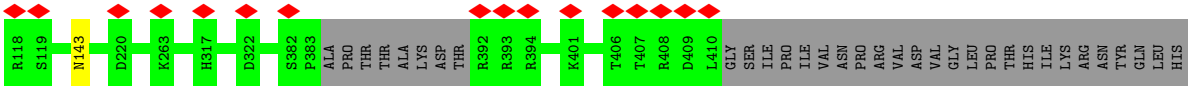
Chain CC: 32% 91% 9%



• Molecule 3: Small ribosomal subunit protein uS5 C-terminal domain-containing protein

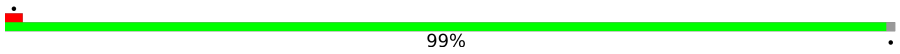
Chain CE:

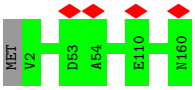




• Molecule 4: bS6m

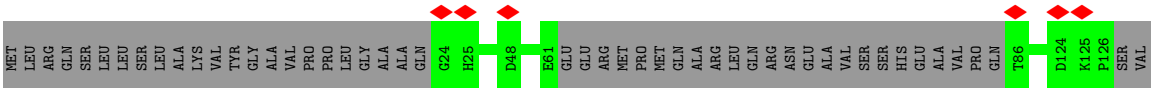
Chain CF:

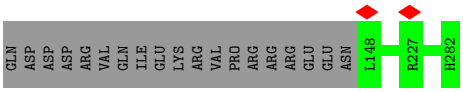




• Molecule 5: 30S ribosomal protein S8

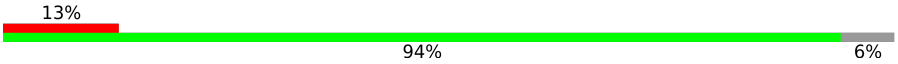
Chain CH:

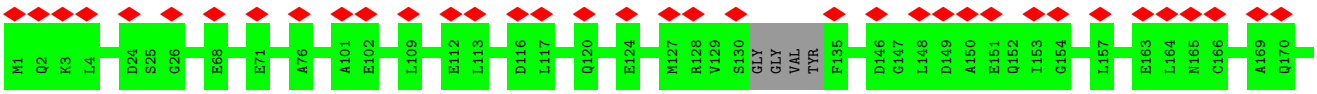


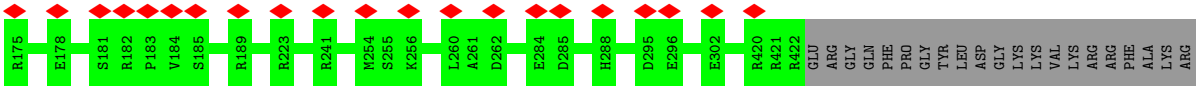


• Molecule 6: Ribosomal protein S9/S16

Chain CI:

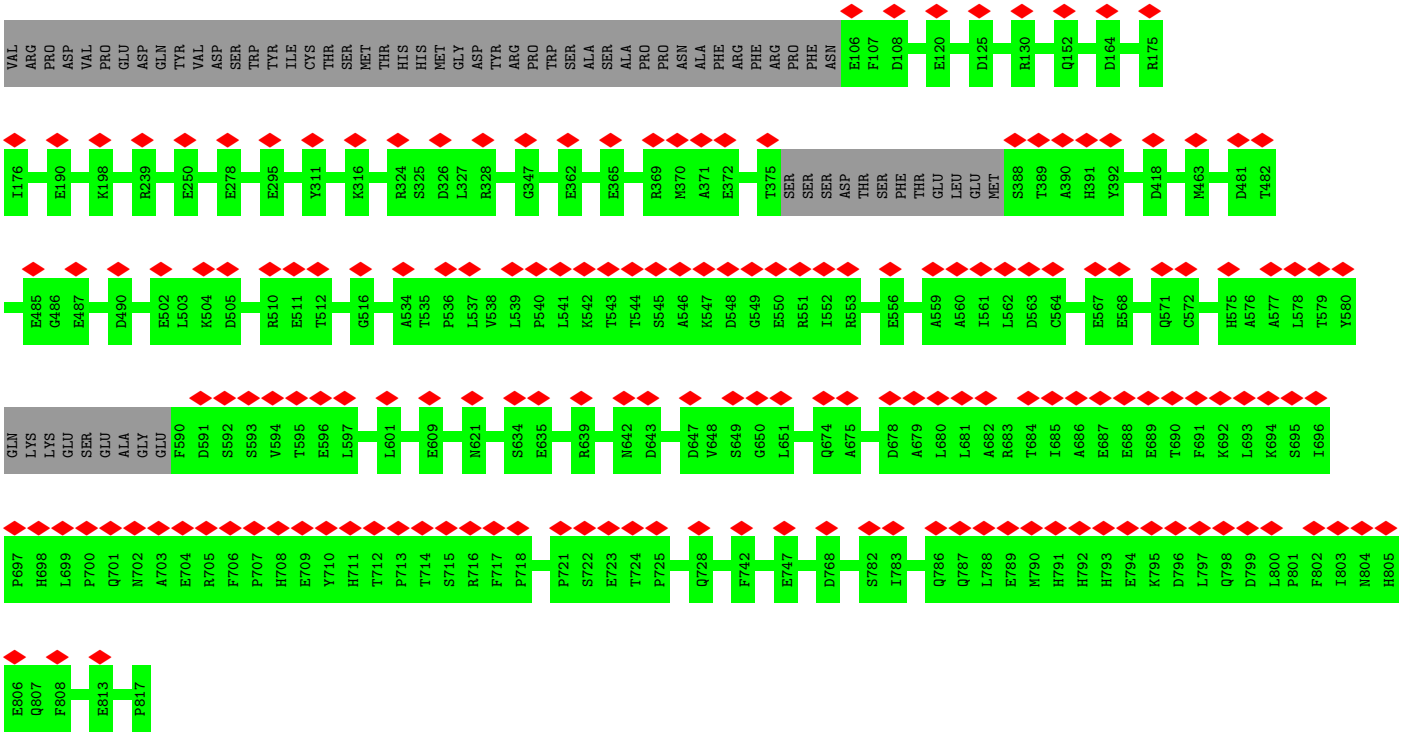






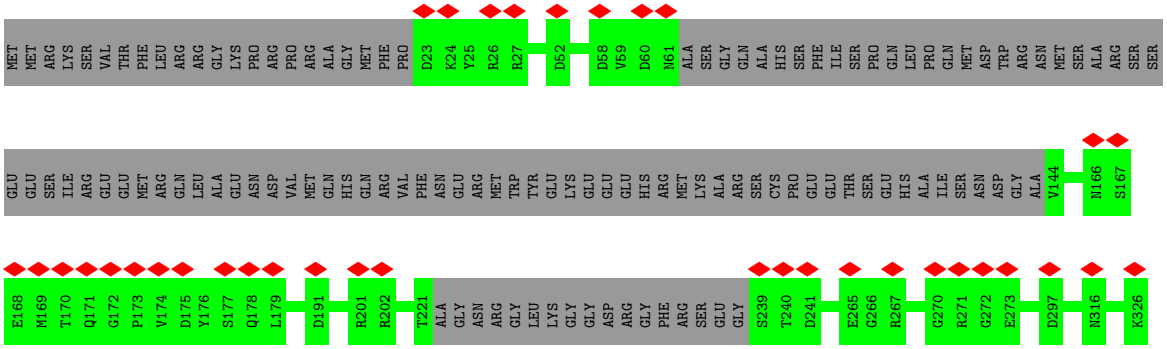
• Molecule 7: LysM domain-containing protein

Chain CJ:



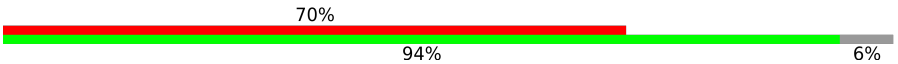
- Molecule 8: uS11m

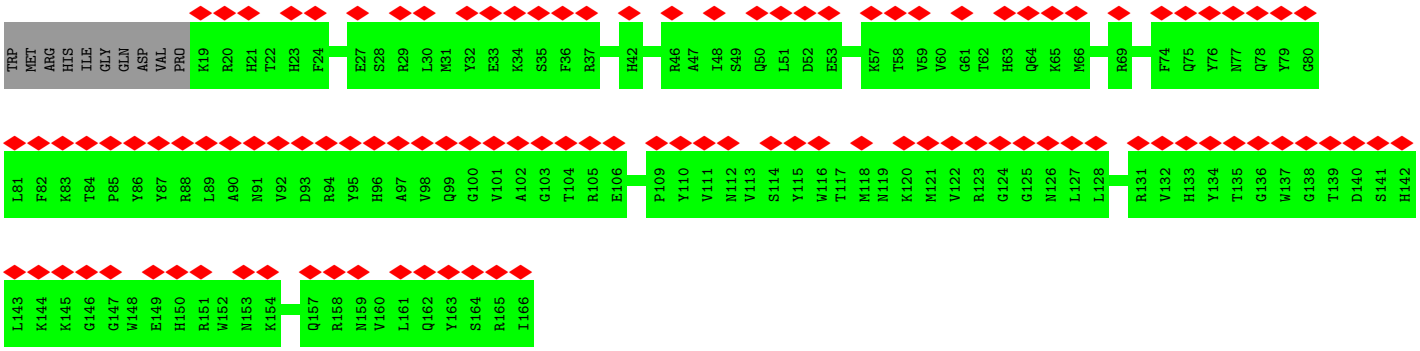
Chain CK:



- Molecule 9: uS14m

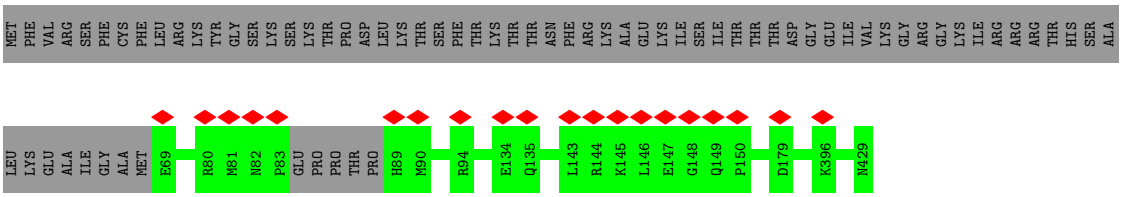
Chain CN:





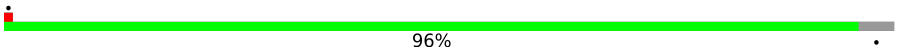
- Molecule 10: Mitochondrial ribosomal protein S15

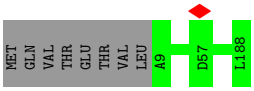
Chain CO:



- Molecule 11: bS16m

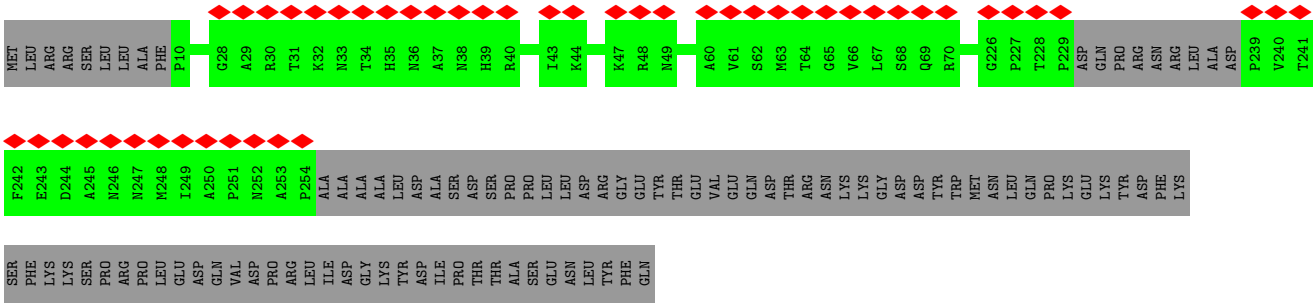
Chain CP:





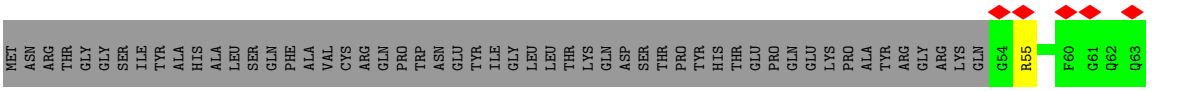
- Molecule 12: uS17m

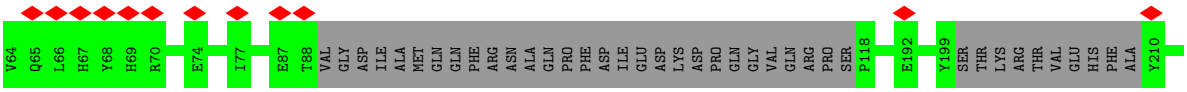
Chain CQ:

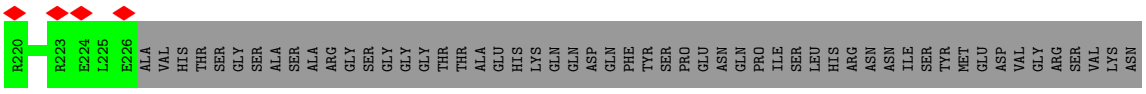


- Molecule 13: Mitochondrial ribosomal protein S18

Chain CR:

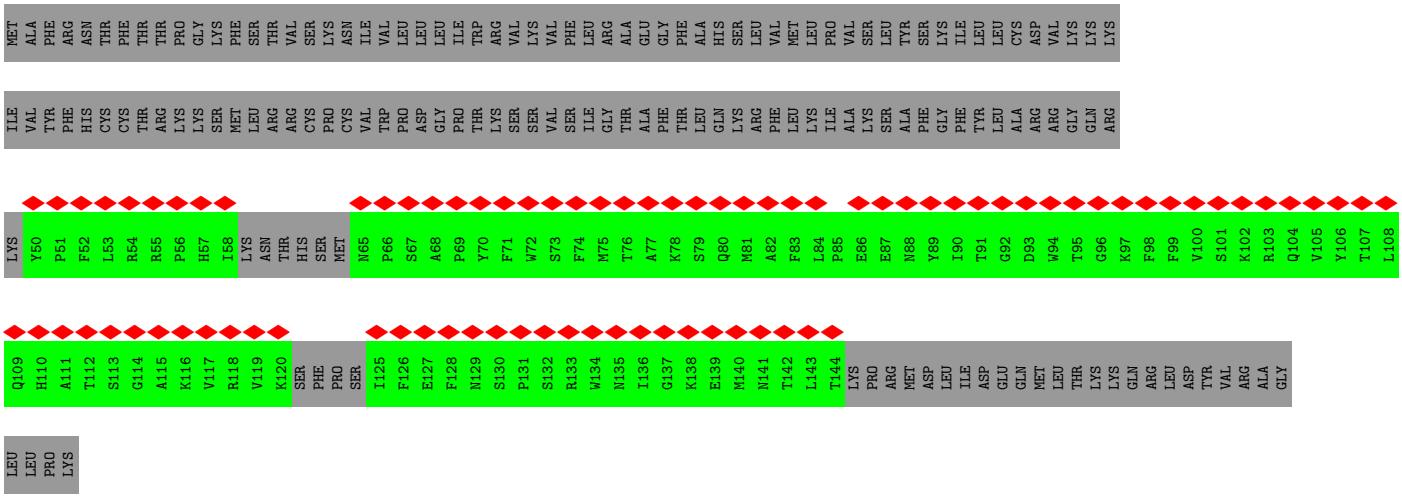






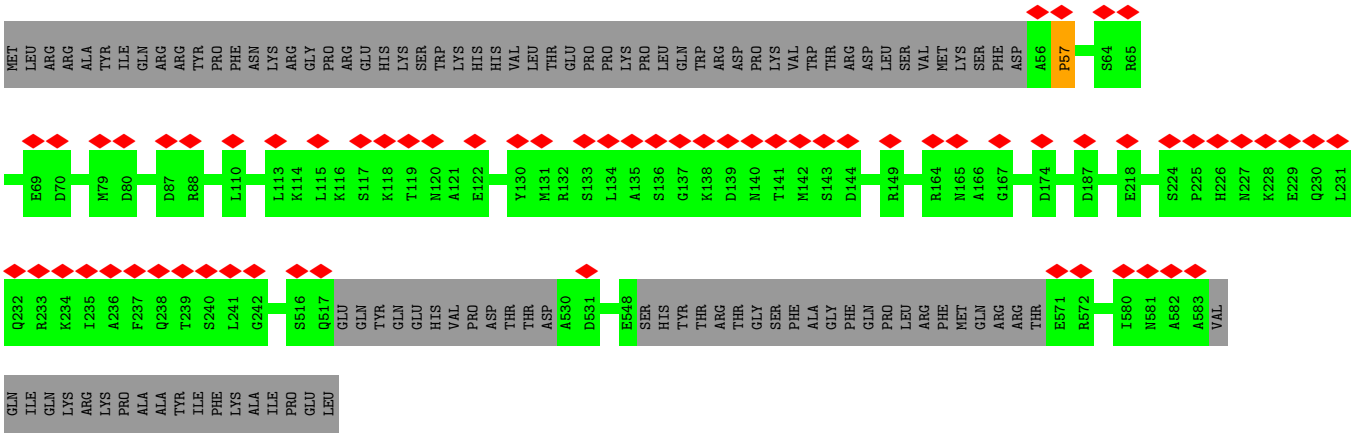
- Molecule 14: uS19m

Chain CS:



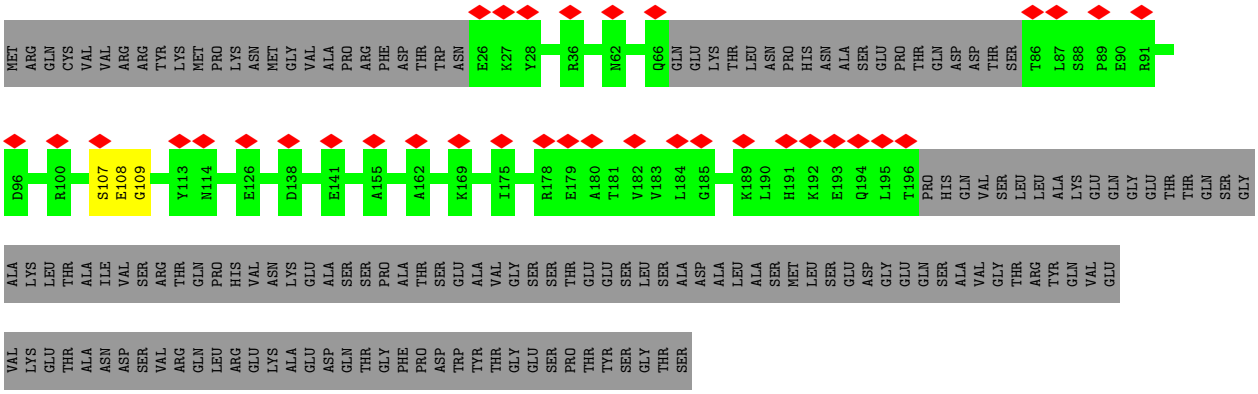
- Molecule 15: Chromosome passenger complex (CPC) protein INCENP N terminal

Chain Ca:



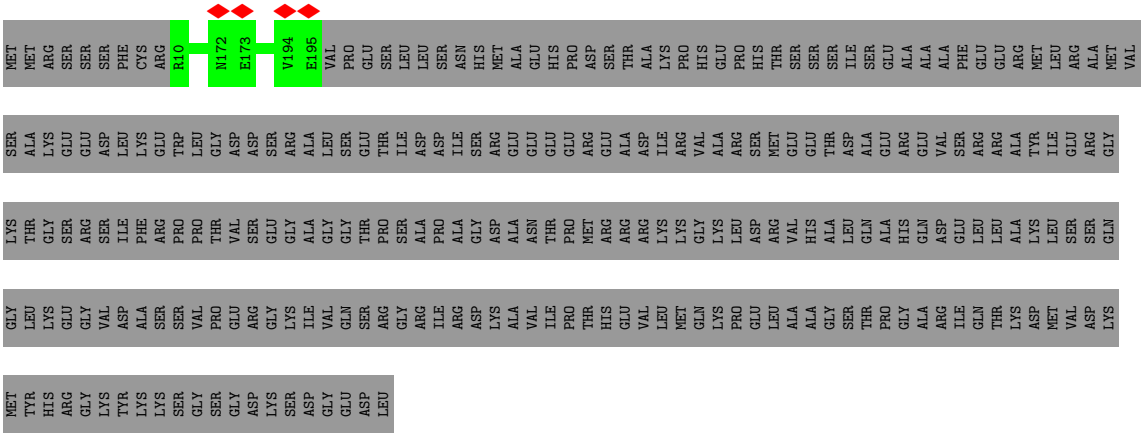
- Molecule 16: mS23

Chain Cb:



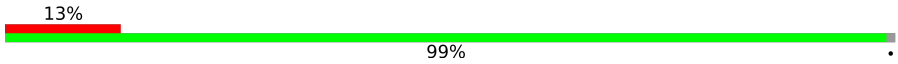
- Molecule 17: mS26

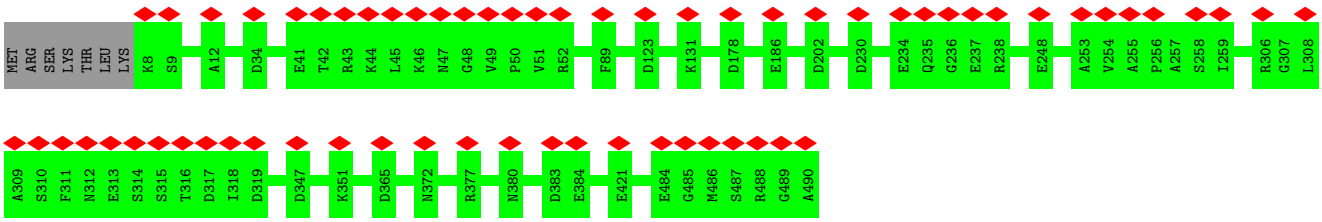
Chain Cd:



- Molecule 18: Mitochondrial SSU ribosomal protein 29

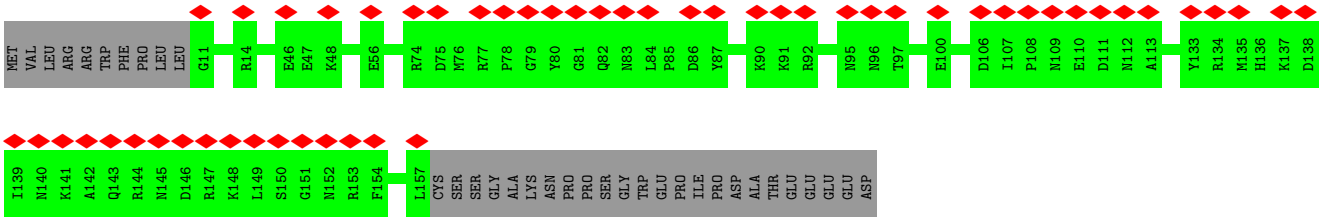
Chain Cg:





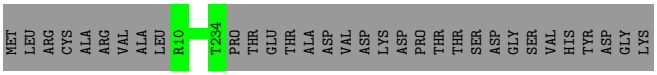
- Molecule 19: mS33

Chain Ci:



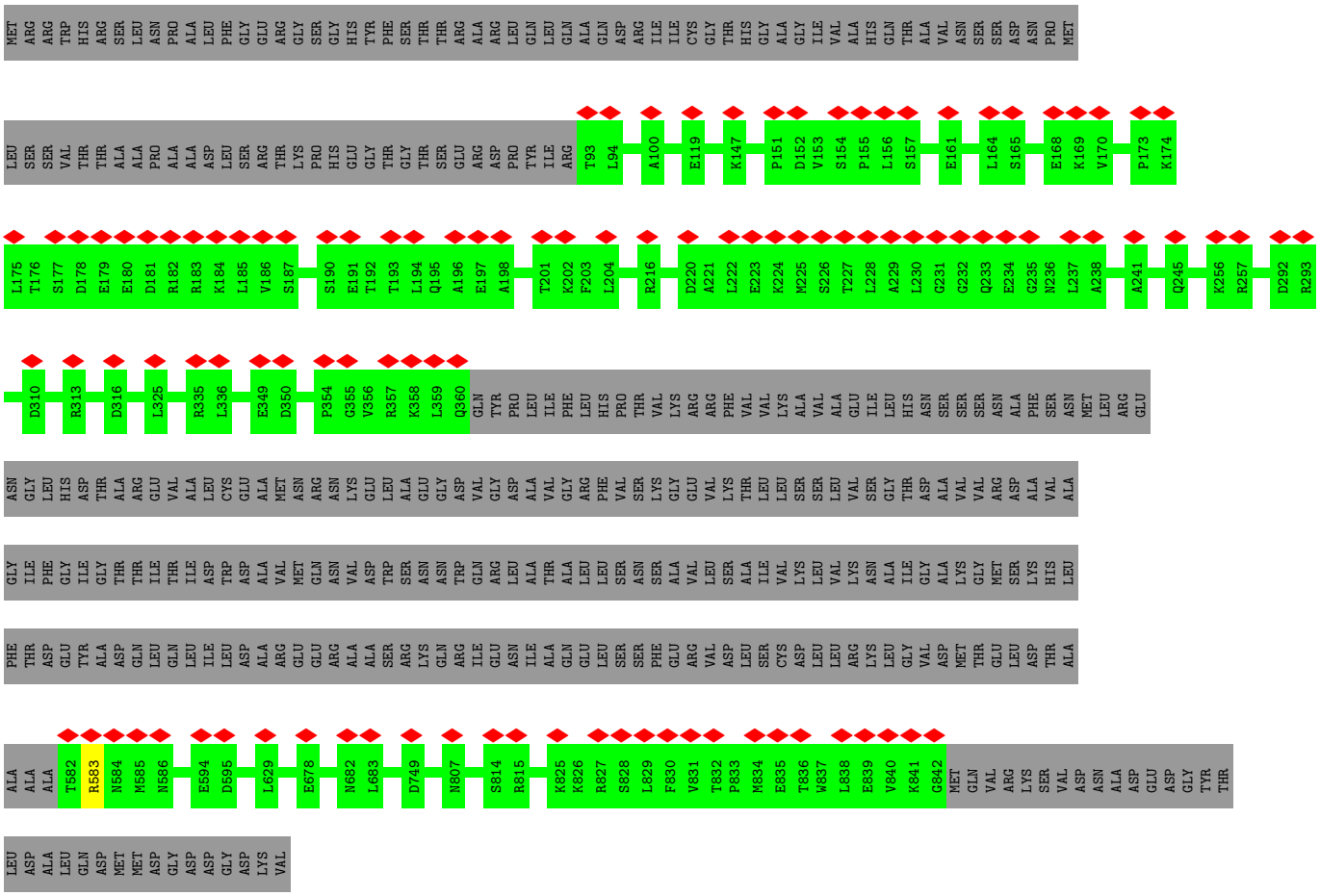
- Molecule 20: mS34

Chain Cj:



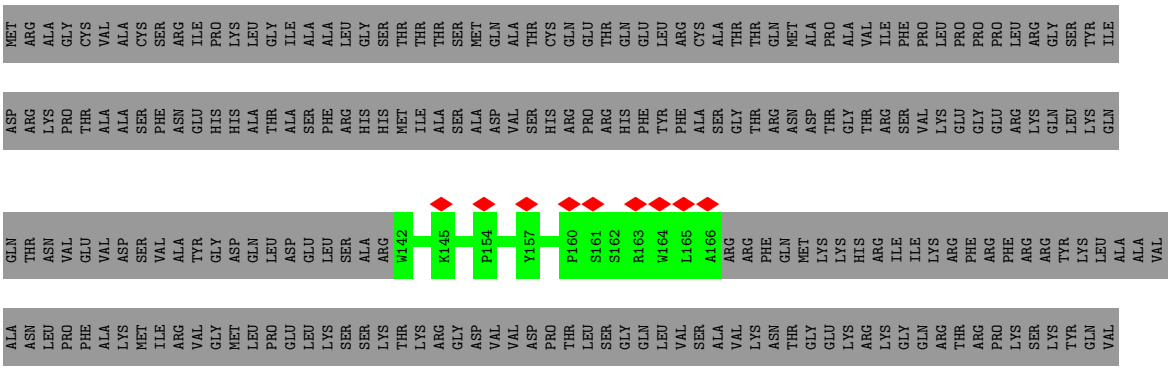
- Molecule 21: mS35

Chain Ck:



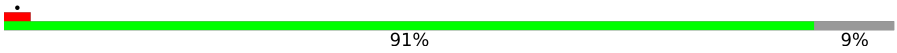
- Molecule 22: mS38

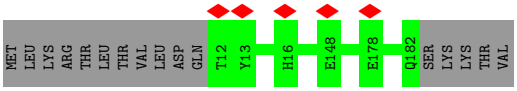
Chain Cn:



- Molecule 23: Protein FYV4, mitochondrial

Chain Cp:





- Molecule 24: mS49

Chain DB: 23% 50% 50%

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

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

PRO HIS ILE GLN SER PRO TYR GLU TYR GLU GLU ALA ALA HIS ARG ARG VAL TRP LEU ASP HIS ASP VAL ASP ARG MET ARG GLU GLU PHE THR GLN HIS ARG ALA SER LEU ARG SER LEU ALA SER ALA GLN GLU ARG GLU GLU LEU LEU ARG SER ARG ALA ALA GLU TYR GLN VAL ALA

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

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

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

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

THR PRO ALA ASP GLU HIS TRP ASN PRO TYR ILE ARG ARG SER THR GLU ASN GLY VAL GLY HIS L442 L443 Q444 D448 R452 E453 D454 K458 G459 E460 Q461 D462 E465 R466 H470 I475 D480 E481 R490 G491 E492 L495 D496 K499 P500 F501 L507 R508

L509 N510 R511 M512 Y513 R514 E517 S520 L521 M522 K523 Q524 R525 P526 E527 F528 L529 E530 L553 E559 E563 R564 D565 D581 E582 R583 H586 V587 N588 D589 D590 E591 M592 K593 V594 S595 V596 E597 T598 L599 G604 V605 Y606 M607 L608 A616 V617 L618 GLY GLY SER

ALA SER VAL ASN LEU HIS LEU TYR HIS LEU ALA ASP GLU MET GLY THR ALA D639 T640 R641 L645 L650 N651 R652 L653 L654 E657 S658 TYR GLN ASN ARG VAL GLY ARG GLY PHE MET ASN HIS VAL VAL GLY ARG ALA PRO GLU PRO VAL V680 P681 H682 E683 Q684 P685 Q686 E687

V688 L689 R690 H691 F692 S693 A694 E695 E696 R697 A698 E701 Q702 H703 V704 K705 E706 Q707 T708 S709 R710 Q711 L712 G713 E714 W715 E716 R717 A718 M719 K720 R721 R722 R723 W724 L725 T726 D727 H728 Q729 Q730 Y731 G732 H733 V734 VAL SER HIS GLY LEU GLU THR SER VAL VAL ASP LEU SER HIS

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

MET THR SER GLU ASP PHE D815 R816 C817 E818 L819 E820 A821 F822 P823 R824 N825 LEU ASN HIS ALA LEU ASN TYR GLY ILE ALA ASN TYR ALA TYR N840 R841 G842 E854 D870 E874 E914 D925 D952 E953 S954 R955 R956 Y957 N958 P959 A960 A961 M962 R963 R964 Y965 V966

D967 V968 T969 D970 P971 F972 N973 E974 K975 T976 S977 N978 T979 E980 D984 K985 Y986 E987 P988 K989 R990 N991 A992 D993 T994 V995 A996 D997 K998 Y999 R1000 T1001 T1002 E1007 I1008 D1009 K1010 R1013 A1017 I1027 S1028 H1029 R1030 R1031 D1032 G1037 R1041 E1052 A1053 D1054 I1058

A1059 E1060 Q1064 D1065 R1090 D1098 D1104 G1105 V1106 T1107 P1108 W1109 K1110 Q1111 A1112 Q1113 K1114 I1115 R1116 T1117 Y1118 W1119 E1120 V1121 R1122 S1123 H1124 H1125 P1126 M1127 P1128 Q1129 F1130 N1131 R1132 P1133 E1134 V1135 A1136 M1137 H1138 R1139 N1140 T1141 V1142 G1143 L1144 L1145 P1146 A1147 H1148 M1149 W1150 E1151 T1152 D1153

K1154 K1155 T1156 G1157 K1158 V1159 K1160 S1161 V1162 K1163 D1164 SER VAL ARG ASP TYR GLN THR LYS THR PRO TYR PRO LYS TRP VAL GLN LEU

- Molecule 25: mS50

Chain DC: 48% 88% 12%

MET PHE ARG VAL ARG ARG LEU ALA GLY PHE ILE GLN CYS SER PRO CYS GLY LYS MET GLY PRO LEU LYS GLN GLN THR ARG ARG TYR THR PRO ILE TRP K34 S35 D36 P37 A38 V39 D40 L45 R46 D47 E48 D49 E50 R51 R52 A56 E57 V58 G59 P60 I61 S62 D63 V64 G65

R73 F74 L80 H81 G90 K91 F92 R93 N94 Q95 Q96 R97 E98 K99 E100 S101 L102 L103 P104 N105 S106 S107 F110 V113 E114 G118 F123 G124 S125 P126 K130 E131 A134 R143 R147 L150 S151 R152 Y158 V159 G160 N163 S164 P165 E166 V167

F168 D169 D170 E171 R174 D182 T183 F184 F185 R186 E187 L191 F195 L196 K197 E198 K199 V200 A209 L210 K211 R212 A213 S214 P215 E216 A217 Y218 D223 Q226 T229 Q230 T231 P234 E244 G245 E246 R247 R248 K249 Q250 K254 A264 F265 F266 K267 D268 V269

L270 S271 E272 D273 V274 K275 K276 Y277 Q278 E279 V280 P281 G282 K283 L284 L285 Q286 K287 V291 D294 V295 I298 H303 E304 R305 W306 L307 K308 G309 R310 V311 W312 T313 S314 L315 T316 E317 E318 E319 R320 E321 A322 Y323 R330 Q334 V335 E336 D337 G338 E339 F340 D341 P342 M343

M344 E345 D346 D347 V348 D349 D350 T351 E352 I353 E359 I363 M364 E365 S369 P370 I371 D372 G373 L374 H375 F376 L379 E380 H384 A385 M386 E390 L391 E392 T398 S399 A400 R401 A404 R410 K411 D415 E420 Q424 T434 L435 D436 L437 G438 A439 G440

R443 P444 H445 E448 L453 N454 K457 F458 L474 H478 A479 G480 S481 L482 K483 D484 L491 T495 K496 P497 L498 S499 N500 S501 L502 D503 Y504 A505 K509 N520 Y527 R535 R542 A543 E544 D545 L546 I547 V551 F558 G559 E560 R561 R562 R563

R567 D568 L569 E572 F573 Q574 R575 L576 A577 V578 P579 V580 E581 R582 V583 I584 V585 A586 N587 P588 V589 S590 A591 L592 L593 E594 S595 G596 A597 D598 P599 D600 E601 K602 P603 V604 E605 G606 E607 K608 V609 N610 M611 W612 P613 L614 G615 A616 K617 R618 V619 V620 L621 Y622 K623 W624 S625 A626

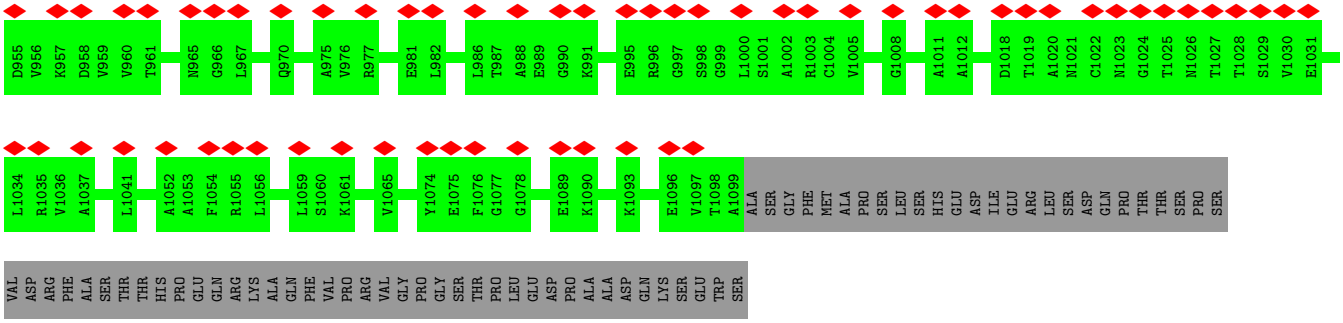
P627 N628 V629 E630 K631 L632 M635 E636 S637 D638 A639 A640 P641 A642 V643 S644 G645 S646 S647 L648 T649 A650 E651 R652 L653 R654 E655 I656 Q657 E658 L659 K660 R661 R662 L665 E666 V667 S668 L669 W670 V673 T674 A675 Q676 E677 R678 K679 Q680 R681 N682 E683 I684 V685 E686 A687 K688 K689

K690 Q691 V692 E693 E694 V695 V696 R697 T698 V699 A703 H706 S714 R715 I716 E717 E718 R719 V720 A721 PHE PRO THR GLU THR SER THR VAL THR ASP THR THR ASN MET LYS GLU GLU THR ASN LYS PRO LEU GLU ASP SER E747 W748 E749 F750 A751 V752 L753 L754 D755 D756 R757 V758

L759 L760 N761 K762 E763 E764 S765 V766 E767 L768 Y769 L770 P771 Y772 R773 D774 A775 N776 G777 E778 L779 L780 A781 Q782 G783 E784 Y785 R786 A787 L788 V789 R790 L794 E795 A796 N797 P798 N799 P802 A803 Y804 V807 G808 Y809 S810 E811 H814 V815 F816 D817 A818 L819 P820 Q821 L822 I823

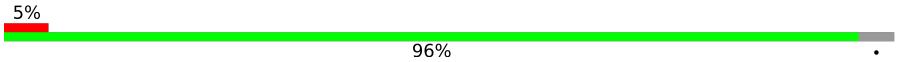
A824 Q825 F826 F827 R828 VAL LYS ASP ALA THR ALA GLU ALA ALA GLY VAL THR H841 I842 P843 A844 A845 D846 F847 T848 P849 F850 C851 A852 F853 L854 R855 D856 A857 G858 L859 D860 V861 P862 L863 R864 C865 E866 F867 E868 A869 G870 Q871 ALA VAL THR THR ASP GLY ASP VAL Y880 M881 D882 Y883

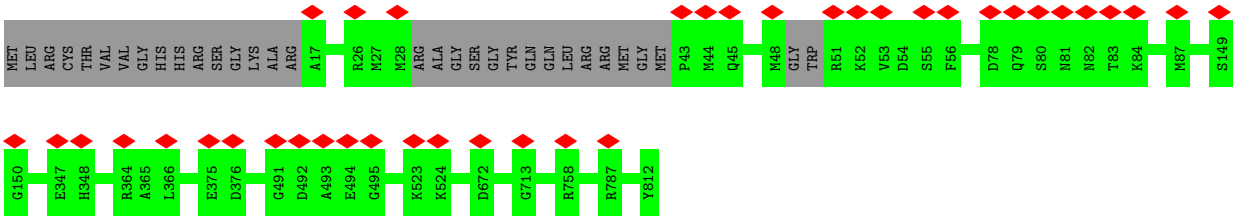
F884 L885 Q886 L887 L888 R889 G890 E891 A892 F893 H894 Q895 S896 H897 A898 Q899 A900 G901 L902 T903 E904 A905 Q906 R907 A908 I909 E910 R914 G923 A924 D925 E926 S927 E928 W929 A930 T931 A932 R933 R934 S935 V936 L937 D938 H939 Q942 H943 E944 R945 E946 F949 P950 N951 E952 M953 L954



- Molecule 26: mS51

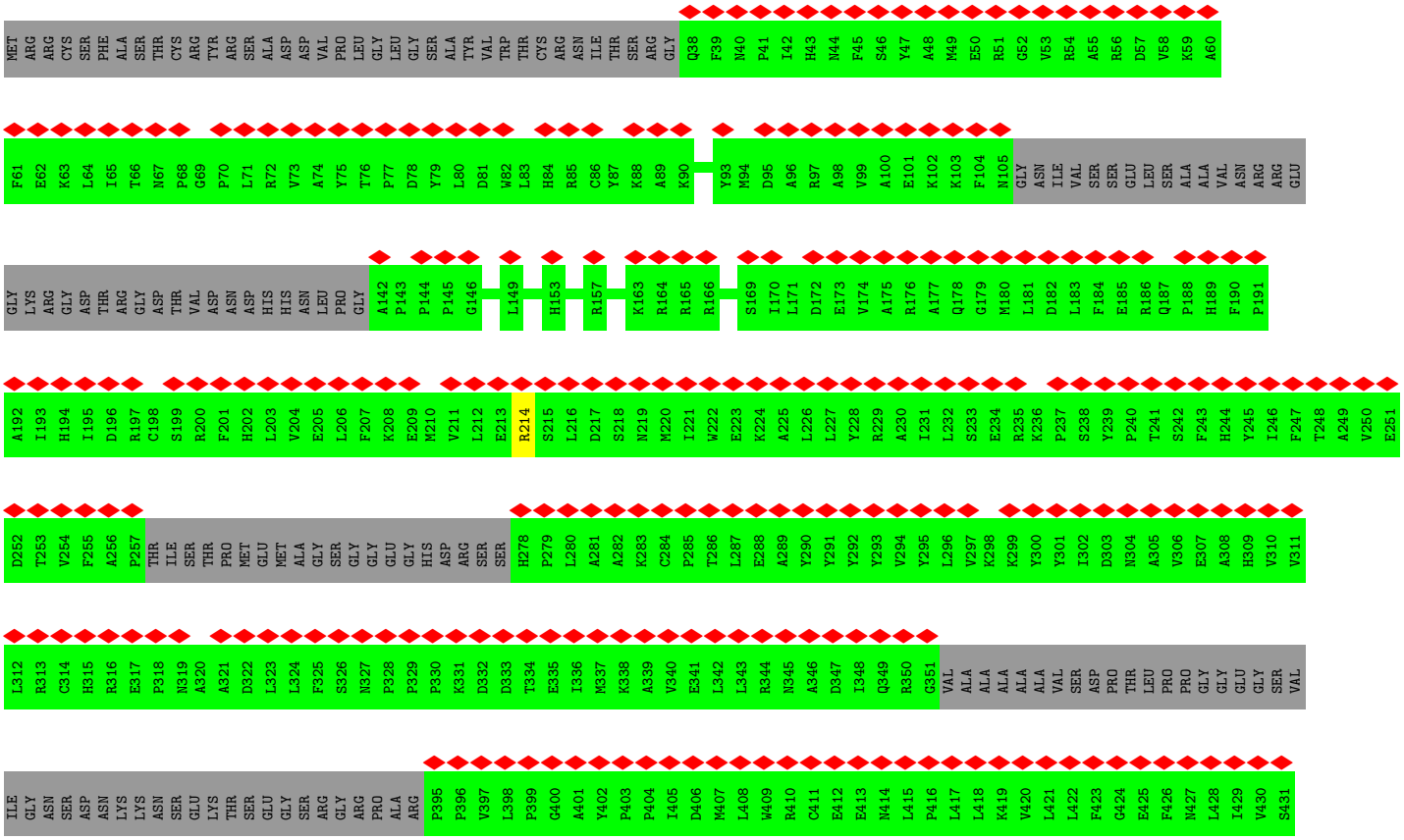
Chain DD:





- Molecule 27: Mitochondrial SSU ribosomal protein

Chain DE:



E432 N433 P434 F435 V436 K437 F438 P439 S440 A441 H442 G443 F444 L445 T446 R447 P448 Y449 S450 T451 D452 S453 S454 R455 T456 L457 A458 D459 G460 M461 S462 L463 A464 N465 V466 M467 A468 E469 K470 R471 G472 H473 L474 L475 P476 S477 L478 P479 R480 N481 T482 A483 T484 S485 I486 D487 A488 R489 A490 Q491

D492 I493 R494 R495 L496 Q497 Q498 K499 H500 H501 R502 D503 D504 I505 V506 S507 F508 Q509 K510 L511 L512 R513 S514 THR HIS ALA GLU ASP SER PRO SER ALA F524 S525 S526 Y527 S528 D529 W530 S531 Y532 F533 N534 P535 R536 A537 V538 R539 A540 E541 E542 R543 D544 R545 L546 T547 R548 K549 A550 V551

E552 A553 L554 K555 L556 Y557 D558 S559 A560 T561 N562 D563 H567 S568 F569 E570 Q573 T577 E582 R583 D584 R585 T586 M587 Y590 L591 P592 T593 L594 P595 H596 I600 D604 I613 G614 D617 R618 N619 S620 S621 E622 E623 K629 E630 L631 E632 K633 R634 Y637

R640 H644 T645 A646 Y649 E652 T653 V654 R655 R656 R659 Q660 K661 D670 N671 T678 T679 I680 L681 R682 D683 K684 H685 D686 V687 T688 D689 V690 T691 K692 T693 L694 N699 K702 Q703 L704 A705 R706 R710 L713 F714 A715 N716 R717 S718 L719 D720 D721 T722

G723 F724 P725 T726 ASP ALA ARG ALA ASP ASP TYR THR ARG TRP MET ALA PRO PRO SER VAL GLY LYS VAL SER LEU

- Molecule 28: mS53

Chain DF: 21% 73% 27%

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

GLY ASN Y63 N64 S65 G66 Y67 C68 T69 E70 R71 T72 H73 V74 L75 E76 E77 N78 T79 V80 S81 I82 I83 P84 R85 R86 E87 L88 E89 K90 Y91 M92 P93 D94 I95 T96 I97 G98 P99 K100 A101 L102 S107 L108 M109 N110 A111 R112 N113 G114 H115 R116 V117 T118 H119 D120 L121 L122 H123

S124 Y125 D126 P127 H128 ILE GLY ARG LEU GLY LYS PRO ALA VAL VAL ASP HIS ASP ASN ILE THR VAL GLU ASP P148 N149 R150 V151 G152 L153 N154 A155 A156 T157 L158 D159 C160 R161 G162 R163 I164 Y165 R188 D189 P193 T194 D195 F196 V197 H198 E199 L202 E220 R223

E255 D256 G257 N258 R297 D309 E342 R347 C348 D349 E360 A364 G365 K366 L370 N371 D372 D373 V374 M375 N376 A377 A410 V411 G412 A413 GLU ASN VAL ARG GLU GLY SER A421 G427 P434 T435 A436 E437 Q444 D449 R460 L485 R489 N490

R491 E492 M493 E494 L509 G510 P522 L523 M524 ARG SER GLY GLY PRO PRO ARG L532 L533 A534 R535 E536 N545 E551 E552 T553 Y554 ARG HIS PRO GLY GLU SER LEU GLN SER ARG TYR LEU ALA LEU Q569 H572 K578 R583 Q587 H591 H592 K593 Q594 Q595 E596

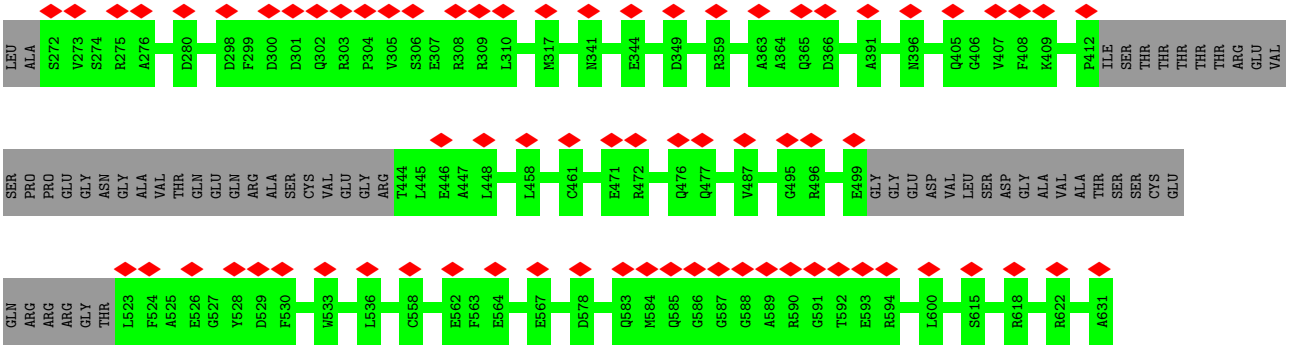
ARG LEU LEU PRO VAL SER THR ALA ALA ILE PRO SER ARG ILE VAL HIS HIS SER VAL MET SER ALA LEU HIS GLY VAL SER GLY LYS GLY GLU PRO ALA ASN ARG SER LEU PHE THR GLY ASN ARG SER ASN ASP SER HIS SER ASN THR GLY VAL ALA SER GLY THR SER ALA CYS THR

ASP GLY ALA GLY SER ALA THR PRO GLU PHE

- Molecule 29: mS54

Chain DG: 16% 89% 11%

MET PHE ARG ARG ALA ILE PRO LEU LEU SER A11 D34 N37 P42 A43 R44 L50 E51 P52 C53 E57 H78 L85 D100 L123 D135 S149 E155 R183 A184 N238 D239 E244 A247 L248 Q249 S263 V264 ASN PRO GLY VAL SER

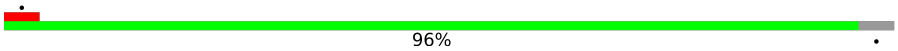


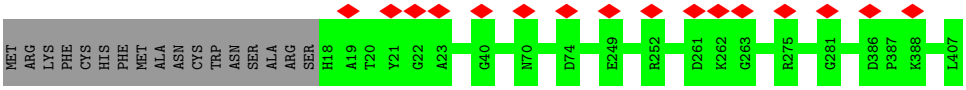
- Molecule 30: mS55

Chain DH:

- Molecule 31: mS56

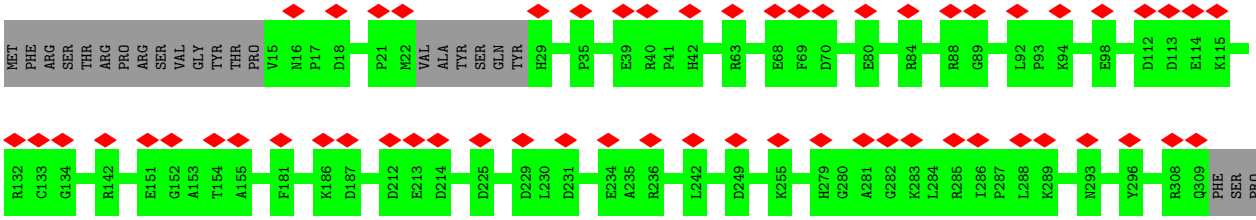
Chain DI:

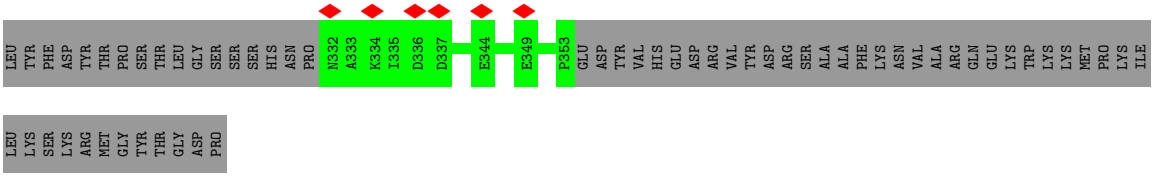




- Molecule 32: mS57

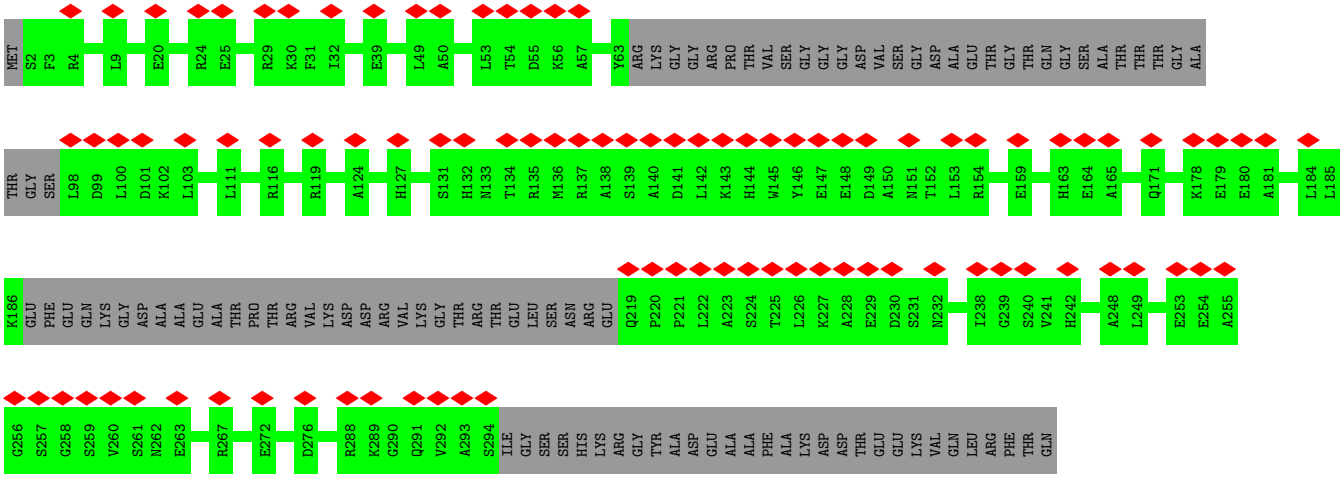
Chain DJ:





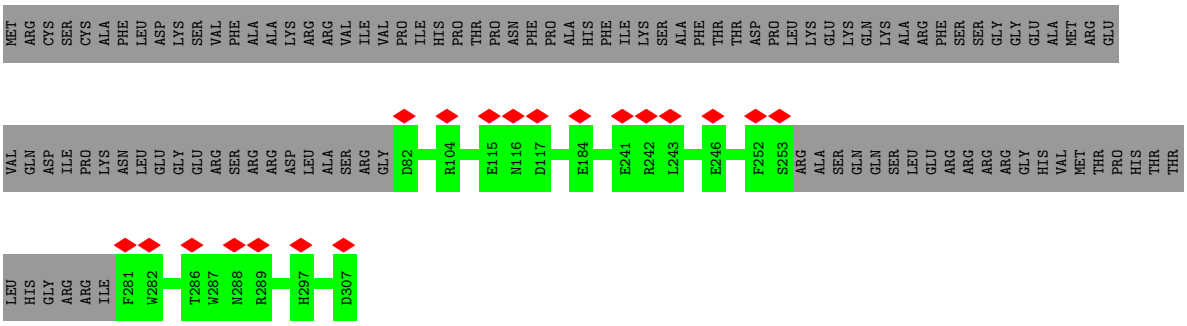
- Molecule 33: mS58

Chain DK:



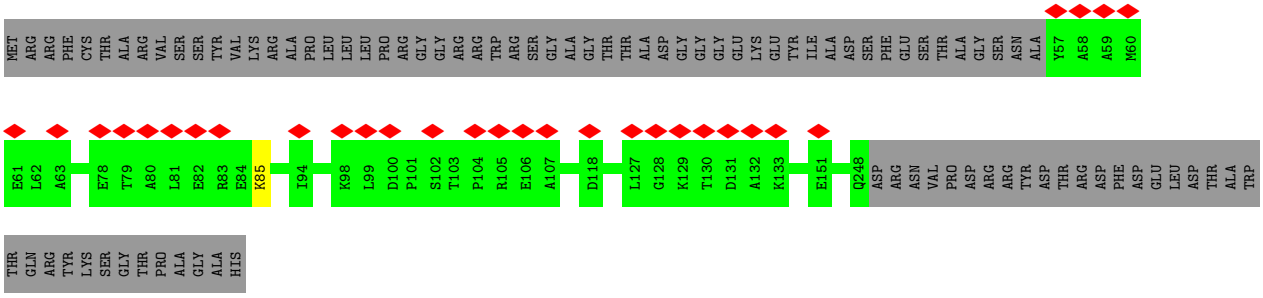
- Molecule 34: mS59

Chain DL:



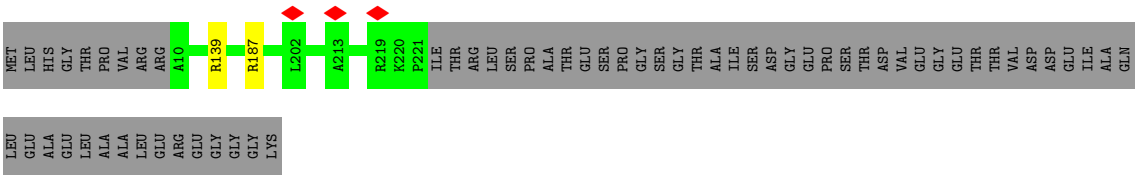
- Molecule 35: mS62

Chain DO:



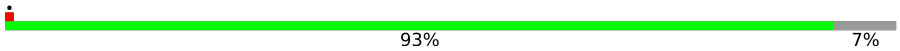
- Molecule 36: mS63

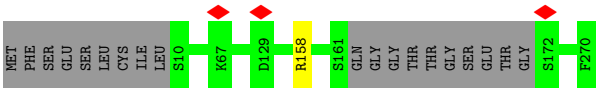
Chain DP:



- Molecule 37: mS65

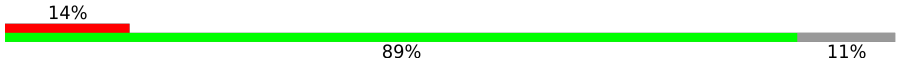
Chain DR:

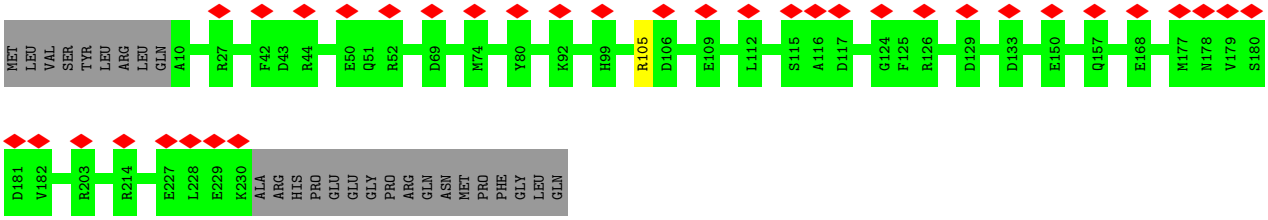




- Molecule 38: Rhodanese domain-containing protein

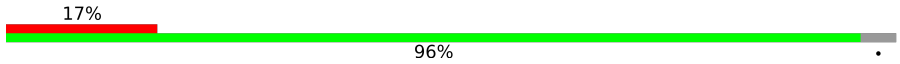
Chain DT:

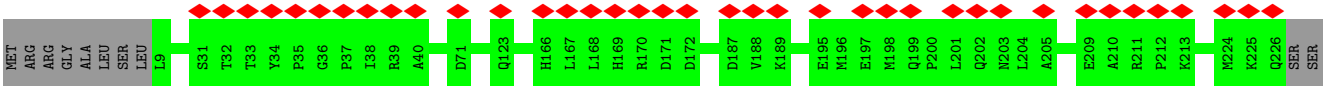




- Molecule 39: Ubiquitin-like domain-containing protein

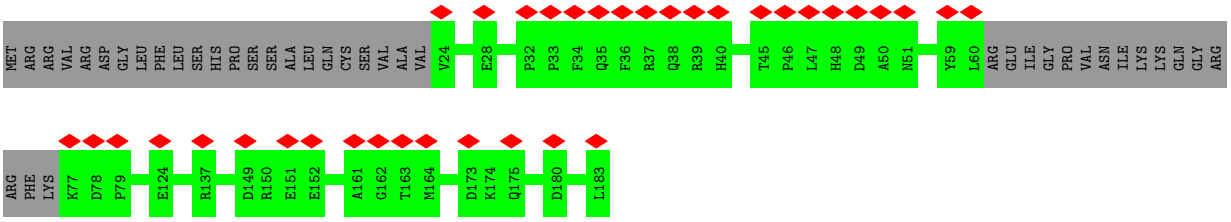
Chain DU:





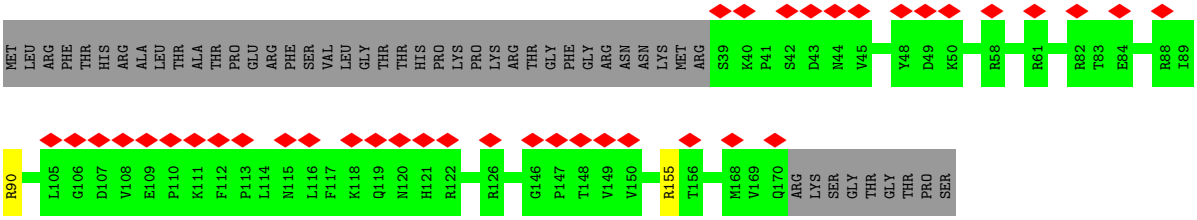
- Molecule 40: mS69

Chain DV:



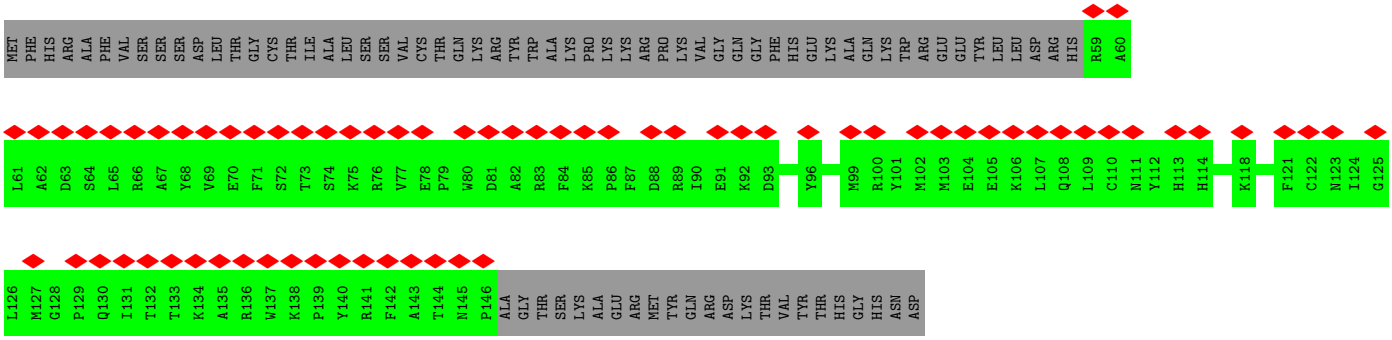
- Molecule 41: mS70

Chain DW:



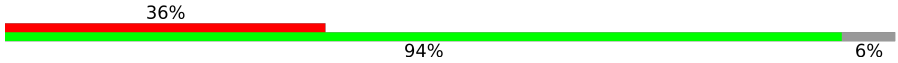
- Molecule 42: mS71

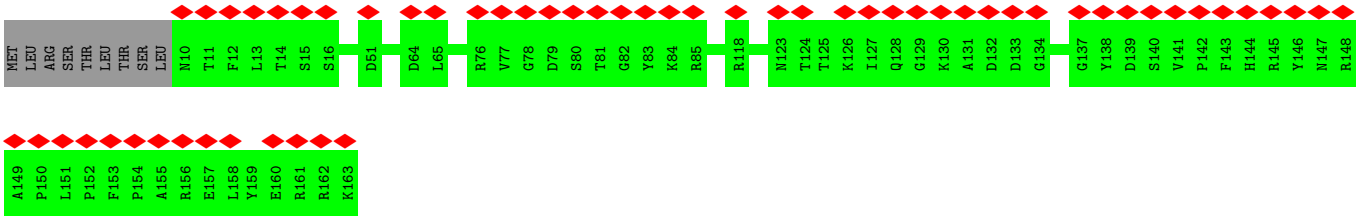
Chain DX:



- Molecule 43: mS72

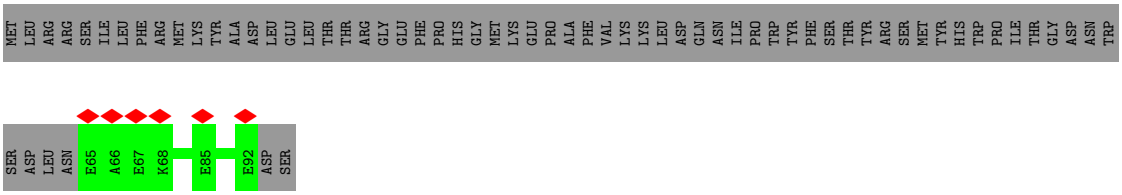
Chain DY:





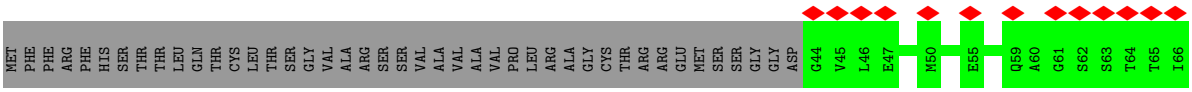
- Molecule 44: mS73

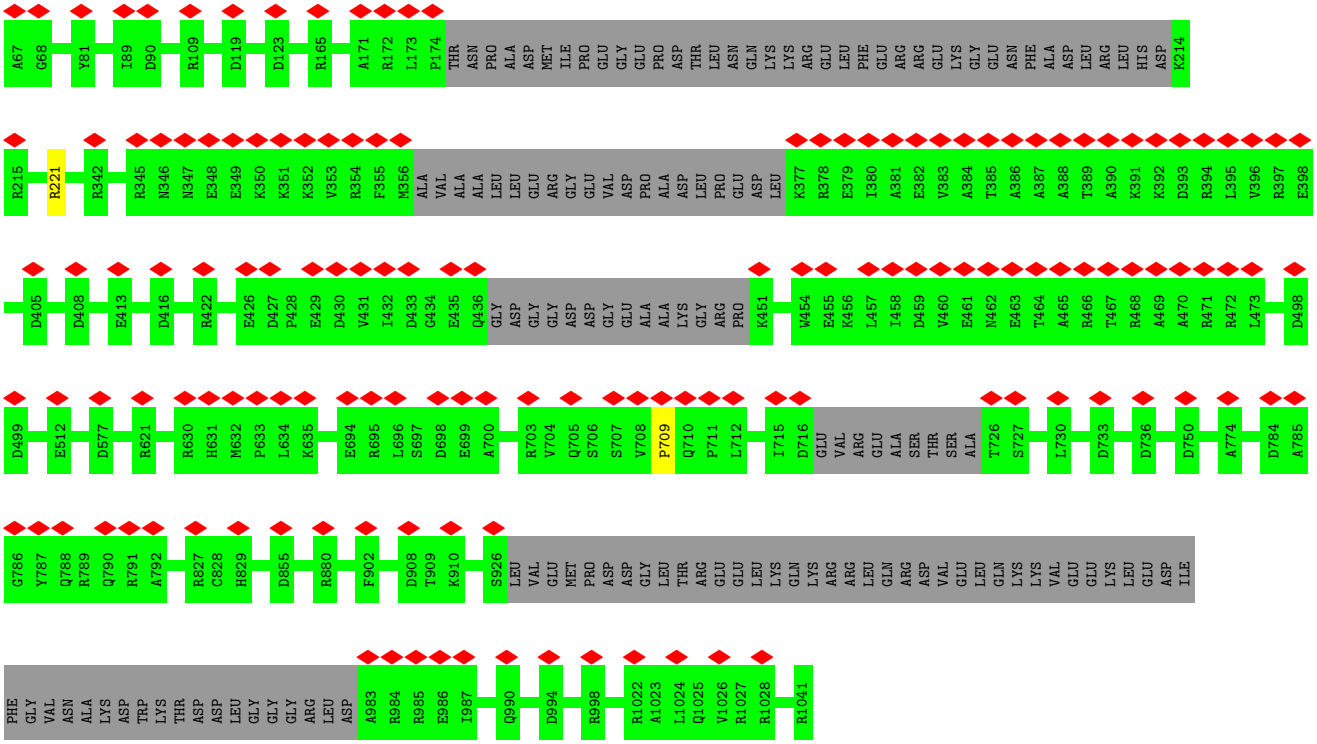
Chain DZ:



- Molecule 45: Mitochondrial small ribosomal subunit Rsm22

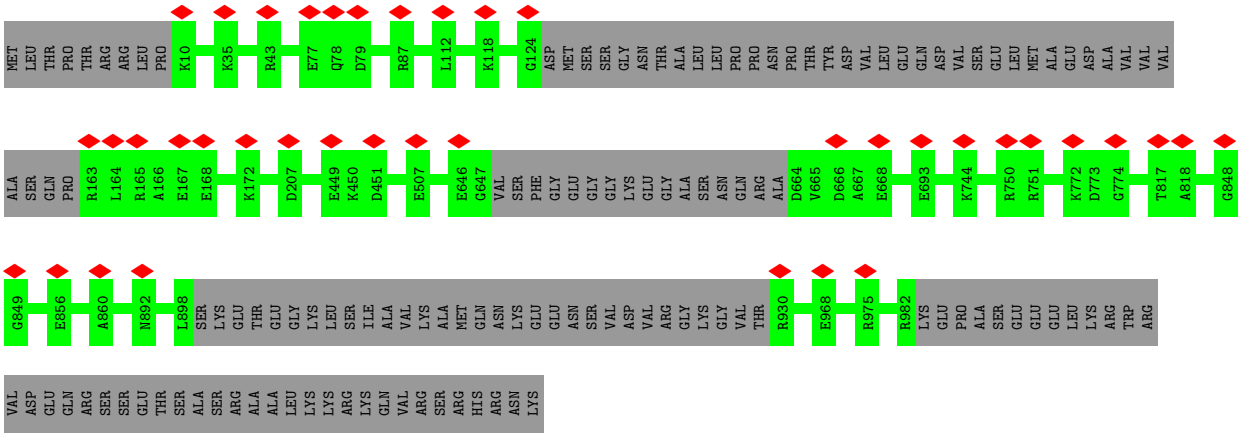
Chain F1:





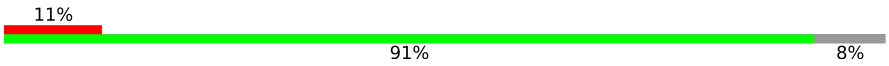
- Molecule 46: Pentacotripeptide-repeat region of PRORP domain-containing protein

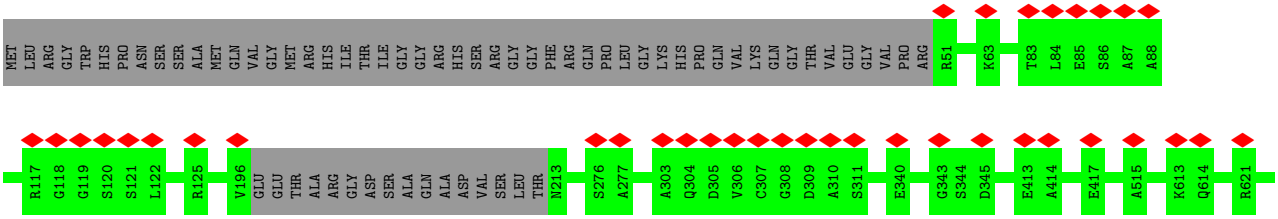
Chain F2:

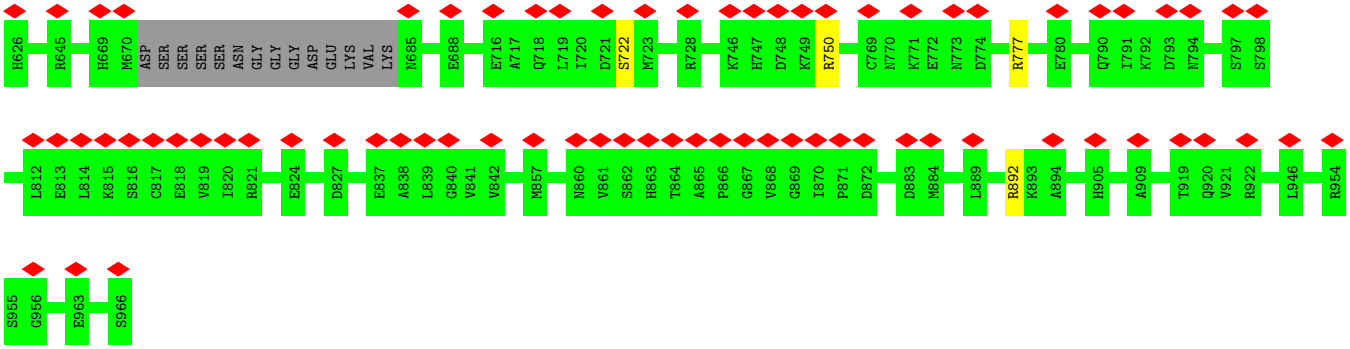


- Molecule 47: mt-SAF3

Chain F3:

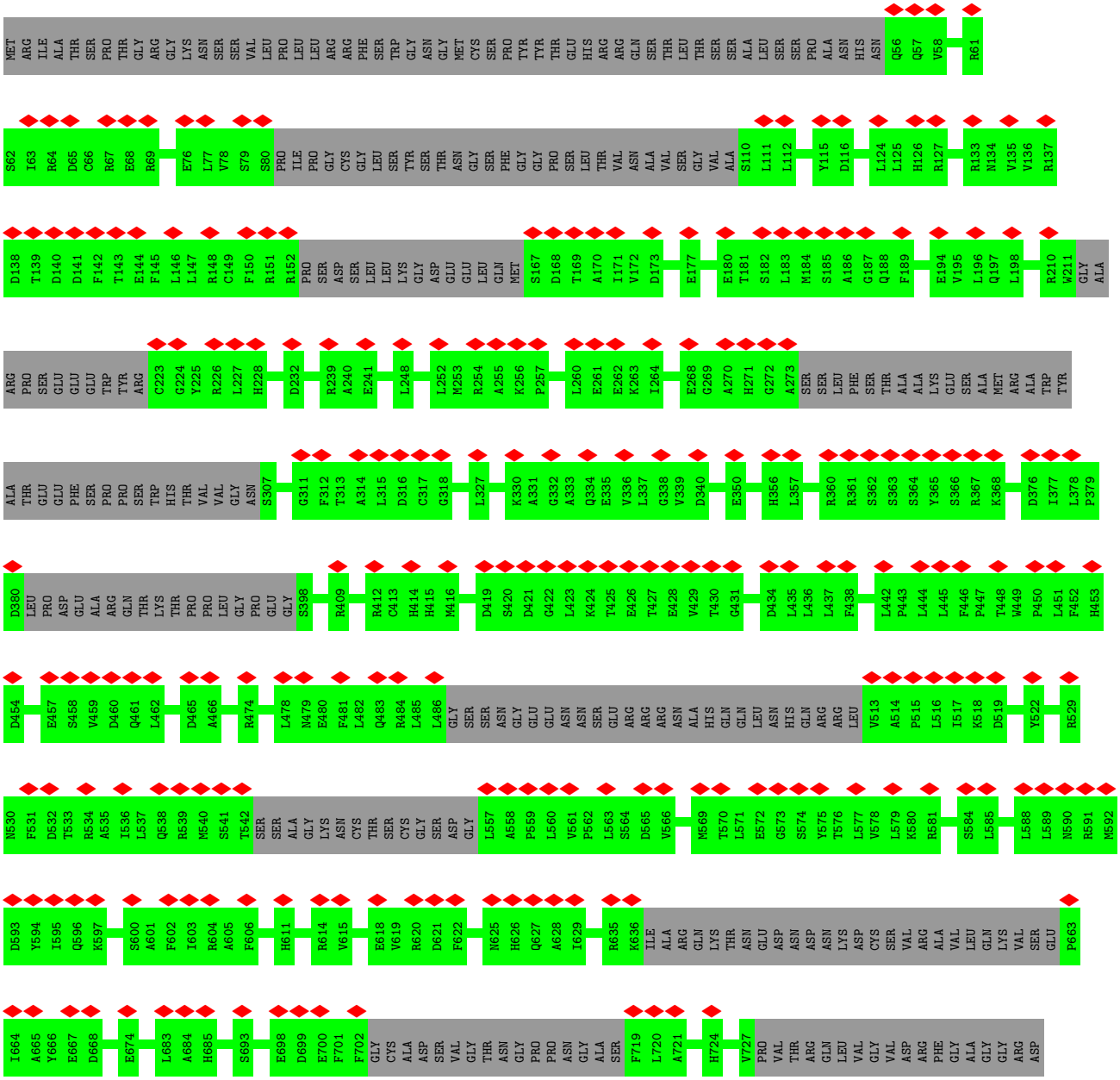


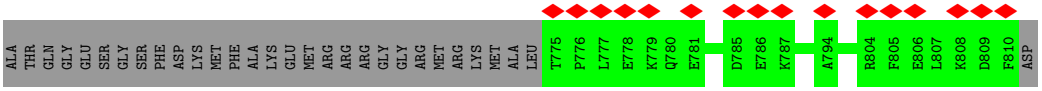




• Molecule 48: Methyltranfer_dom domain-containing protein

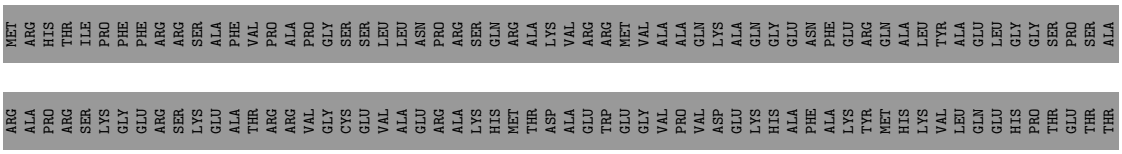
Chain F4:

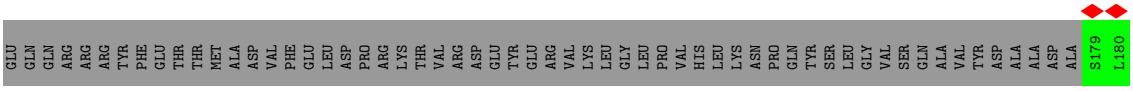


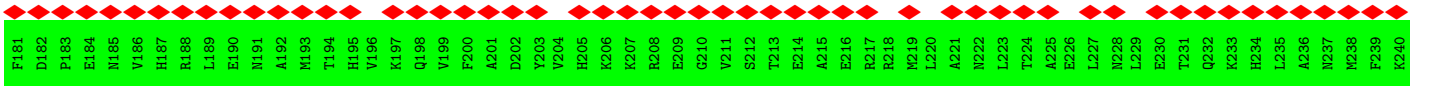


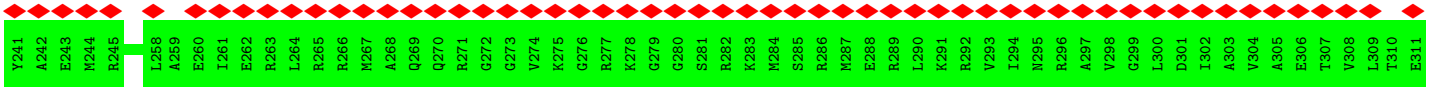
• Molecule 49: Kinteoplast poly(A) polymerase complex 1 subunit

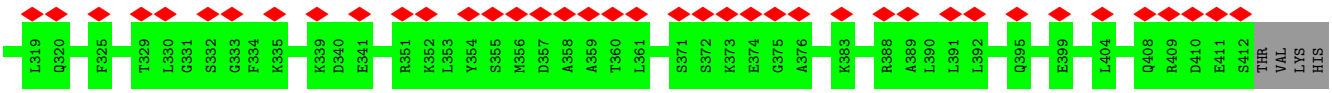
Chain F5:

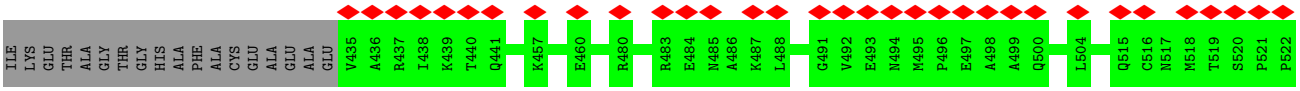


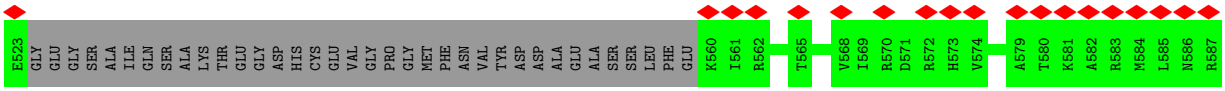


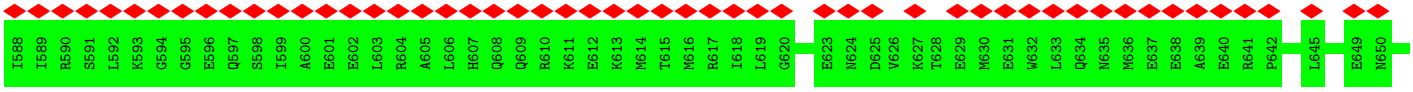


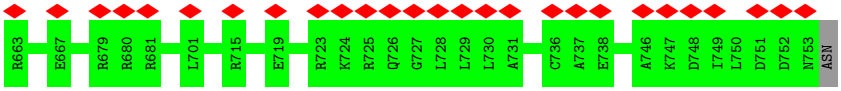






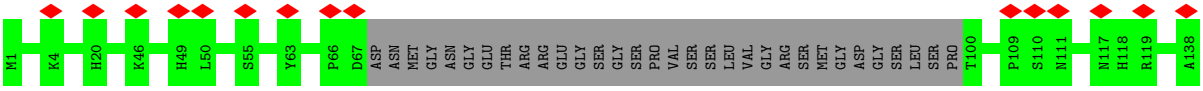


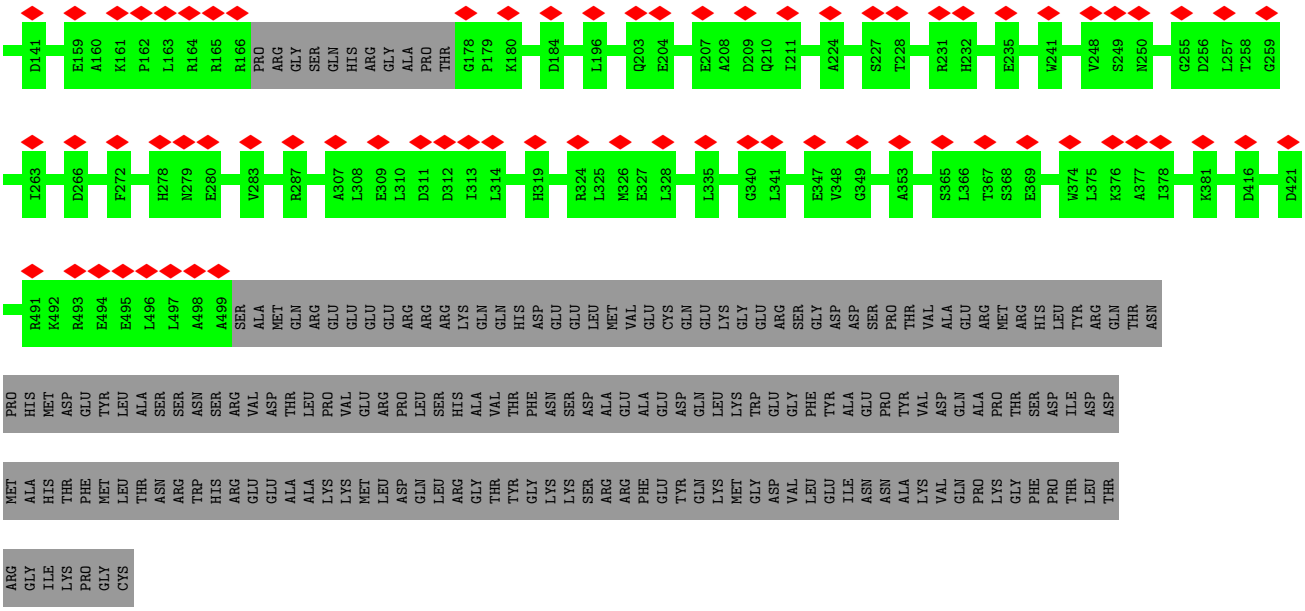




• Molecule 50: DUF4460 domain-containing protein

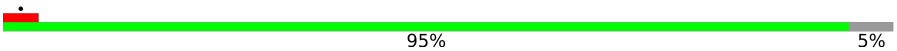
Chain F6:

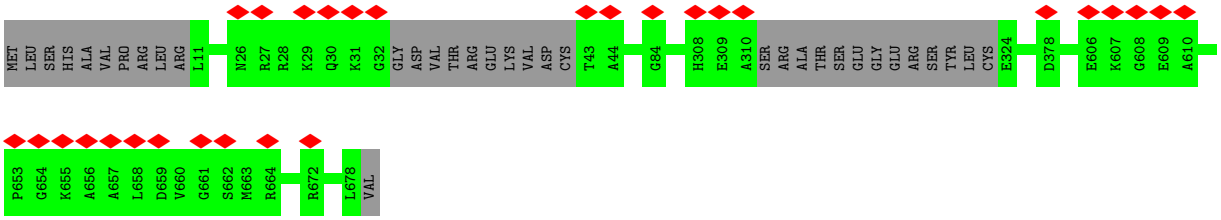




- Molecule 51: mt-SAF7 (KRIPP10)

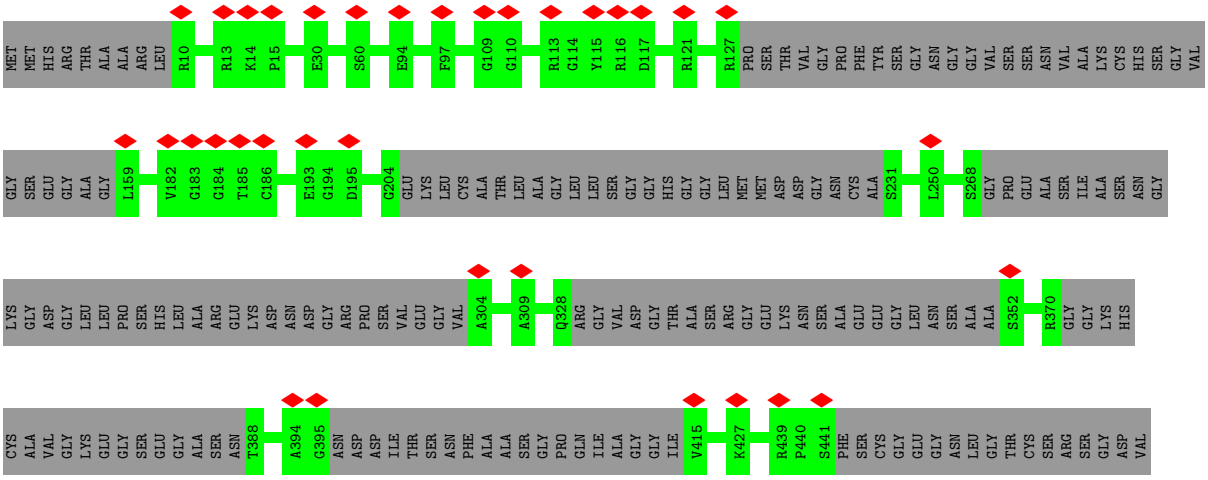
Chain F7:

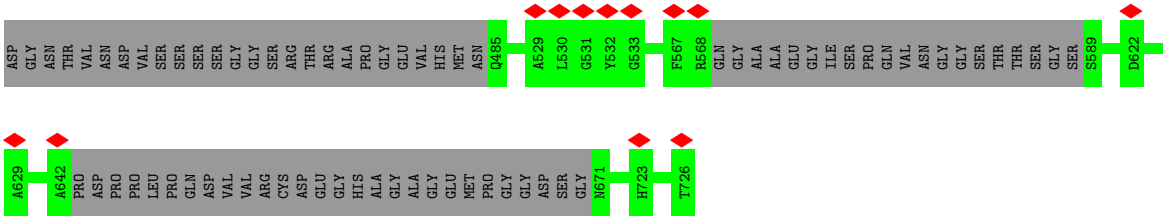




- Molecule 52: Cupin type-1 domain-containing protein

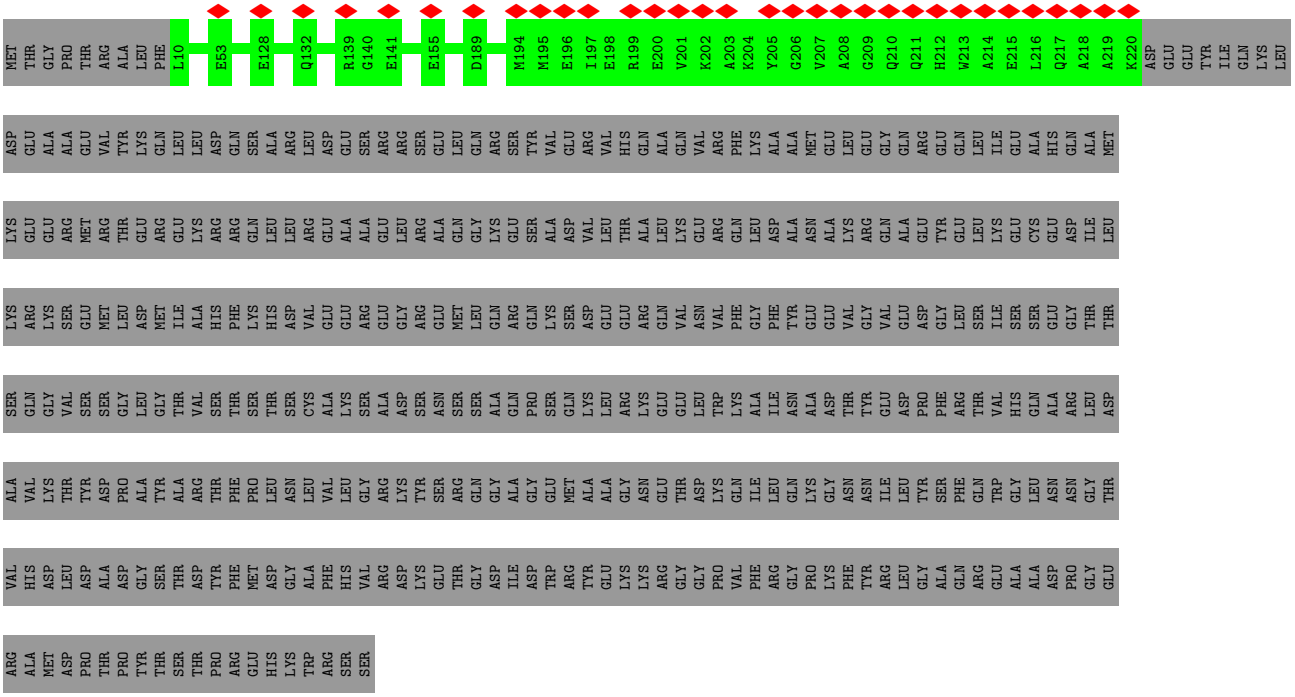
Chain F8:





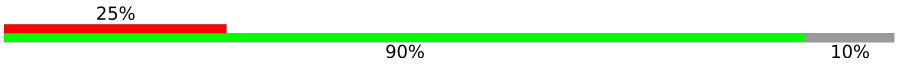
• Molecule 53: Trichohyalin

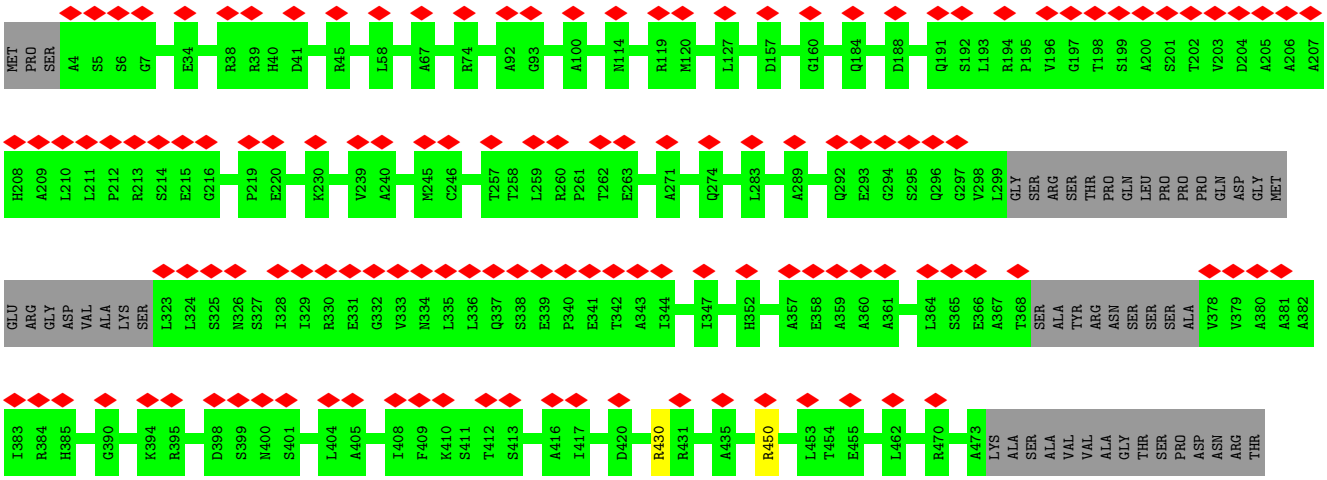
Chain F9:

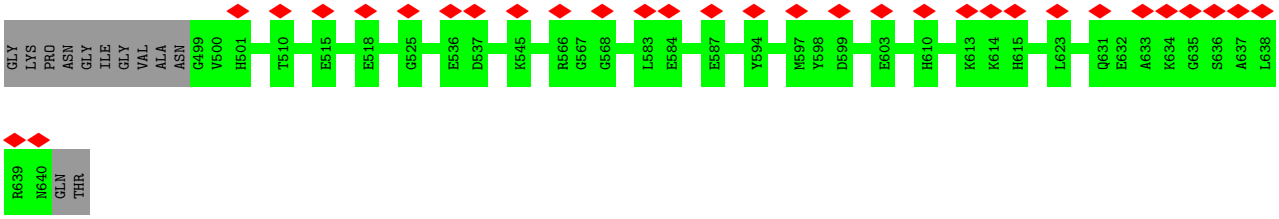


• Molecule 54: mt-SAF10

Chain FA:

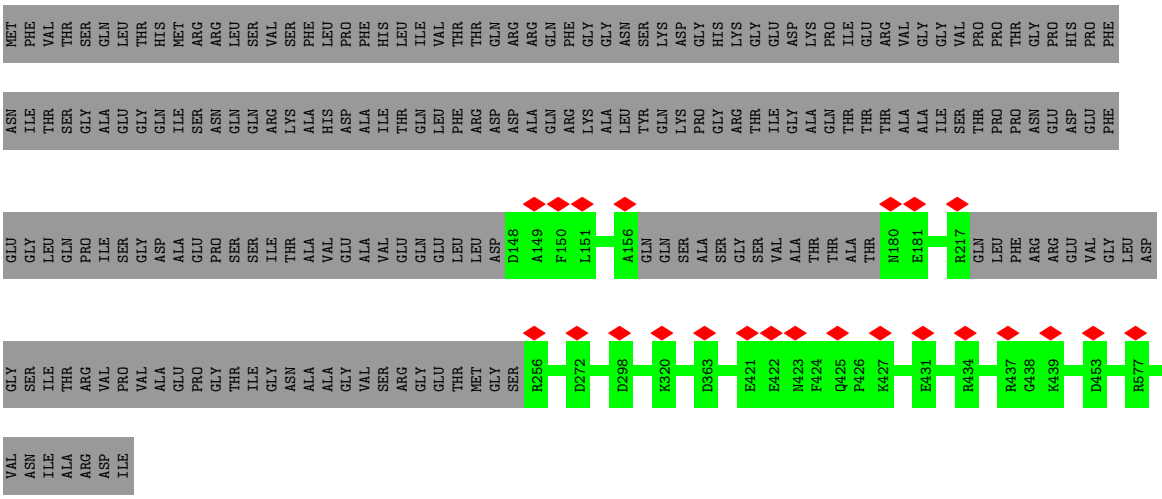






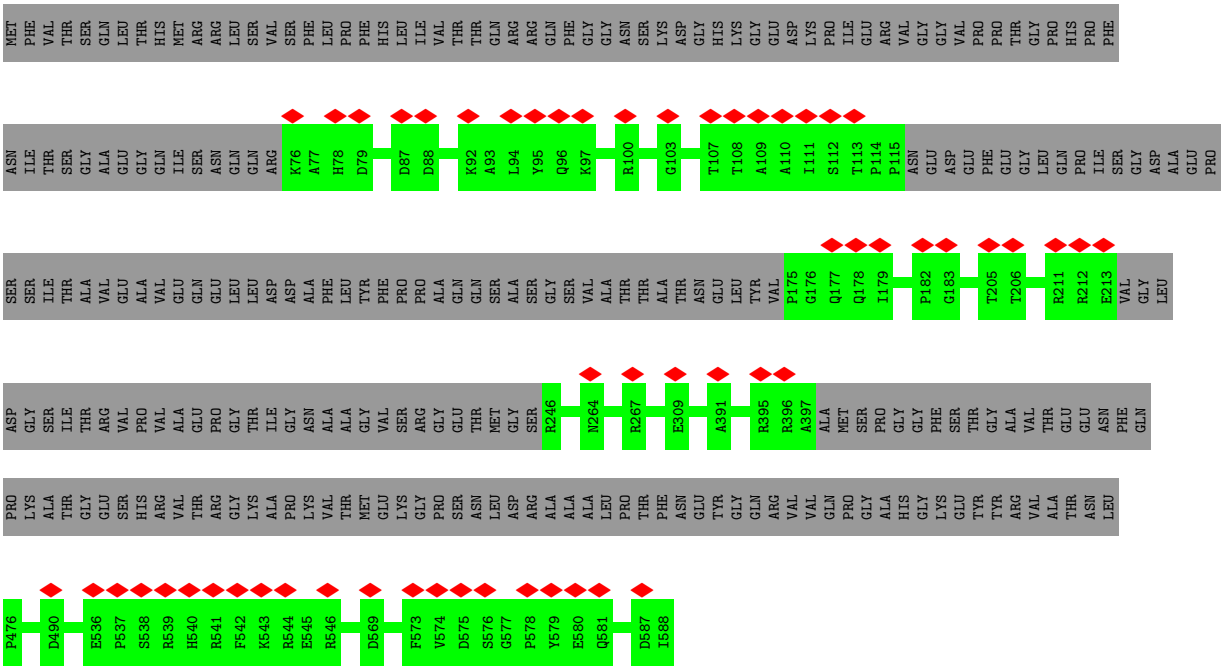
• Molecule 55: tRNA pseudouridine synthase A-like protein

Chain FB:



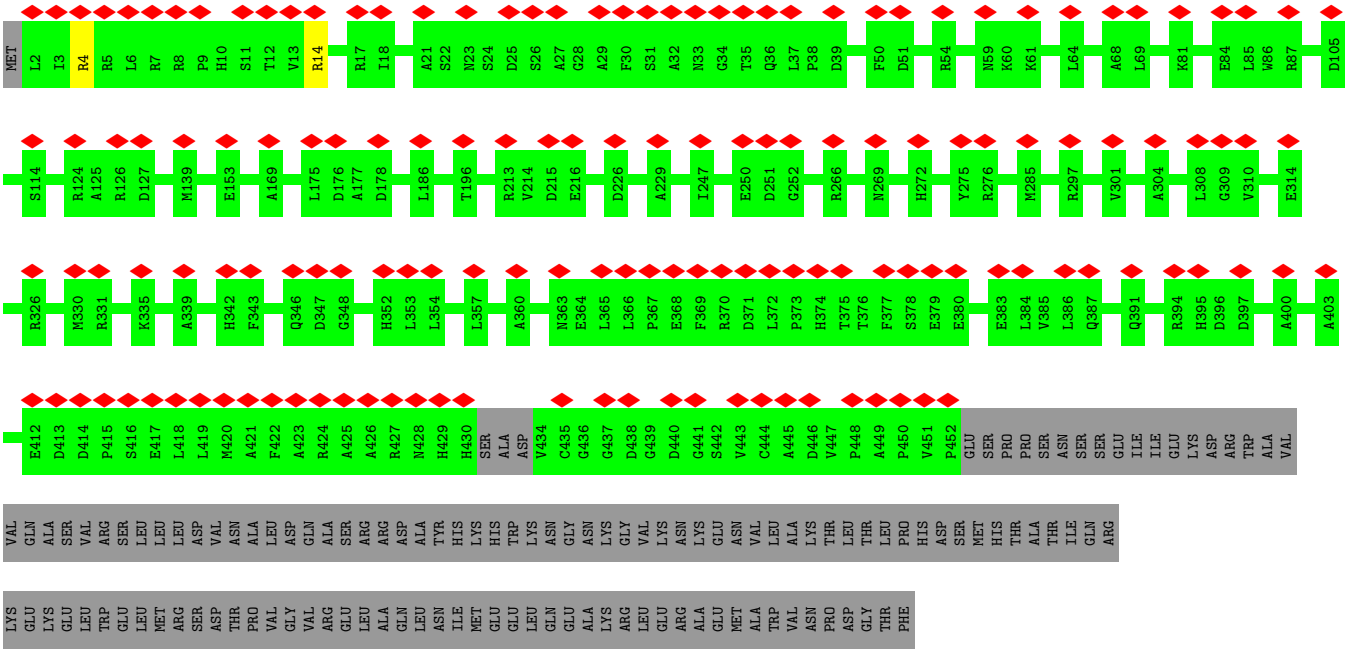
• Molecule 55: tRNA pseudouridine synthase A-like protein

Chain FC:



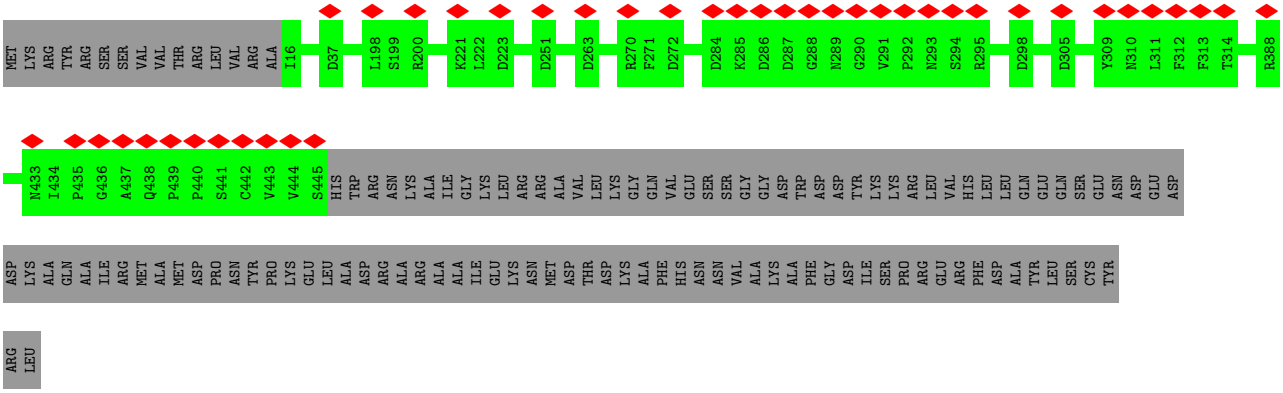
• Molecule 56: PPR_long domain-containing protein

Chain FD:



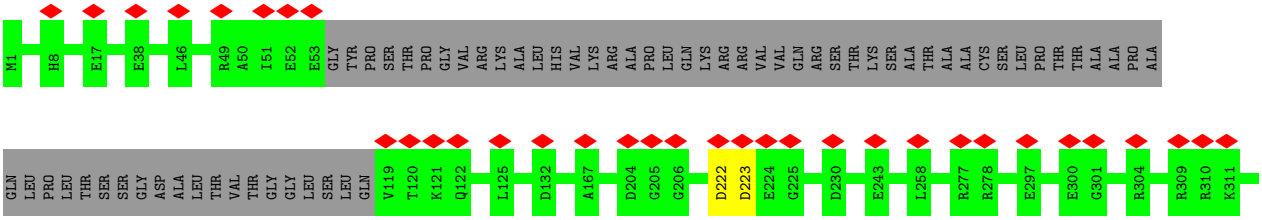
- Molecule 57: mt-SAF13

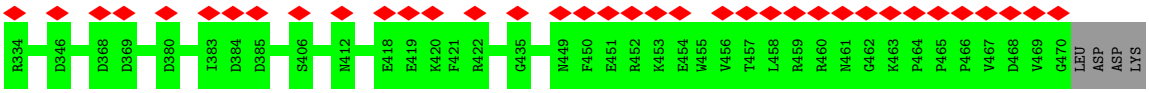
Chain FE:



- Molecule 58: S-adenosyl-methyltransferase mraW-like protein

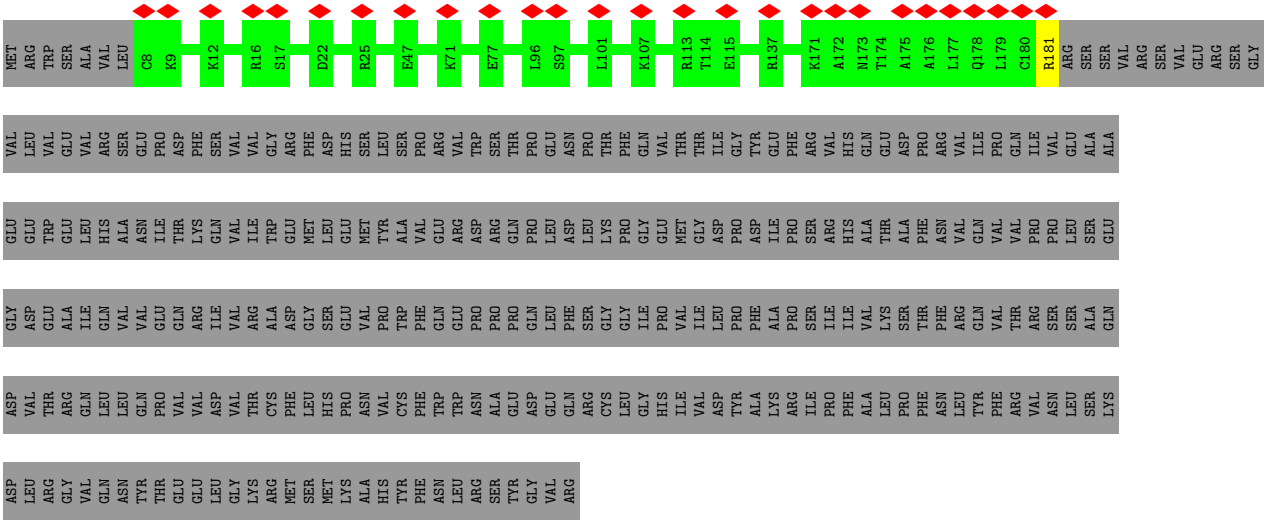
Chain FF:





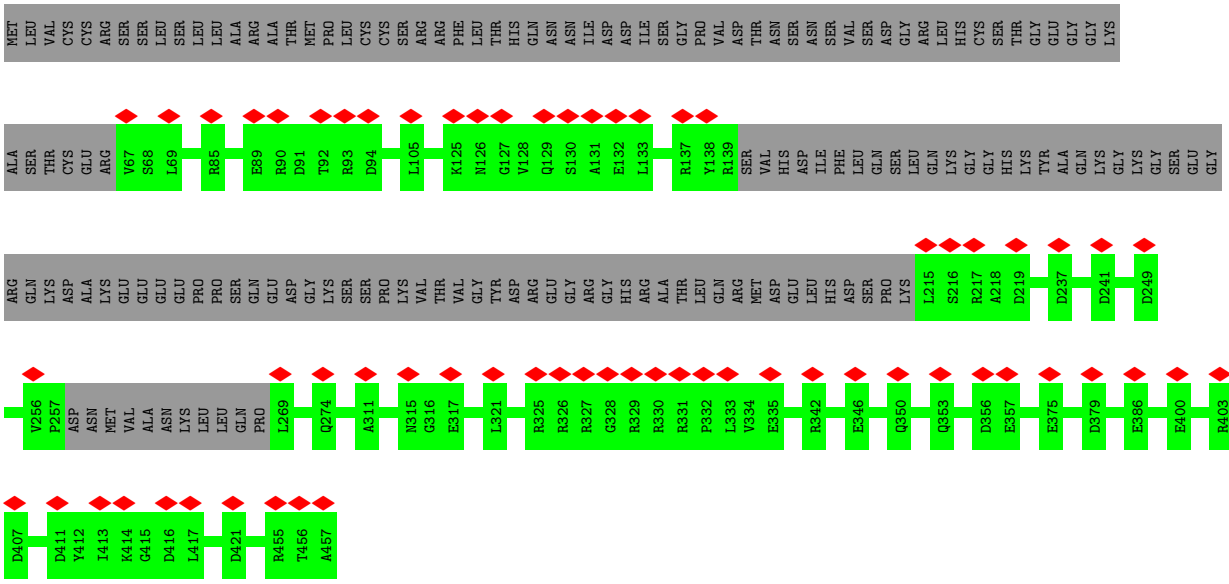
- Molecule 59: mt-SAF15

Chain FG:



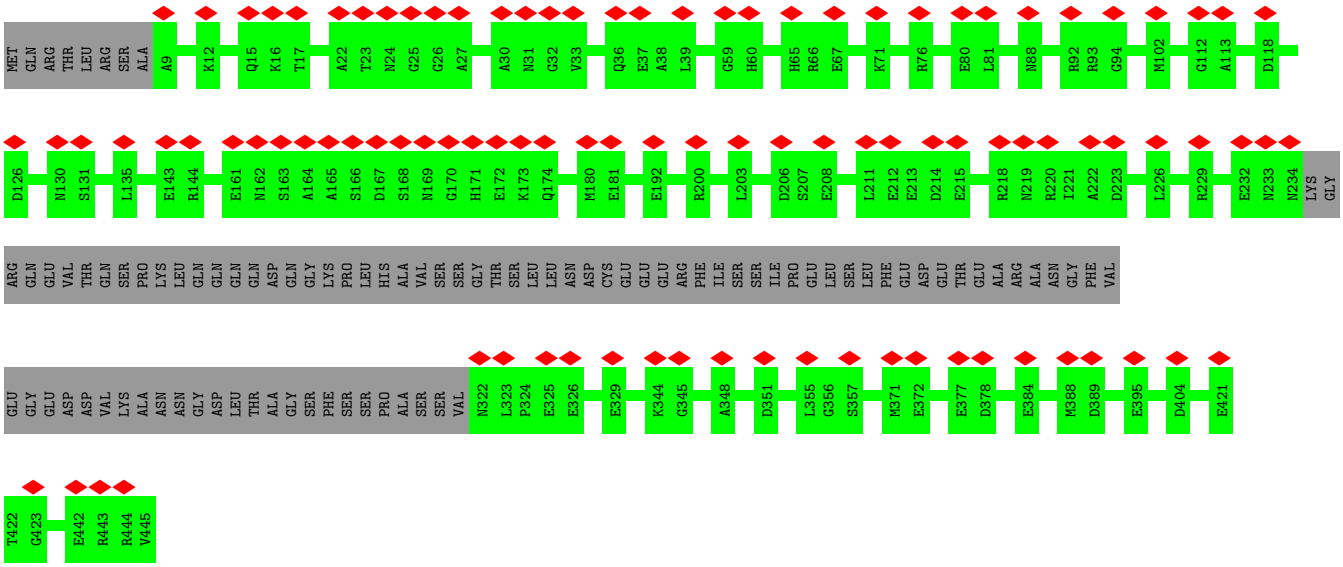
- Molecule 60: mt-SAF16 (P32)

Chain FH:



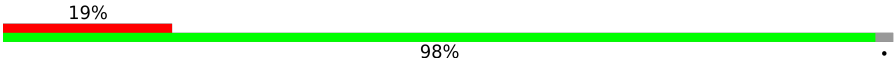
- Molecule 61: mt-SAF17

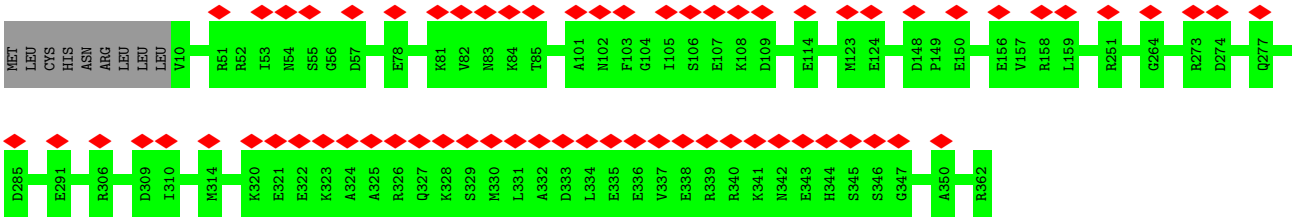
Chain FI:



- Molecule 62: mt-SAF18 (RbfA)

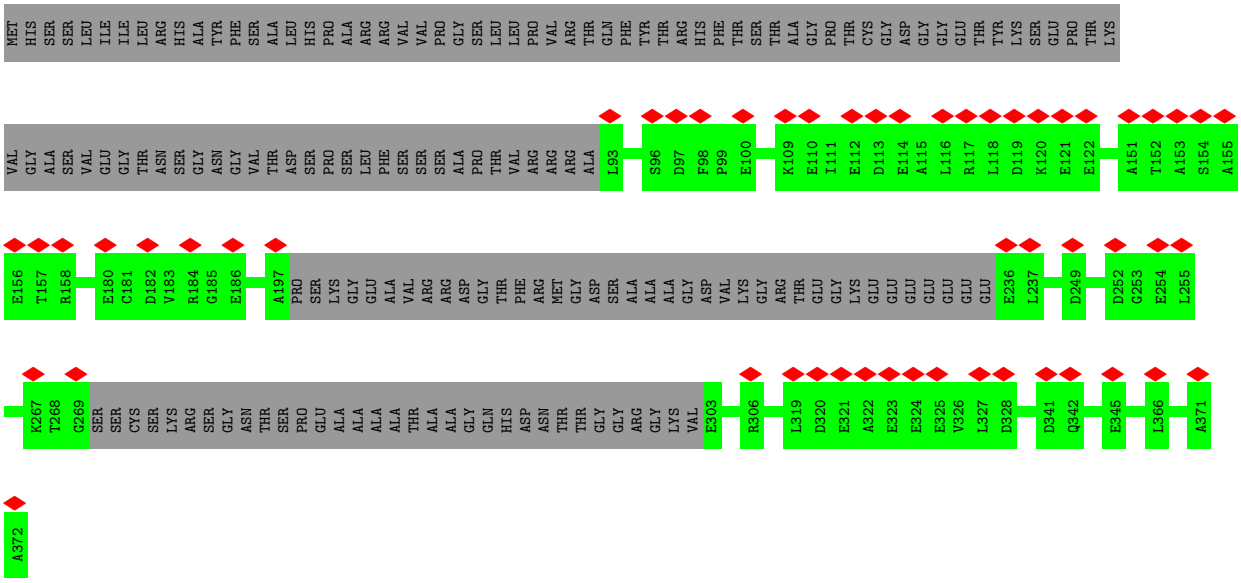
Chain FJ:





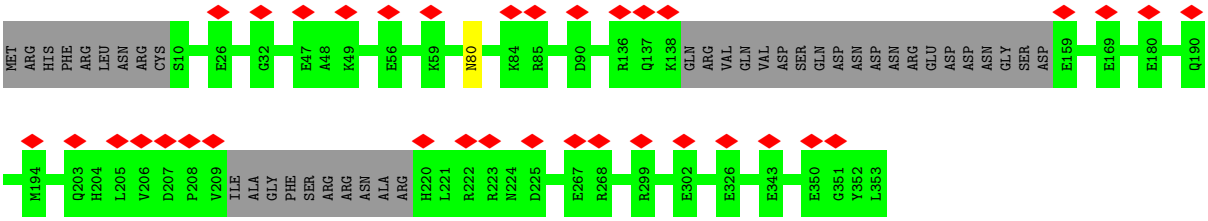
- Molecule 63: Mitochondrial glycoprotein

Chain FK:



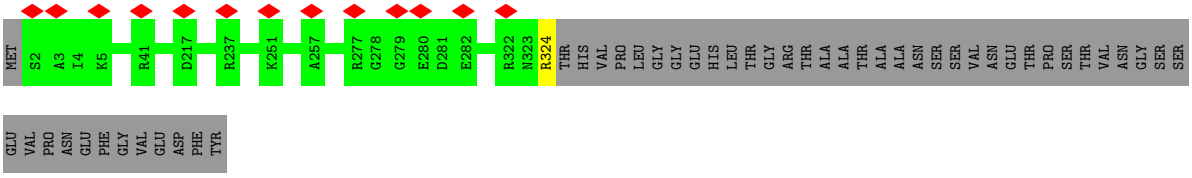
- Molecule 64: Metallo-beta-lactamase domain-containing protein

Chain FL:



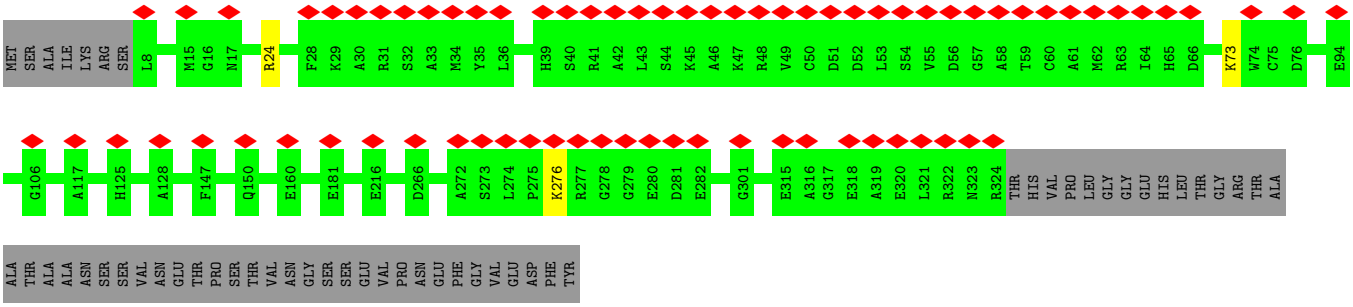
- Molecule 65: mt-SAF21

Chain FM:



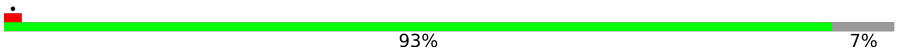
- Molecule 65: mt-SAF21

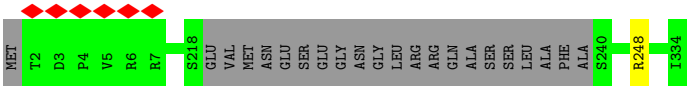
Chain FN:



- Molecule 66: mt-SAF22

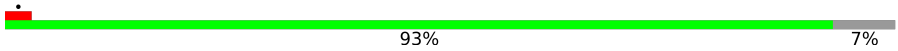
Chain FO:

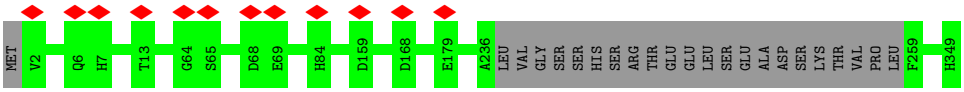




- Molecule 67: ADP-ribosylglycohydrolase

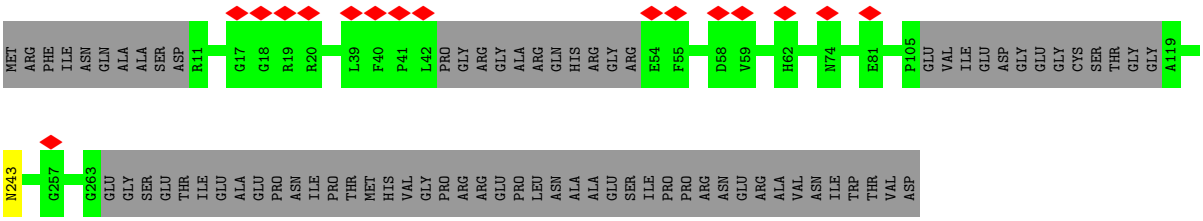
Chain FP:





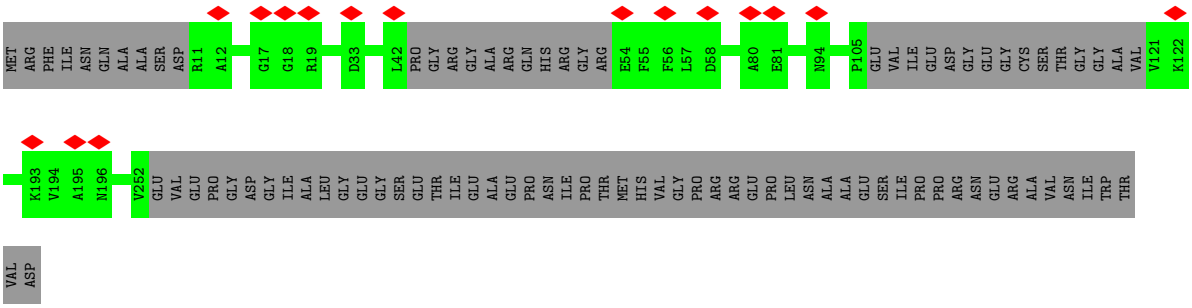
- Molecule 68: Potassium voltage-gated channel, putative

Chain FQ:



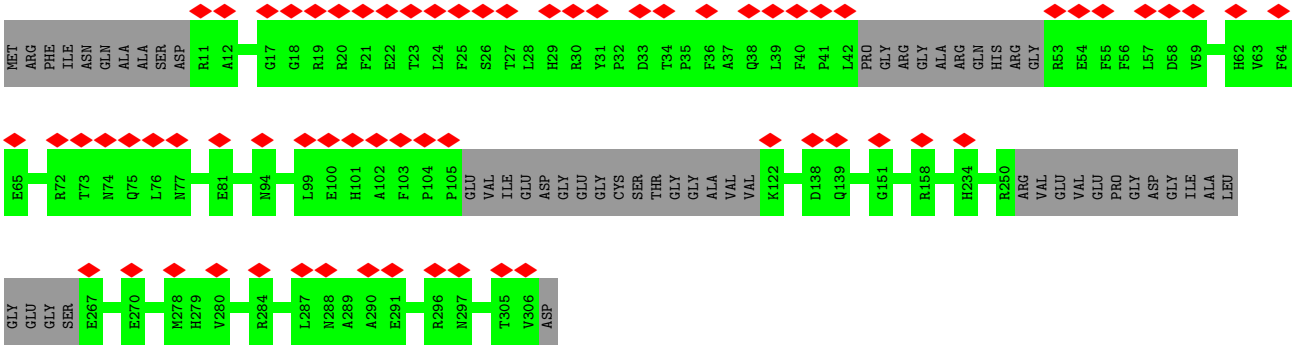
- Molecule 68: Potassium voltage-gated channel, putative

Chain FR:



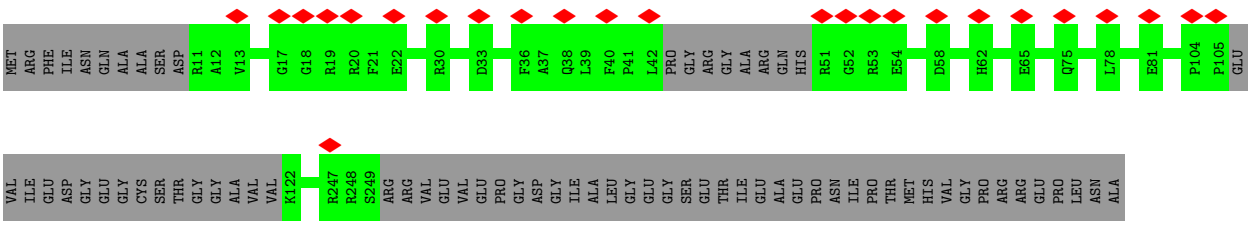
- Molecule 68: Potassium voltage-gated channel, putative

Chain FS:



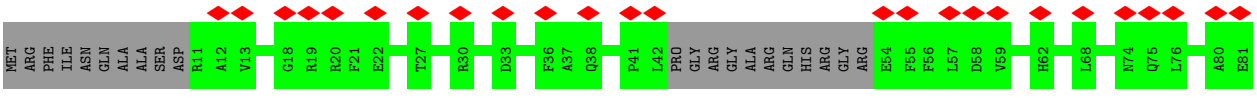
- Molecule 68: Potassium voltage-gated channel, putative

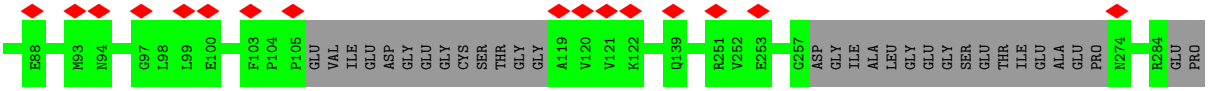
Chain FT:



• Molecule 68: Potassium voltage-gated channel, putative

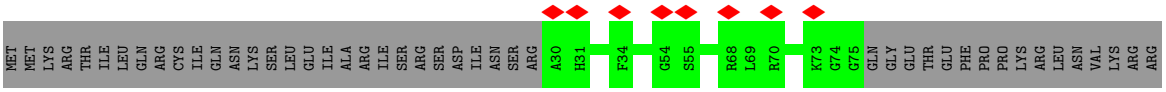
Chain FU:

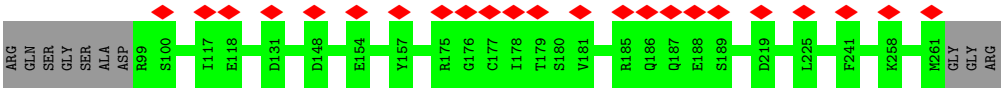




• Molecule 69: mt-SAF25

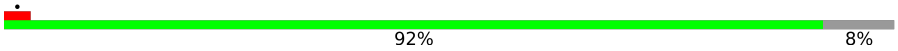
Chain FV:

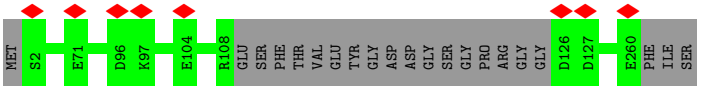




• Molecule 70: Low molecular weight protein tyrosine phosphatase

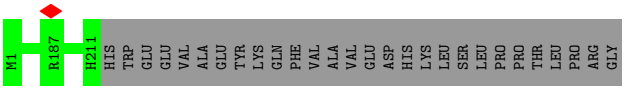
Chain FW:





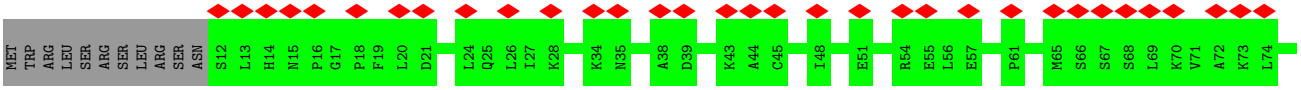
• Molecule 71: PPR_long domain-containing protein

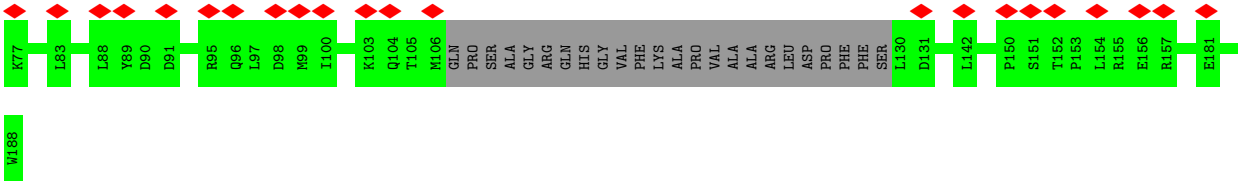
Chain FX:



• Molecule 72: mt-SAF28

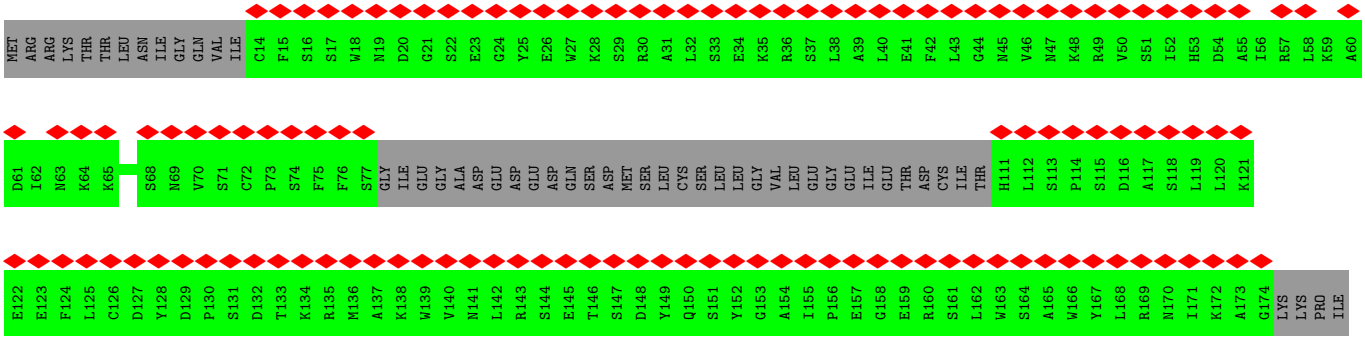
Chain FY:





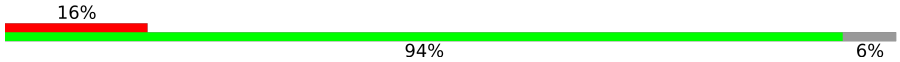
• Molecule 73: mt-SAF29

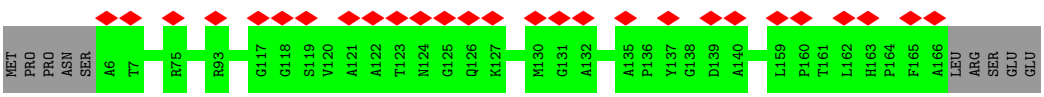
Chain FZ:



• Molecule 74: mt-SAF30

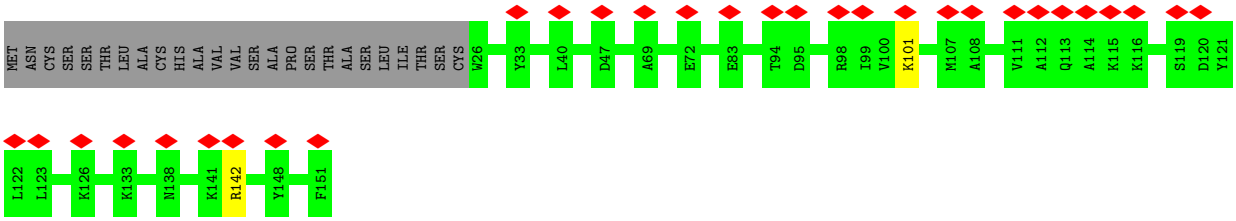
Chain Fa:





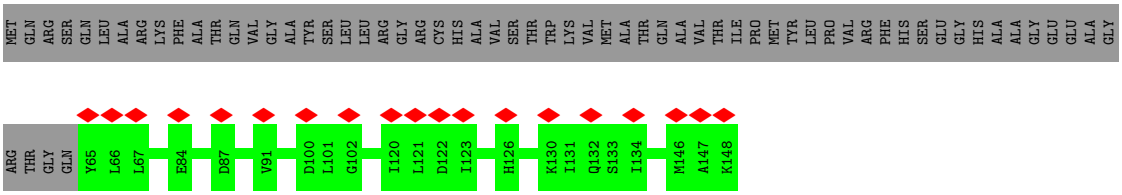
• Molecule 75: Complex 1 protein (LYR family)

Chain Fb:



• Molecule 76: Acyl carrier protein

Chain Fc:



• Molecule 77: Probable Zinc-ribbon domain-containing protein

Chain Fd: 64% 36%

MET ARG HIS PHE GLY PRO SER ILE ALA HIS PHE PRO LEU SER ALA ASN GLN LEU ARG PHE K21 K31 N111 GLY LYS ARG ALA VAL ALA ASP GLY ALA LEU GLU GLY GLU MET ASP SER GLN LEU ARG PRO LYS ARG PRO VAL MET PHE ASN MET ARG THR LYS TYR

- Molecule 78: mt-SAF34

Chain Fe: 24% 97%

MET S2 Y13 S14 F15 T26 ASN CYS THR L30 N31 K32 R33 M34 K35 D36 R39 L40 E41 D49 F50 D51 R52 E53 R54 R55 R78 R84 C85 A86 D87 R95 M96 V97 D98 R102 L107 R108 E109 S110 P111 V112 E113 R120 R123

- Molecule 79: mt-SAF38

Chain Fi: 65% 66% 34%

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

ALA ARG MET HIS GLY THR ALA ASP SER THR MET ALA THR ALA GLY ASP SER SER GLN ASN ASN SER VAL MET ASP S86 P87 R88 W89 L90 R91 N92 P93 D94 E95 L96 C97 V98 A99 A100 L101 R102 R103 S104 R105 D106 V107 N108 K109 I110 N111 S112 Y113 V114 A115 T116 Y117 K118 F119 D120

D121 P122 Q123 W124 A125 P126 L127 L128 L129 P130 E131 V132 T133 L134 ARG PRO GLN VAL ASN SER THR GLY ASP LYS PRO ASN GLY GLY ASN GLU ALA ALA ALA ASP VAL VAL SER VAL GLY PRO SER VAL SER ALA THR PRO GLU SER THR PRO PRO PRO PRO PRO SER SER SER SER SER SER

PRO TYR SER CYS HIS ALA ASP CYS VAL SER I191 S192 H193 N194 K195 M196 I197 M198 L199 E200 C201 M202 S203 R204 H205 V206 N207 F208 S209 L210 R211 H212 I213 V214 Q215 K216 G217 H218 G219 I220 Y221 L222 I223 Y224 H225 A226 Q227 H228 S229 I230 L231 Q232 P233 K234 G235 L236 V237 E238 Q239 S240

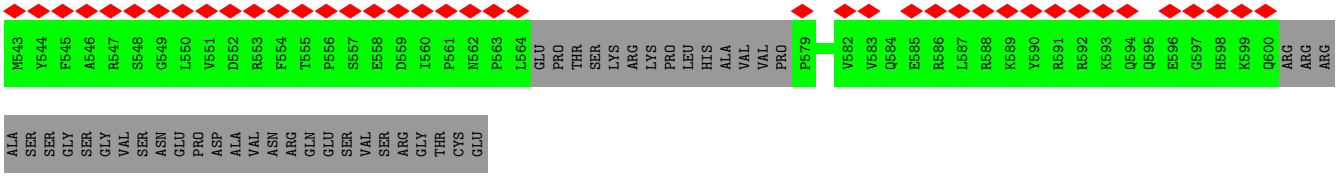
F241 V242 T243 C244 S245 F246 G247 I248 R249 L253 R254 T255 D256 I257 V258 H259 V260 G261 P262 I263 D264 A265 A266 D267 V268 M269 E270 L271 Q272 P273 S274 E275 G276 H277 D278 H279 P280 R281 C282 C283 F284 N285 L286 Y287 Q288 K289 S290 D291 V292 R293 R294 G295 V296 I297 A298 V299 S300 Q301 V302

E303 G304 Y305 G306 T307 W308 F309 Q310 R311 K312 P313 M314 L315 W316 Q317 R318 S319 R320 R321 I322 G323 A324 L325 Q326 S327 Q328 L329 G330 A331 F332 A333 Y334 D335 L336 V337 D338 P339 H340 E341 V342 G343 K344 W345 R346 D347 C348 E349 V350 S351 L352 L353 A354 P355 H356 M357 R358 F359 F360 R361 N362

G363 L364 N365 G366 A367 E368 A369 V370 G371 I372 I373 A374 S375 S376 Q377 V378 A379 Q380 Q381 R382 R383 L384 Y385 L386 G387 E388 F389 E390 A391 P392 A393 I394 T395 A396 L397 D398 A399 V400 Q401 Q402 L403 A404 H405 A406 S407 A408 L409 R410 C411 K412 L413 V414 T415 P416 V417 V418 ASP PRO ASN GLY

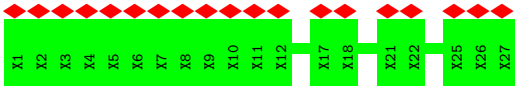
VAL GLY GLY THR GLY SER GLY SER LEU GLY ASP GLU ASN MET ASP LYS HIS I440 D441 M442 E443 T444 L445 L446 P447 L448 S449 W450 A451 T452 R453 T454 P455 P456 P457 Y458 Y459 P460 L461 E462 A463 D464 L465 P466 F467 K468 L469 Q470 M471 S472 R473 P474 T475 V476 F477 A478 GLU SER HIS GLN

GLN ASN GLN A486 Y487 P488 T489 G490 G491 T492 V493 G494 S495 P496 F497 V498 R499 G500 A501 P502 M503 M504 M505 F506 E507 Y508 N509 M510 H511 Q512 G513 V514 D515 H516 Y517 V518 Y519 D520 D521 A522 P523 S524 A525 R526 P527 M528 K529 W530 W531 S532 Q533 K534 S535 N536 M537 P538 Y539 S540 G541 Y542



• Molecule 80: UNK-A

Chain UA: 70% 100%



• Molecule 81: UNK-B

Chain UB: 33% 100%

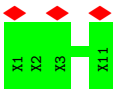
• Molecule 82: UNK-C

Chain UC: 100%

There are no outlier residues recorded for this chain.

• Molecule 83: UNK-F

Chain UF: 27% 100%

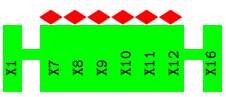


• Molecule 84: UNK-G,J

Chain UG: 12% 100%

• Molecule 84: UNK-G,J

Chain UJ: 38% 100%



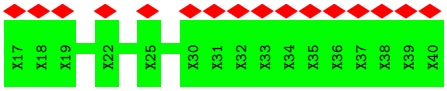
• Molecule 85: UNK-I

Chain UI: 100%

There are no outlier residues recorded for this chain.

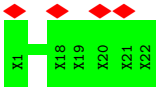
• Molecule 86: UNK-K

Chain UK: 67% 100%



• Molecule 87: UNK-L

Chain UL: 18% 100%



• Molecule 88: UNK-M,Q

Chain UM: 11% 100%

• Molecule 88: UNK-M,Q

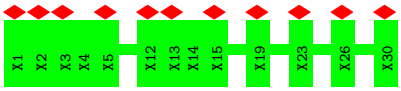
Chain UQ: 22% 100%

• Molecule 89: UNK-N

Chain UN: 14% 100%

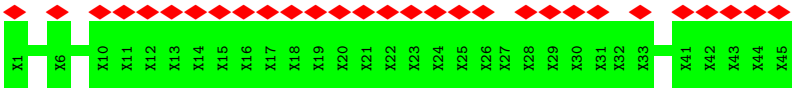
• Molecule 90: UNK-O

Chain UO: 37% 100%



• Molecule 91: UNK-P

Chain UP: 64% 100%

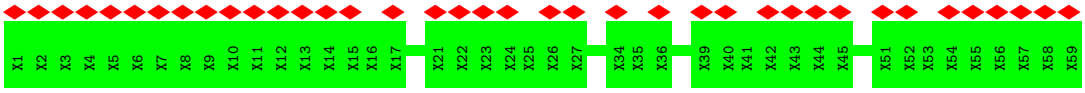


• Molecule 92: UNK-Y

Chain UY: 98% 98%

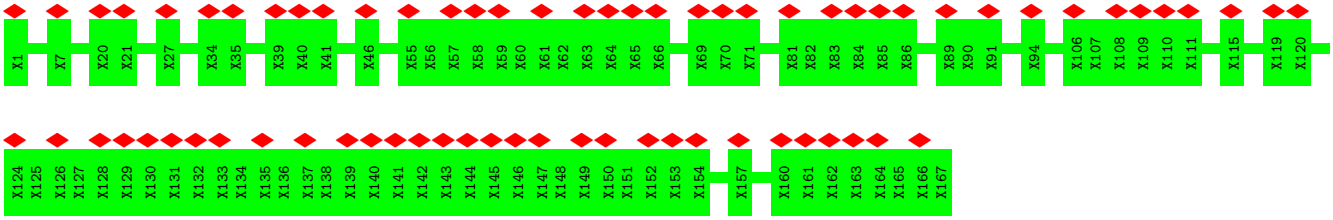
• Molecule 93: UNK-d

Chain Ud: 64% 100%



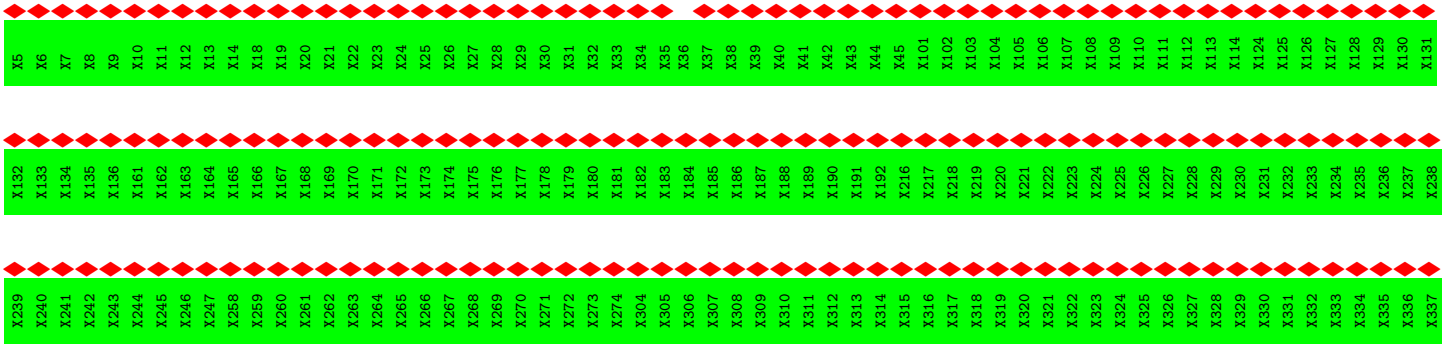
• Molecule 94: UNK-g

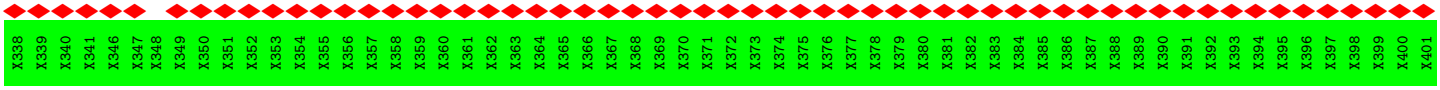
Chain Ug: 42% 100%

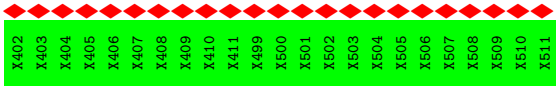


• Molecule 95: UNK-h

Chain Uh: 99% 100%

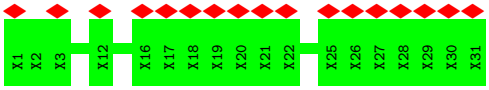






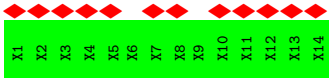
- Molecule 96: UNK-k

Chain Uk:



- Molecule 97: UNK-l

Chain Ul:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	104838	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.613	Depositor
Minimum map value	-0.285	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, MG, SAM, ZN, ACO, PO4, GTP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	CA	0.23	0/11345	0.70	0/17617
2	CC	0.27	0/603	0.46	0/814
3	CE	0.27	0/3095	0.54	0/4184
4	CF	0.27	0/1344	0.54	0/1813
5	CH	0.26	0/1797	0.57	0/2421
6	CI	0.26	0/3388	0.51	0/4576
7	CJ	0.25	0/5781	0.50	0/7862
8	CK	0.26	0/1722	0.53	0/2321
9	CN	0.24	0/1287	0.49	0/1740
10	CO	0.27	0/3044	0.52	0/4104
11	CP	0.27	0/1533	0.53	0/2074
12	CQ	0.27	0/1985	0.51	0/2687
13	CR	0.26	0/1189	0.53	0/1609
14	CS	0.25	0/731	0.46	0/987
15	Ca	0.27	0/4351	0.52	1/5880 (0.0%)
16	Cb	0.28	0/1298	0.55	0/1744
17	Cd	0.27	0/1671	0.48	0/2246
18	Cg	0.26	0/4032	0.48	0/5475
19	Ci	0.25	0/1256	0.52	0/1695
20	Cj	0.28	0/1834	0.51	0/2499
21	Ck	0.24	0/4340	0.50	0/5871
22	Cn	0.28	0/223	0.48	0/305
23	Cp	0.27	0/1496	0.51	0/2030
24	DB	0.25	0/5108	0.55	0/6905
25	DC	0.25	0/8359	0.49	0/11333
26	DD	0.27	0/6621	0.51	0/8972
27	DE	0.25	0/4710	0.51	0/6396
28	DF	0.24	0/4031	0.52	0/5459
29	DG	0.25	0/4633	0.52	0/6280
30	DH	0.24	0/4169	0.51	0/5641
31	DI	0.26	0/3244	0.52	0/4395
32	DJ	0.25	0/2599	0.48	0/3519

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	DK	0.25	0/1828	0.49	0/2474
34	DL	0.27	0/1664	0.53	0/2247
35	DO	0.26	0/1576	0.51	0/2124
36	DP	0.26	0/1851	0.51	0/2507
37	DR	0.28	0/2093	0.53	0/2853
38	DT	0.26	0/1982	0.49	0/2685
39	DU	0.27	0/1777	0.52	0/2412
40	DV	0.25	0/1246	0.51	0/1691
41	DW	0.25	0/1172	0.50	0/1599
42	DX	0.24	0/765	0.51	0/1030
43	DY	0.26	0/1334	0.54	0/1810
44	DZ	0.24	0/247	0.40	0/333
45	F1	0.25	0/7134	0.55	0/9607
46	F2	0.26	0/7256	0.50	0/9804
47	F3	0.25	0/6980	0.50	0/9447
48	F4	0.25	0/4358	0.50	0/5894
49	F5	0.25	0/3829	0.48	0/5192
50	F6	0.26	0/3728	0.50	0/5060
51	F7	0.26	0/5227	0.50	0/7077
52	F8	0.27	0/3747	0.53	0/5074
53	F9	0.26	0/1737	0.53	0/2333
54	FA	0.24	0/4509	0.49	0/6141
55	FB	0.26	0/3190	0.54	0/4328
55	FC	0.25	0/2889	0.55	0/3913
56	FD	0.25	0/3604	0.50	0/4905
57	FE	0.27	0/3583	0.51	0/4872
58	FF	0.26	0/3307	0.53	0/4461
59	FG	0.24	0/1429	0.52	0/1926
60	FH	0.27	0/2445	0.53	0/3315
61	FI	0.25	0/2847	0.53	0/3842
62	FJ	0.26	0/2987	0.54	0/4030
63	FK	0.27	0/1757	0.50	0/2390
64	FL	0.26	0/2567	0.53	0/3479
65	FM	0.25	0/2462	0.52	0/3326
65	FN	0.25	0/2417	0.51	0/3267
66	FO	0.27	0/2647	0.57	0/3579
67	FP	0.27	0/2593	0.49	0/3544
68	FQ	0.26	0/1886	0.54	0/2562
68	FR	0.26	0/1800	0.53	0/2444
68	FS	0.26	0/2110	0.53	0/2869
68	FT	0.25	0/1790	0.54	0/2429
68	FU	0.26	0/1939	0.54	0/2633
69	FV	0.27	0/1668	0.49	0/2265

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
70	FW	0.25	0/2036	0.55	0/2751
71	FX	0.25	0/1693	0.49	0/2287
72	FY	0.25	0/1267	0.50	0/1715
73	FZ	0.29	0/966	0.51	0/1305
74	Fa	0.26	0/1351	0.53	0/1837
75	Fb	0.25	0/1104	0.50	0/1487
76	Fc	0.27	0/679	0.46	0/923
77	Fd	0.26	0/743	0.49	0/1007
78	Fe	0.26	0/1035	0.58	0/1389
79	Fi	0.25	0/3438	0.52	0/4660
All	All	0.26	0/235088	0.53	1/320588 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
58	FF	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	Ca	57	PRO	N-CA-CB	5.75	110.20	103.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
58	FF	222	ASP	Peptide

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	
2	CC	63/74 (85%)	61 (97%)	2 (3%)	0	100	100
3	CE	364/435 (84%)	341 (94%)	23 (6%)	0	100	100
4	CF	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
5	CH	208/282 (74%)	197 (95%)	11 (5%)	0	100	100
6	CI	414/443 (94%)	404 (98%)	10 (2%)	0	100	100
7	CJ	685/817 (84%)	664 (97%)	21 (3%)	0	100	100
8	CK	199/326 (61%)	190 (96%)	9 (4%)	0	100	100
9	CN	146/158 (92%)	141 (97%)	5 (3%)	0	100	100
10	CO	352/429 (82%)	339 (96%)	13 (4%)	0	100	100
11	CP	178/188 (95%)	172 (97%)	6 (3%)	0	100	100
12	CQ	232/336 (69%)	226 (97%)	6 (3%)	0	100	100
13	CR	128/320 (40%)	127 (99%)	1 (1%)	0	100	100
14	CS	79/244 (32%)	73 (92%)	6 (8%)	0	100	100
15	Ca	488/602 (81%)	465 (95%)	22 (4%)	1 (0%)	44	71
16	Cb	148/311 (48%)	136 (92%)	9 (6%)	3 (2%)	6	28
17	Cd	184/440 (42%)	176 (96%)	8 (4%)	0	100	100
18	Cg	481/490 (98%)	461 (96%)	20 (4%)	0	100	100
19	Ci	145/181 (80%)	138 (95%)	7 (5%)	0	100	100
20	Cj	223/257 (87%)	216 (97%)	7 (3%)	0	100	100
21	Ck	525/874 (60%)	511 (97%)	14 (3%)	0	100	100
22	Cn	23/250 (9%)	20 (87%)	3 (13%)	0	100	100
23	Cp	169/187 (90%)	162 (96%)	7 (4%)	0	100	100
24	DB	578/1181 (49%)	553 (96%)	25 (4%)	0	100	100
25	DC	1013/1165 (87%)	990 (98%)	23 (2%)	0	100	100
26	DD	774/812 (95%)	741 (96%)	33 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	DE	571/747 (76%)	522 (91%)	48 (8%)	1 (0%)	44	71
28	DF	477/666 (72%)	465 (98%)	12 (2%)	0	100	100
29	DG	552/631 (88%)	531 (96%)	21 (4%)	0	100	100
30	DH	489/581 (84%)	471 (96%)	18 (4%)	0	100	100
31	DI	388/407 (95%)	379 (98%)	9 (2%)	0	100	100
32	DJ	305/396 (77%)	296 (97%)	9 (3%)	0	100	100
33	DK	221/324 (68%)	217 (98%)	4 (2%)	0	100	100
34	DL	195/307 (64%)	193 (99%)	2 (1%)	0	100	100
35	DO	190/282 (67%)	179 (94%)	11 (6%)	0	100	100
36	DP	210/274 (77%)	194 (92%)	16 (8%)	0	100	100
37	DR	247/270 (92%)	233 (94%)	14 (6%)	0	100	100
38	DT	219/247 (89%)	197 (90%)	22 (10%)	0	100	100
39	DU	216/228 (95%)	203 (94%)	13 (6%)	0	100	100
40	DV	140/183 (76%)	130 (93%)	10 (7%)	0	100	100
41	DW	130/179 (73%)	124 (95%)	6 (5%)	0	100	100
42	DX	86/169 (51%)	79 (92%)	7 (8%)	0	100	100
43	DY	152/163 (93%)	146 (96%)	6 (4%)	0	100	100
44	DZ	26/94 (28%)	24 (92%)	2 (8%)	0	100	100
45	F1	848/1041 (82%)	811 (96%)	36 (4%)	1 (0%)	48	76
46	F2	880/1024 (86%)	845 (96%)	35 (4%)	0	100	100
47	F3	880/966 (91%)	843 (96%)	36 (4%)	1 (0%)	48	76
48	F4	500/811 (62%)	480 (96%)	20 (4%)	0	100	100
49	F5	511/754 (68%)	483 (94%)	28 (6%)	0	100	100
50	F6	450/676 (67%)	432 (96%)	18 (4%)	0	100	100
51	F7	639/679 (94%)	612 (96%)	27 (4%)	0	100	100
52	F8	455/726 (63%)	439 (96%)	16 (4%)	0	100	100
53	F9	209/608 (34%)	206 (99%)	3 (1%)	0	100	100
54	FA	572/642 (89%)	553 (97%)	19 (3%)	0	100	100
55	FB	377/588 (64%)	362 (96%)	15 (4%)	0	100	100
55	FC	336/588 (57%)	320 (95%)	16 (5%)	0	100	100
56	FD	444/579 (77%)	424 (96%)	20 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	FE	428/553 (77%)	418 (98%)	10 (2%)	0	100	100
58	FF	401/474 (85%)	378 (94%)	22 (6%)	1 (0%)	44	71
59	FG	172/463 (37%)	158 (92%)	14 (8%)	0	100	100
60	FH	299/457 (65%)	274 (92%)	25 (8%)	0	100	100
61	FI	346/445 (78%)	338 (98%)	8 (2%)	0	100	100
62	FJ	351/362 (97%)	340 (97%)	11 (3%)	0	100	100
63	FK	203/372 (55%)	194 (96%)	9 (4%)	0	100	100
64	FL	308/353 (87%)	289 (94%)	19 (6%)	0	100	100
65	FM	321/370 (87%)	309 (96%)	12 (4%)	0	100	100
65	FN	315/370 (85%)	309 (98%)	6 (2%)	0	100	100
66	FO	308/334 (92%)	294 (96%)	14 (4%)	0	100	100
67	FP	322/349 (92%)	309 (96%)	13 (4%)	0	100	100
68	FQ	223/307 (73%)	216 (97%)	7 (3%)	0	100	100
68	FR	210/307 (68%)	203 (97%)	7 (3%)	0	100	100
68	FS	246/307 (80%)	238 (97%)	8 (3%)	0	100	100
68	FT	209/307 (68%)	203 (97%)	6 (3%)	0	100	100
68	FU	226/307 (74%)	209 (92%)	17 (8%)	0	100	100
69	FV	205/264 (78%)	194 (95%)	11 (5%)	0	100	100
70	FW	238/263 (90%)	226 (95%)	12 (5%)	0	100	100
71	FX	209/239 (87%)	199 (95%)	10 (5%)	0	100	100
72	FY	150/189 (79%)	143 (95%)	7 (5%)	0	100	100
73	FZ	124/178 (70%)	119 (96%)	5 (4%)	0	100	100
74	Fa	159/171 (93%)	152 (96%)	7 (4%)	0	100	100
75	Fb	124/151 (82%)	123 (99%)	1 (1%)	0	100	100
76	Fc	82/148 (55%)	79 (96%)	3 (4%)	0	100	100
77	Fd	89/143 (62%)	84 (94%)	5 (6%)	0	100	100
78	Fe	115/123 (94%)	112 (97%)	3 (3%)	0	100	100
79	Fi	407/629 (65%)	384 (94%)	23 (6%)	0	100	100
All	All	26661/35727 (75%)	25542 (96%)	1111 (4%)	8 (0%)	100	100

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	Ca	57	PRO
16	Cb	107	SER
45	F1	709	PRO
47	F3	722	SER
16	Cb	109	GLY

5.3.2 Protein sidechains (i)

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	
2	CC	66/73 (90%)	66 (100%)	0	100	100
3	CE	317/372 (85%)	316 (100%)	1 (0%)	91	94
4	CF	143/144 (99%)	143 (100%)	0	100	100
5	CH	187/246 (76%)	187 (100%)	0	100	100
6	CI	353/372 (95%)	353 (100%)	0	100	100
7	CJ	609/723 (84%)	609 (100%)	0	100	100
8	CK	182/284 (64%)	182 (100%)	0	100	100
9	CN	134/143 (94%)	134 (100%)	0	100	100
10	CO	313/377 (83%)	313 (100%)	0	100	100
11	CP	160/168 (95%)	160 (100%)	0	100	100
12	CQ	208/297 (70%)	208 (100%)	0	100	100
13	CR	120/279 (43%)	119 (99%)	1 (1%)	79	87
14	CS	76/220 (34%)	76 (100%)	0	100	100
15	Ca	441/543 (81%)	441 (100%)	0	100	100
16	Cb	131/267 (49%)	131 (100%)	0	100	100
17	Cd	169/381 (44%)	169 (100%)	0	100	100
18	Cg	424/432 (98%)	424 (100%)	0	100	100
19	Ci	130/160 (81%)	130 (100%)	0	100	100
20	Cj	192/219 (88%)	192 (100%)	0	100	100
21	Ck	464/747 (62%)	463 (100%)	1 (0%)	92	95

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	Cn	20/210 (10%)	20 (100%)	0	100	100
23	Cp	159/175 (91%)	159 (100%)	0	100	100
24	DB	532/1027 (52%)	531 (100%)	1 (0%)	92	95
25	DC	862/986 (87%)	862 (100%)	0	100	100
26	DD	687/712 (96%)	687 (100%)	0	100	100
27	DE	464/644 (72%)	464 (100%)	0	100	100
28	DF	418/559 (75%)	418 (100%)	0	100	100
29	DG	486/543 (90%)	486 (100%)	0	100	100
30	DH	436/505 (86%)	436 (100%)	0	100	100
31	DI	349/364 (96%)	349 (100%)	0	100	100
32	DJ	270/347 (78%)	270 (100%)	0	100	100
33	DK	189/262 (72%)	189 (100%)	0	100	100
34	DL	170/263 (65%)	170 (100%)	0	100	100
35	DO	159/229 (69%)	158 (99%)	1 (1%)	84	90
36	DP	190/239 (80%)	188 (99%)	2 (1%)	70	82
37	DR	222/237 (94%)	221 (100%)	1 (0%)	86	91
38	DT	205/228 (90%)	204 (100%)	1 (0%)	86	91
39	DU	179/201 (89%)	179 (100%)	0	100	100
40	DV	132/166 (80%)	132 (100%)	0	100	100
41	DW	123/163 (76%)	121 (98%)	2 (2%)	58	76
42	DX	79/149 (53%)	79 (100%)	0	100	100
43	DY	137/146 (94%)	137 (100%)	0	100	100
44	DZ	23/84 (27%)	23 (100%)	0	100	100
45	F1	746/895 (83%)	745 (100%)	1 (0%)	92	96
46	F2	750/866 (87%)	750 (100%)	0	100	100
47	F3	746/809 (92%)	743 (100%)	3 (0%)	89	93
48	F4	469/704 (67%)	469 (100%)	0	100	100
49	F5	324/642 (50%)	324 (100%)	0	100	100
50	F6	401/590 (68%)	401 (100%)	0	100	100
51	F7	546/576 (95%)	546 (100%)	0	100	100
52	F8	381/557 (68%)	381 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	F9	171/506 (34%)	171 (100%)	0	100	100
54	FA	478/527 (91%)	476 (100%)	2 (0%)	89	93
55	FB	327/493 (66%)	327 (100%)	0	100	100
55	FC	298/493 (60%)	298 (100%)	0	100	100
56	FD	379/494 (77%)	377 (100%)	2 (0%)	86	91
57	FE	382/486 (79%)	382 (100%)	0	100	100
58	FF	345/400 (86%)	345 (100%)	0	100	100
59	FG	153/414 (37%)	152 (99%)	1 (1%)	81	88
60	FH	259/390 (66%)	259 (100%)	0	100	100
61	FI	299/380 (79%)	299 (100%)	0	100	100
62	FJ	314/323 (97%)	314 (100%)	0	100	100
63	FK	182/308 (59%)	182 (100%)	0	100	100
64	FL	275/310 (89%)	274 (100%)	1 (0%)	89	93
65	FM	254/292 (87%)	253 (100%)	1 (0%)	89	93
65	FN	249/292 (85%)	246 (99%)	3 (1%)	67	80
66	FO	273/290 (94%)	272 (100%)	1 (0%)	89	93
67	FP	265/286 (93%)	265 (100%)	0	100	100
68	FQ	202/264 (76%)	201 (100%)	1 (0%)	86	91
68	FR	194/264 (74%)	194 (100%)	0	100	100
68	FS	227/264 (86%)	227 (100%)	0	100	100
68	FT	192/264 (73%)	192 (100%)	0	100	100
68	FU	209/264 (79%)	209 (100%)	0	100	100
69	FV	182/231 (79%)	182 (100%)	0	100	100
70	FW	218/234 (93%)	218 (100%)	0	100	100
71	FX	169/195 (87%)	169 (100%)	0	100	100
72	FY	136/165 (82%)	136 (100%)	0	100	100
73	FZ	86/156 (55%)	86 (100%)	0	100	100
74	Fa	140/150 (93%)	140 (100%)	0	100	100
75	Fb	114/135 (84%)	112 (98%)	2 (2%)	54	74
76	Fc	78/127 (61%)	78 (100%)	0	100	100
77	Fd	76/119 (64%)	76 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Fe	111/115 (96%)	111 (100%)	0	100	100
79	Fi	361/537 (67%)	361 (100%)	0	100	100
All	All	23271/30693 (76%)	23242 (100%)	29 (0%)	92	96

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	F3	892	ARG
75	Fb	101	LYS
56	FD	4	ARG
65	FN	276	LYS
54	FA	450	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
38	DT	167	ASN
54	FA	145	GLN
75	Fb	102	HIS
41	DW	99	HIS
49	F5	485	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	492/620 (79%)	198 (40%)	6 (1%)

5 of 198 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CA	3	A
1	CA	4	A
1	CA	5	U
1	CA	7	A
1	CA	10	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	285	A
1	CA	295	G
1	CA	483	A
1	CA	27	A
1	CA	4	A

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 11 ligands modelled in this entry, 5 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	$\#\|Z\| > 2$
101	SAM	FF	501	-	24,29,29	1.20	3 (12%)	23,42,42	1.64	4 (17%)
100	SF4	F1	1101	45	0,12,12	-	-	-		
102	ACO	F3	1001	-	45,53,53	4.06	14 (31%)	56,79,79	2.18	6 (10%)
101	SAM	F1	1102	-	24,29,29	1.20	3 (12%)	23,42,42	1.60	4 (17%)
104	PO4	FW	301	-	4,4,4	0.99	0	6,6,6	0.41	0
98	GTP	Cg	501	99	26,34,34	1.13	2 (7%)	32,54,54	1.71	7 (21%)

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
100	SF4	F1	1101	45	-	-	0/6/5/5
101	SAM	FF	501	-	-	5/12/33/33	0/3/3/3
102	ACO	F3	1001	-	-	21/47/67/67	0/3/3/3
101	SAM	F1	1102	-	-	3/12/33/33	0/3/3/3
98	GTP	Cg	501	99	-	0/18/38/38	0/3/3/3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
102	F3	1001	ACO	O4B-C1B	17.32	1.65	1.41
102	F3	1001	ACO	C2B-C1B	-14.37	1.32	1.53
102	F3	1001	ACO	C9P-N8P	7.16	1.49	1.33
102	F3	1001	ACO	O4B-C4B	-6.70	1.30	1.45
102	F3	1001	ACO	C5P-N4P	5.21	1.45	1.33

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
102	F3	1001	ACO	C5A-C6A-N6A	11.16	137.31	120.35
102	F3	1001	ACO	N6A-C6A-N1A	-7.60	102.80	118.57
101	FF	501	SAM	N3-C2-N1	-5.83	119.57	128.68
101	F1	1102	SAM	N3-C2-N1	-5.47	120.14	128.68
102	F3	1001	ACO	N3A-C2A-N1A	-5.27	120.44	128.68

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
101	F1	1102	SAM	CB-CG-SD-CE
101	F1	1102	SAM	CB-CG-SD-C5'
101	F1	1102	SAM	C4'-C5'-SD-CG
101	FF	501	SAM	N-CA-CB-CG
101	FF	501	SAM	C-CA-CB-CG

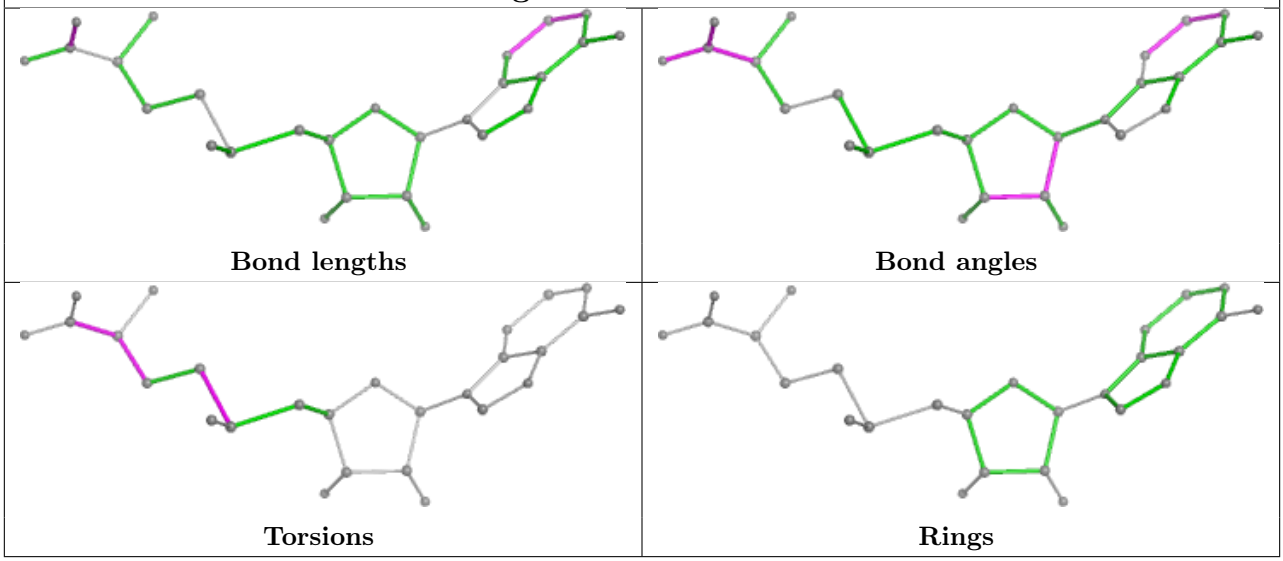
There are no ring outliers.

No monomer is involved in short contacts.

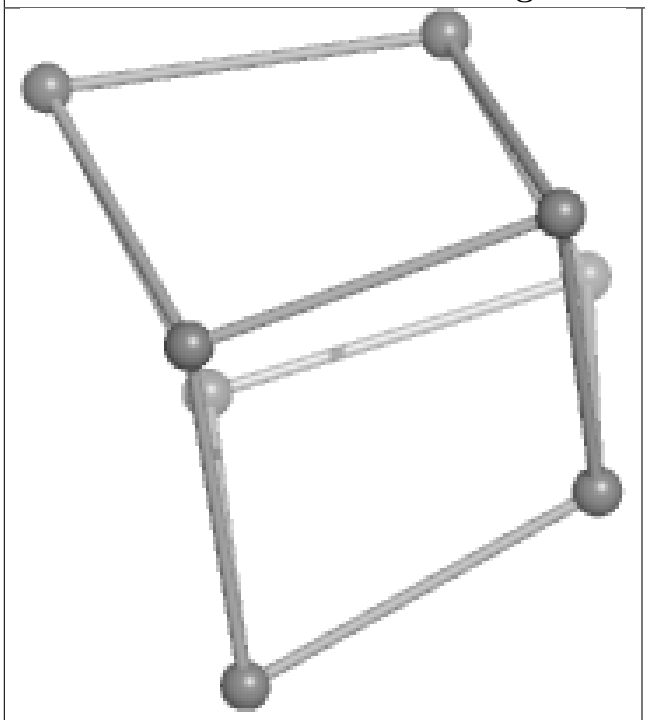
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

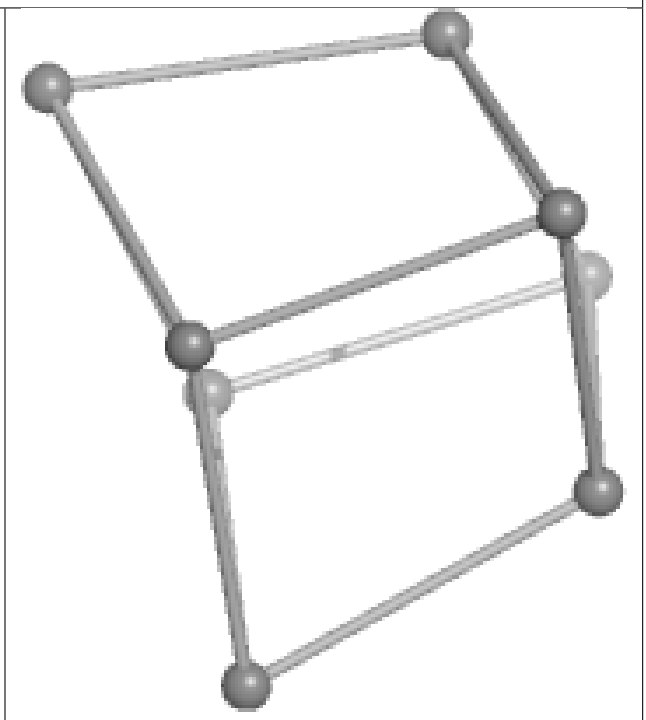
Ligand SAM FF 501



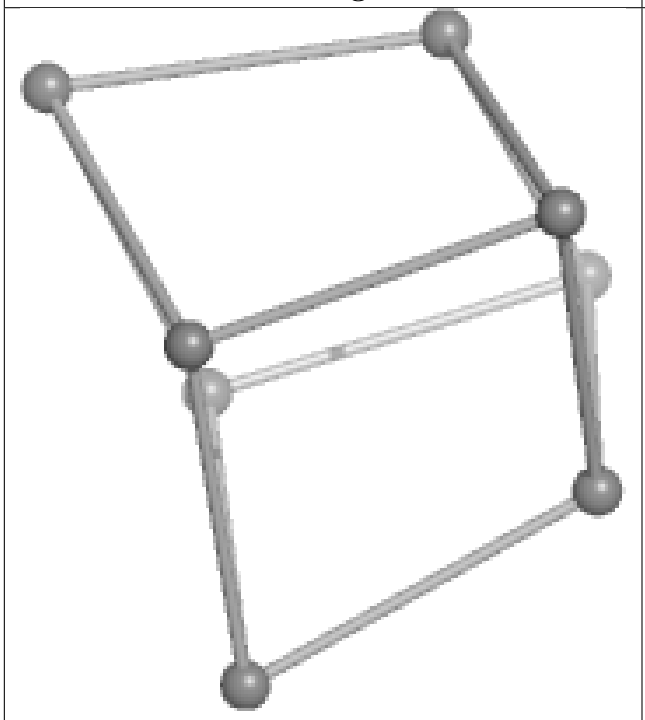
Ligand SF4 F1 1101



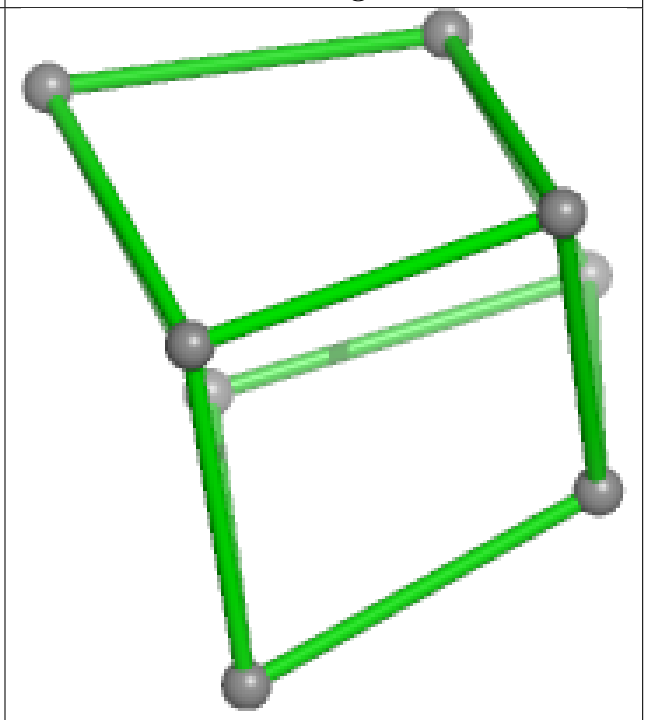
Bond lengths



Bond angles

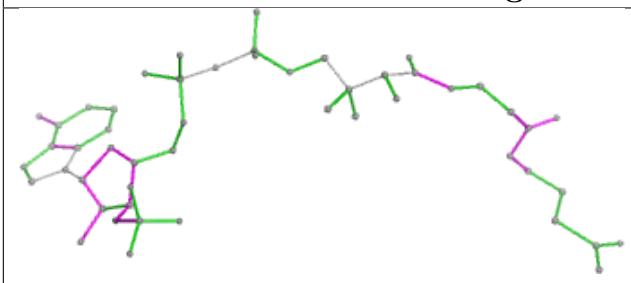


Torsions

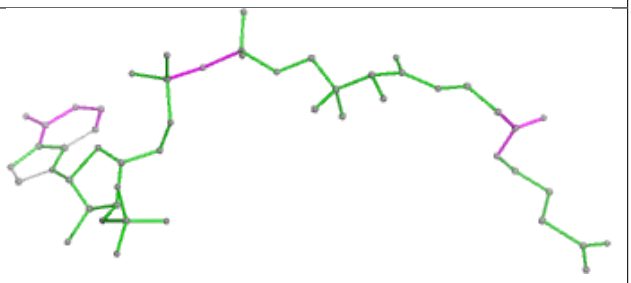


Rings

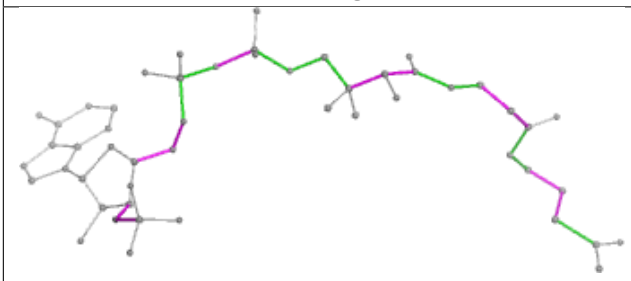
Ligand ACO F3 1001



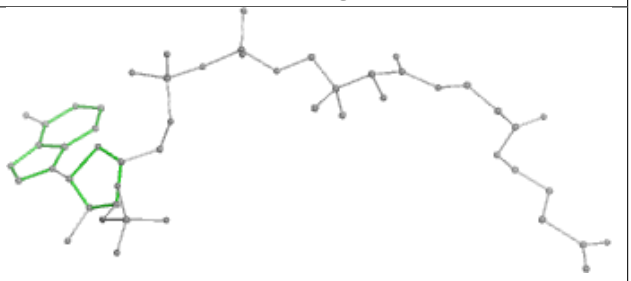
Bond lengths



Bond angles

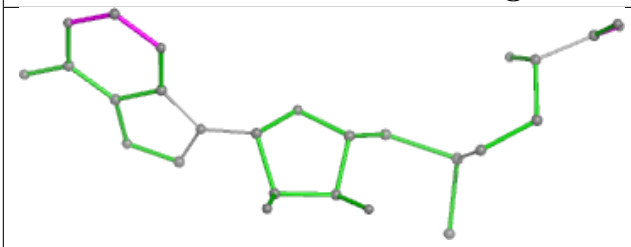


Torsions

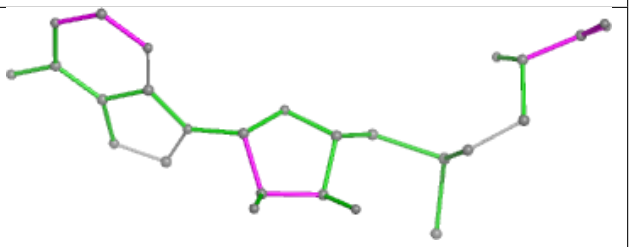


Rings

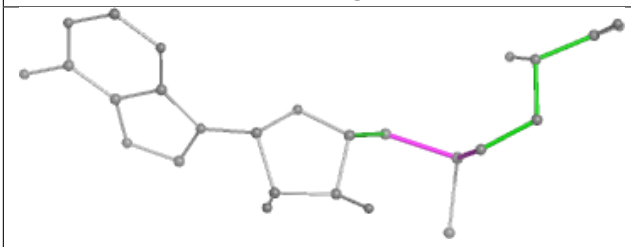
Ligand SAM F1 1102



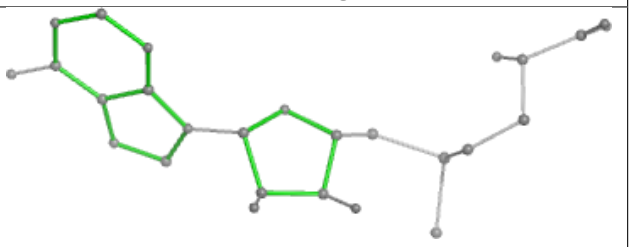
Bond lengths



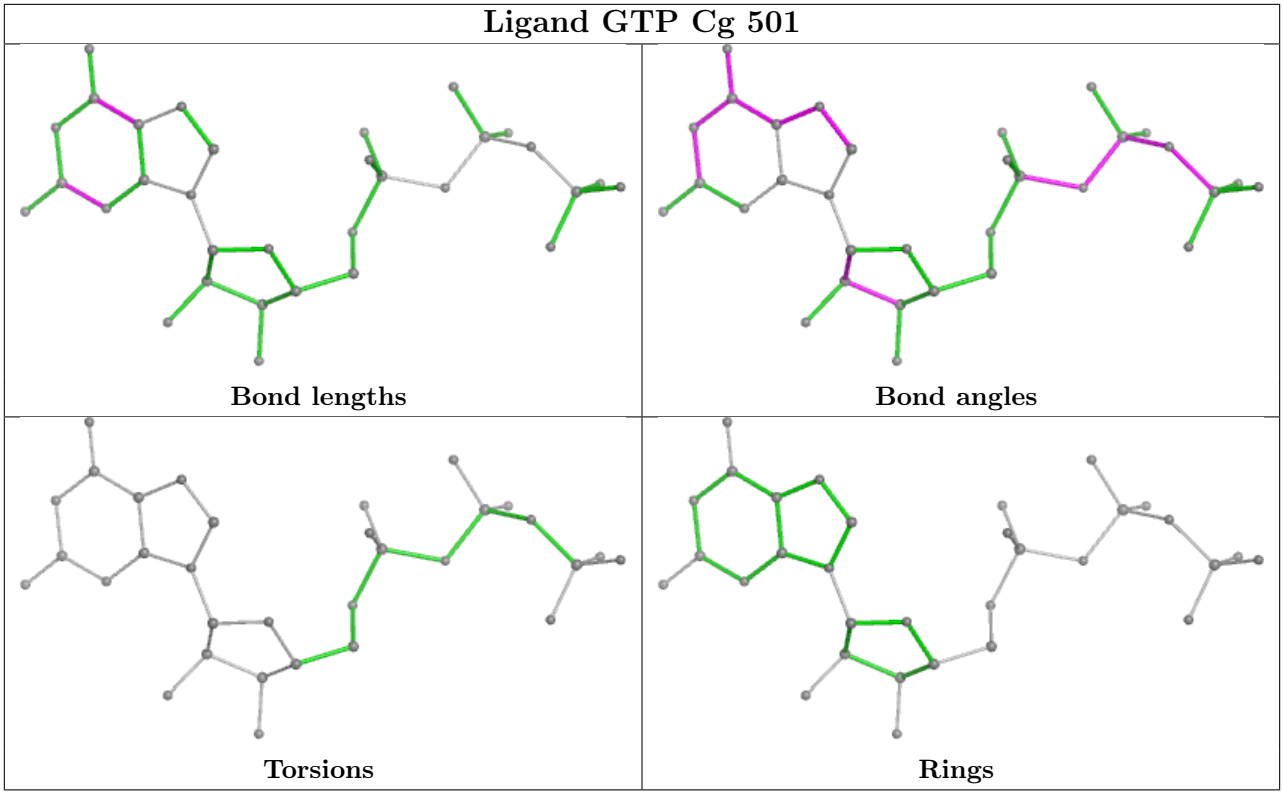
Bond angles



Torsions



Rings



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
94	Ug	10
95	Uh	9
92	UY	3

The worst 5 of 22 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	UY	421:UNK	C	439:UNK	N	57.87
1	UY	405:UNK	C	411:UNK	N	41.49
1	Uh	411:UNK	C	499:UNK	N	40.91
1	Ug	129:UNK	C	130:UNK	N	34.53
1	Uh	274:UNK	C	304:UNK	N	29.82

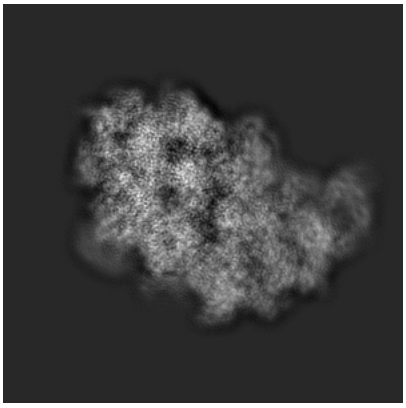
6 Map visualisation (i)

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

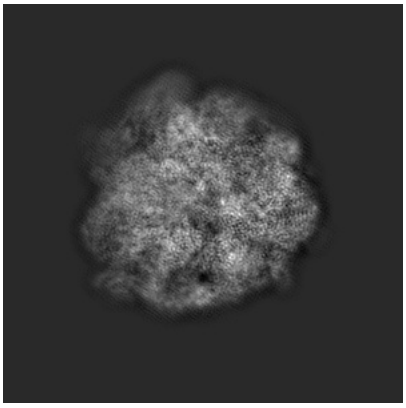
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

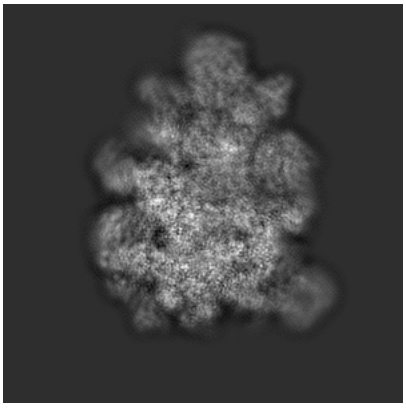
6.1.1 Primary map



X



Y

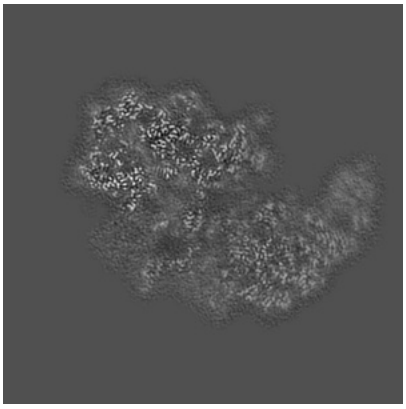


Z

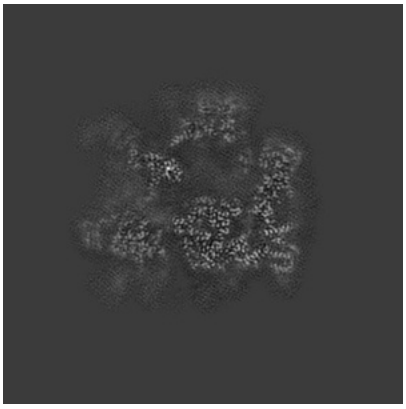
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

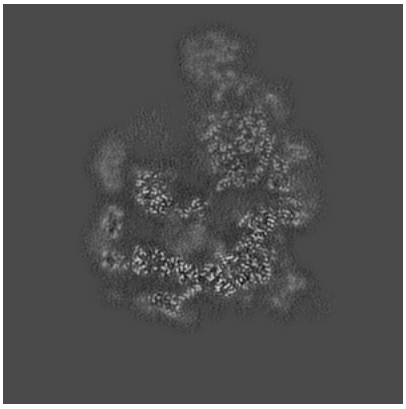
6.2.1 Primary map



X Index: 160



Y Index: 160

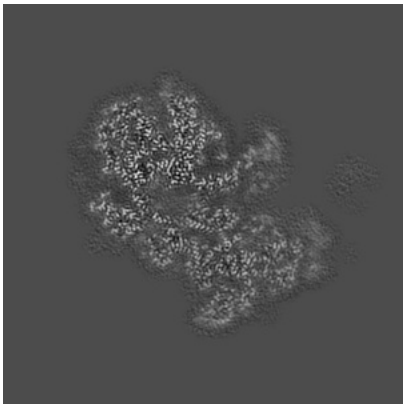


Z Index: 160

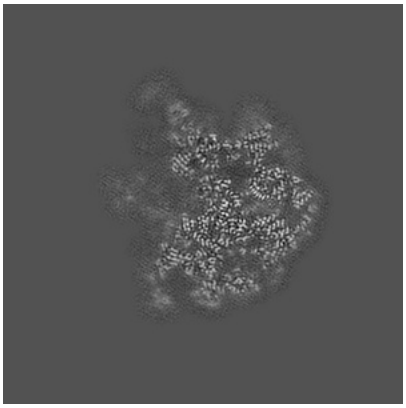
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

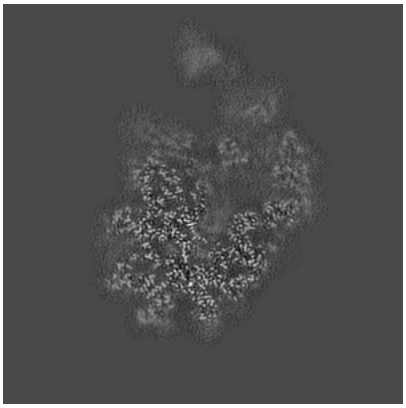
6.3.1 Primary map



X Index: 137



Y Index: 109

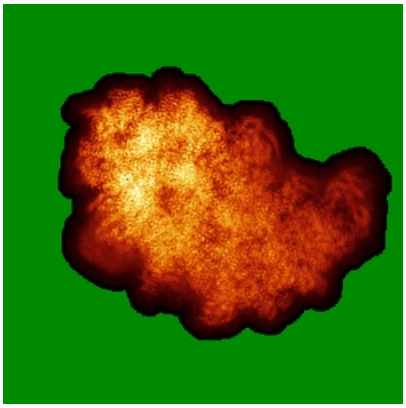


Z Index: 181

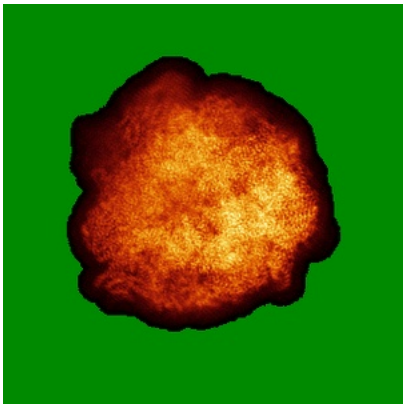
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

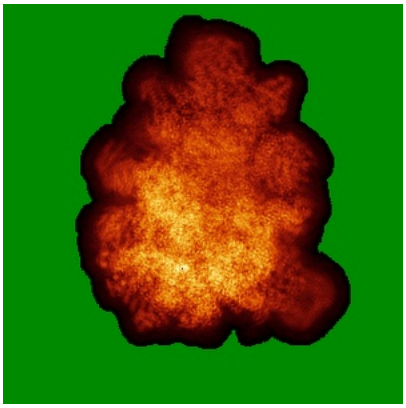
6.4.1 Primary map



X



Y

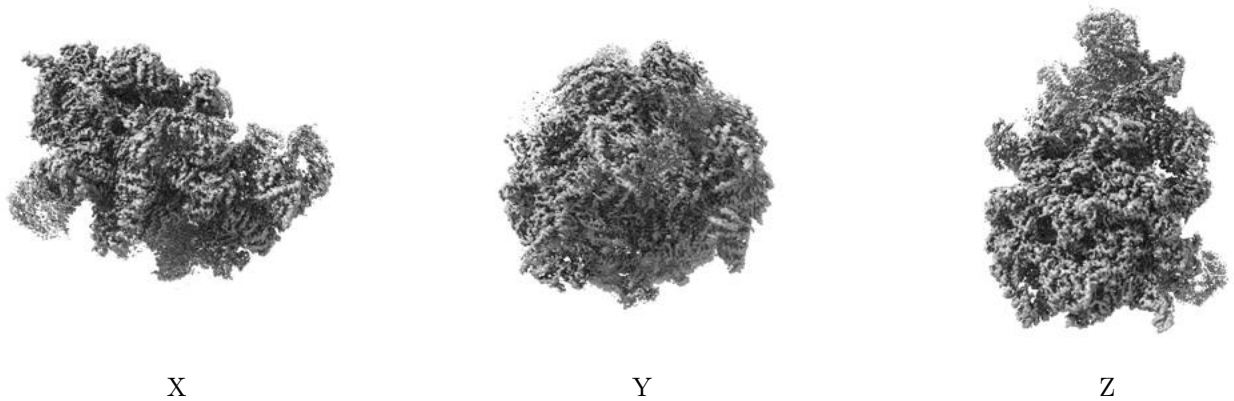


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



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

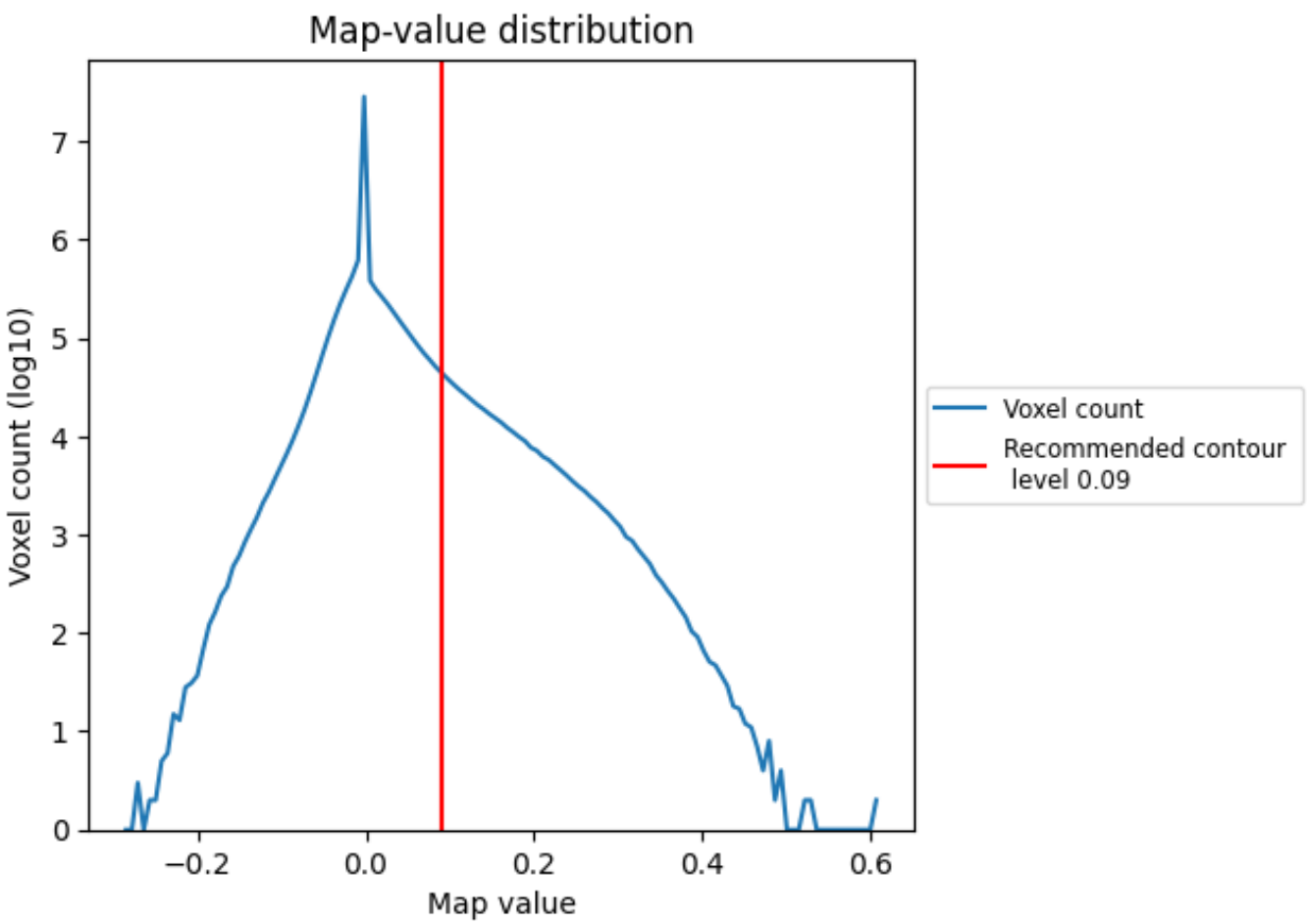
6.6 Mask visualisation (i)

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

7 Map analysis (i)

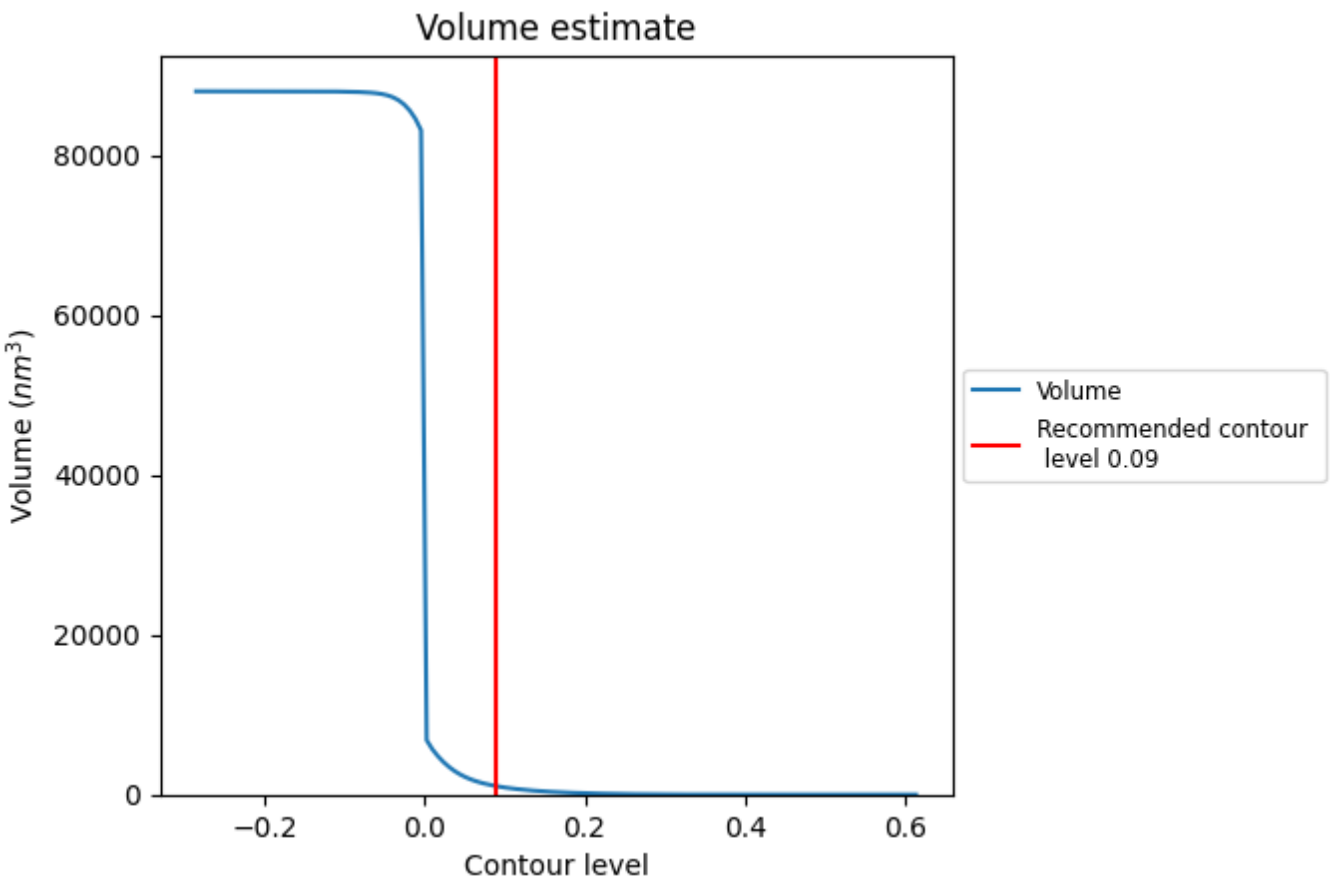
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

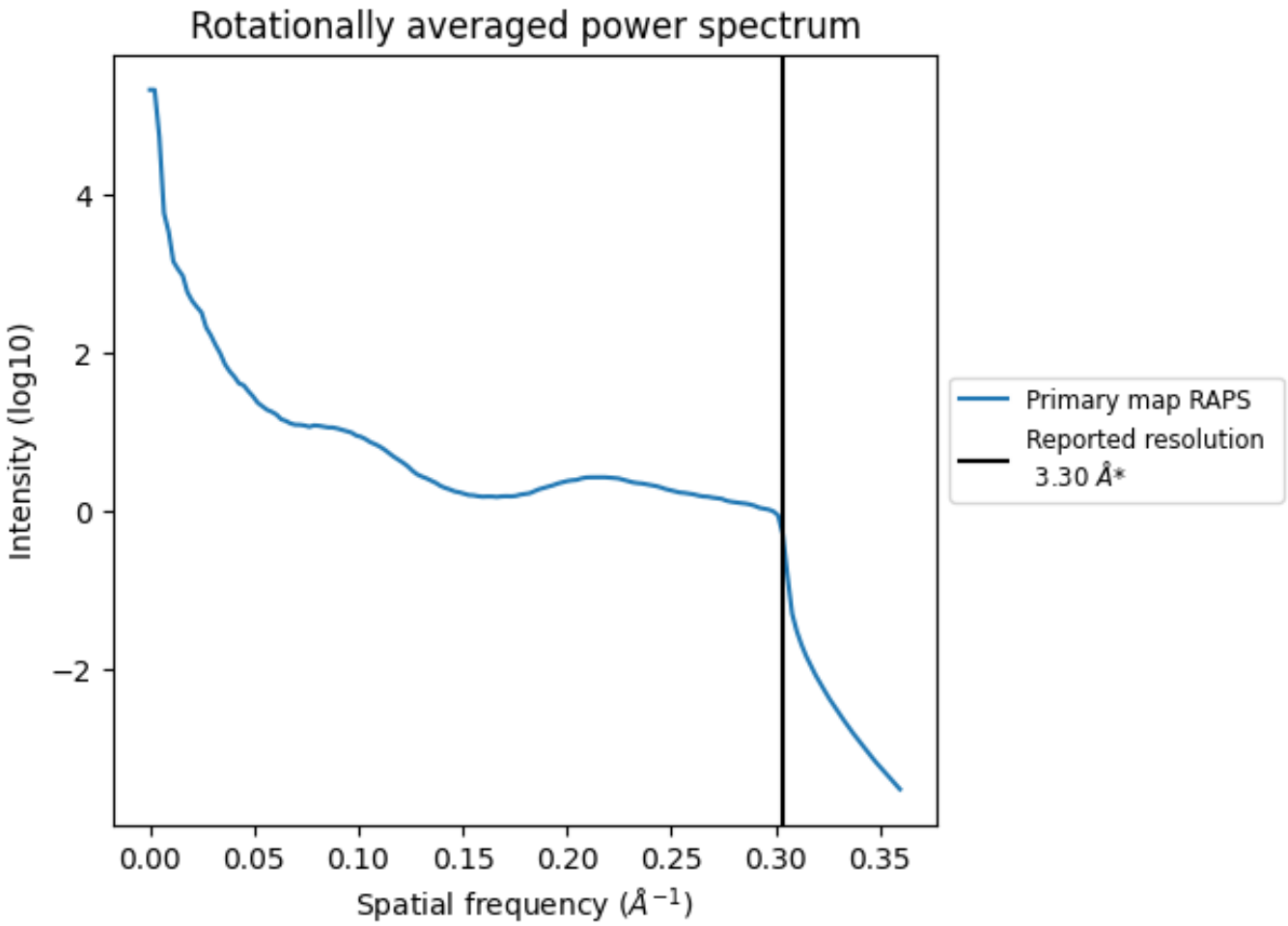
7.2 Volume estimate (i)



The volume at the recommended contour level is 1051 nm^3; this corresponds to an approximate mass of 949 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

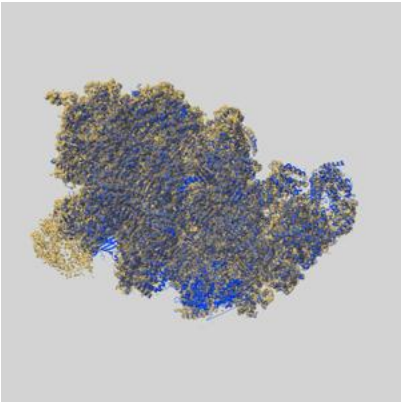
8 Fourier-Shell correlation (i)

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

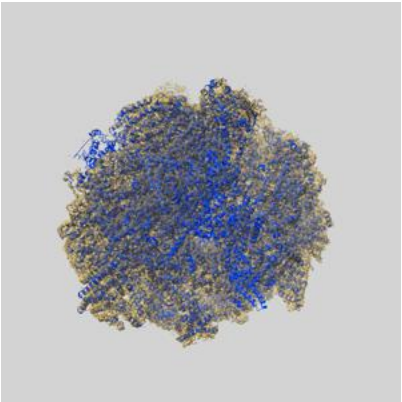
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-10180 and PDB model 9HNY. Per-residue inclusion information can be found in section 3 on page 27.

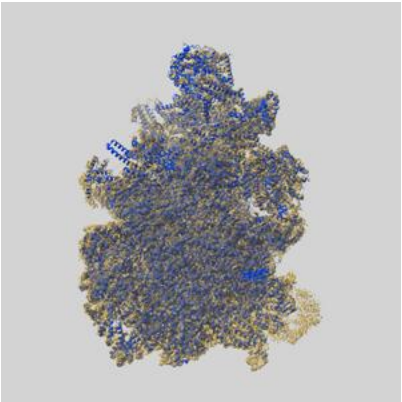
9.1 Map-model overlay (i)



X



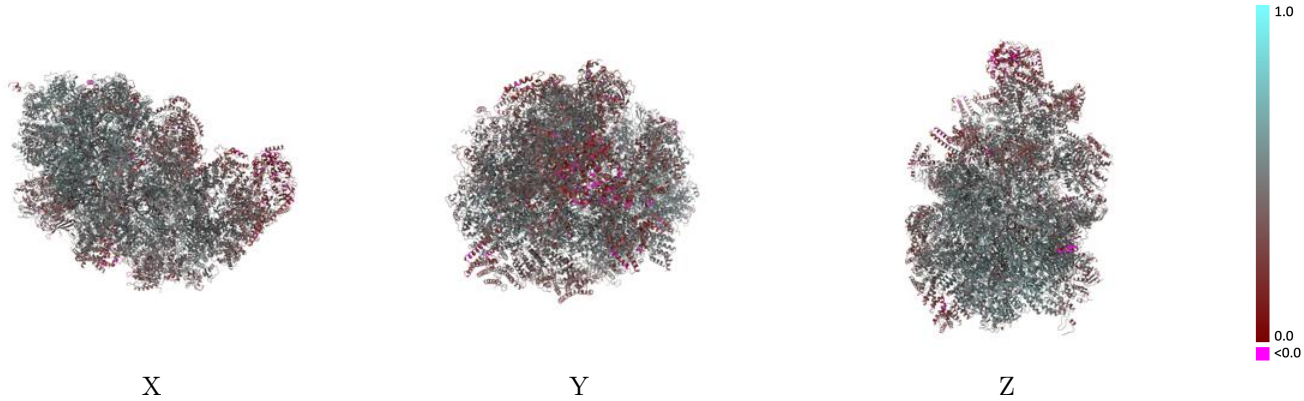
Y



Z

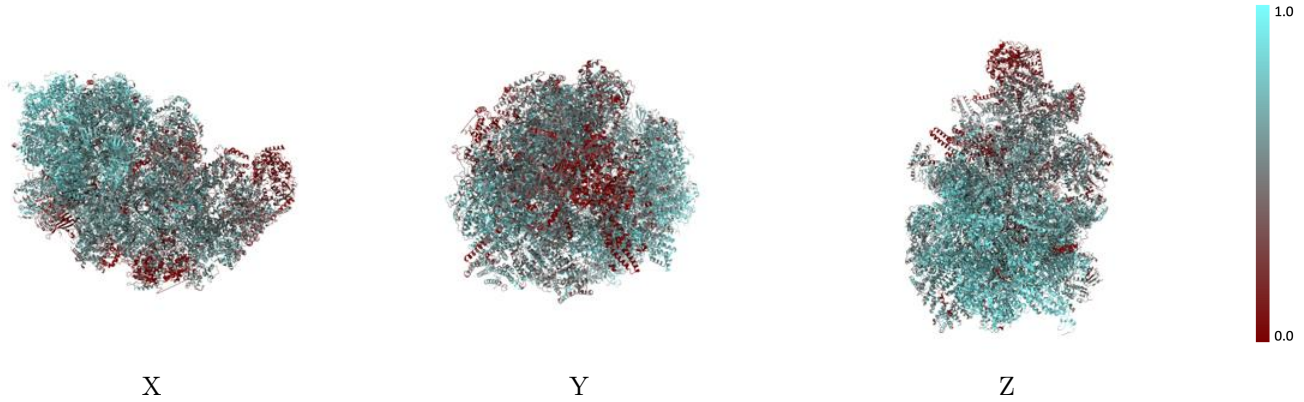
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



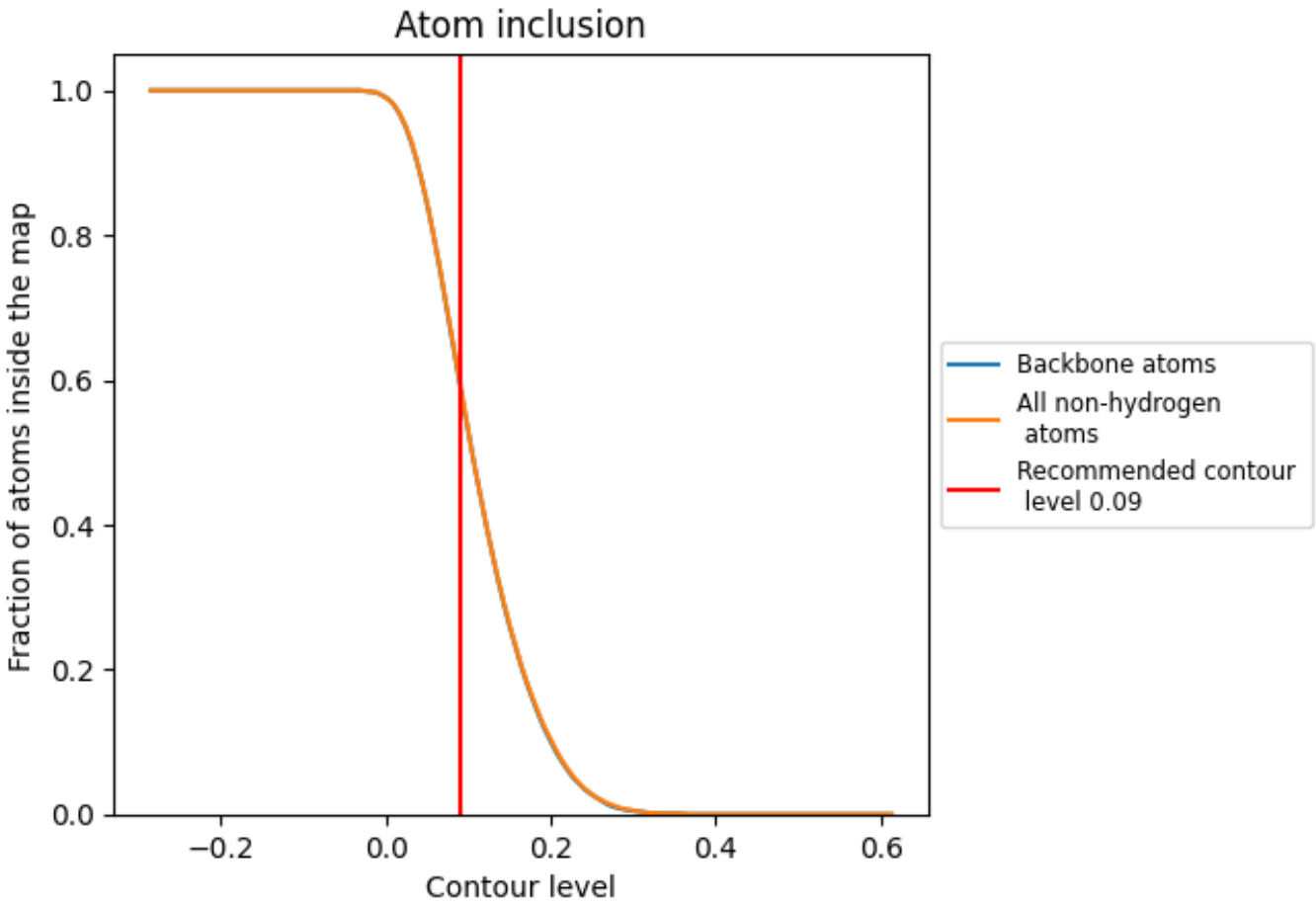
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



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

9.4 Atom inclusion (i)



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

9.5 Map-model fit summary (i)

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

Chain	Atom inclusion	Q-score
All	0.5940	0.4590
CA	0.6720	0.4820
CC	0.4410	0.4800
CE	0.7040	0.5180
CF	0.7400	0.5050
CH	0.7910	0.5470
CI	0.6450	0.4850
CJ	0.5700	0.4790
CK	0.6240	0.4620
CN	0.2720	0.4680
CO	0.7710	0.5260
CP	0.8140	0.5480
CQ	0.6780	0.5230
CR	0.6580	0.4700
CS	0.0120	0.3370
Ca	0.6930	0.4860
Cb	0.5820	0.4160
Cd	0.8130	0.5330
Cg	0.6490	0.4730
Ci	0.5250	0.4880
Cj	0.8440	0.5440
Ck	0.5960	0.4500
Cn	0.4530	0.4740
Cp	0.7760	0.5220
DB	0.4250	0.4100
DC	0.3700	0.3290
DD	0.7960	0.5310
DE	0.2210	0.2520
DF	0.5230	0.4640
DG	0.5930	0.4080
DH	0.5240	0.4680
DI	0.7570	0.4970
DJ	0.5810	0.4510
DK	0.4480	0.4070
DL	0.6880	0.5240

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
DO	0.6440	0.4180
DP	0.8280	0.4920
DR	0.8260	0.5280
DT	0.6040	0.5060
DU	0.6880	0.4980
DV	0.5720	0.4810
DW	0.5440	0.4570
DX	0.2190	0.3910
DY	0.5000	0.4540
DZ	0.5870	0.4890
F1	0.5990	0.4900
F2	0.7520	0.4980
F3	0.6940	0.4550
F4	0.4200	0.3880
F5	0.3830	0.3400
F6	0.5730	0.3700
F7	0.7580	0.4980
F8	0.7120	0.4940
F9	0.6670	0.4860
FA	0.5270	0.4170
FB	0.7210	0.5220
FC	0.6430	0.4520
FD	0.4780	0.4050
FE	0.7200	0.5220
FF	0.5950	0.4950
FG	0.6330	0.4970
FH	0.5780	0.4650
FI	0.5160	0.4700
FJ	0.6120	0.4960
FK	0.5730	0.4660
FL	0.6190	0.5260
FM	0.7130	0.4870
FN	0.5510	0.3910
FO	0.8250	0.5430
FP	0.7990	0.5030
FQ	0.7190	0.4880
FR	0.6840	0.4850
FS	0.5830	0.4480
FT	0.6670	0.4560
FU	0.6140	0.4460
FV	0.6050	0.4660
FW	0.7640	0.5180

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
FX	0.8150	0.4960
FY	0.5230	0.4310
FZ	0.1370	0.3760
Fa	0.6630	0.5190
Fb	0.5750	0.3460
Fc	0.5470	0.3300
Fd	0.7780	0.5080
Fe	0.5190	0.4630
Fi	0.0260	0.3430
UA	0.3260	0.2760
UB	0.6670	0.4610
UC	0.8400	0.5010
UF	0.6360	0.4620
UG	0.7620	0.4630
UI	0.8750	0.5310
UJ	0.5500	0.4920
UK	0.3080	0.4190
UL	0.7360	0.4790
UM	0.7110	0.4770
UN	0.7710	0.4670
UO	0.5530	0.3720
UP	0.3420	0.3700
UQ	0.6220	0.4100
UY	0.0190	0.3990
Ud	0.3590	0.4010
Ug	0.5290	0.3820
Uh	0.0520	0.4180
Uk	0.3810	0.4290
Ul	0.2140	0.3520