wwPDB EM Validation Summary Report ⓘ

Jun 8, 2022 – 07:46 pm BST

PDB ID	:	7PKT
EMDB ID	:	EMD-13480
Title	:	Large subunit of the Chlamydomonas reinhardtii mitoribosome
Authors	:	Waltz, F.; Soufari, H.; Hashem, Y.
Deposited on	:	2021-08-26
Resolution	:	3.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

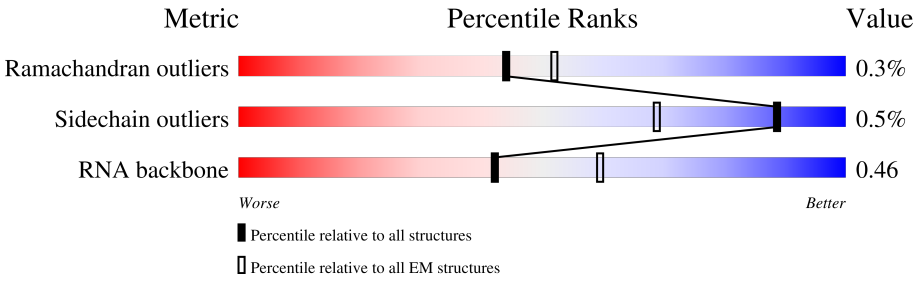
EMDB validation analysis	:	0.0.1.dev8
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

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 3.00 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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	a	383	55% 68% 31%
2	b	417	24% 72% 27%
3	c	427	15% 73% · 26%
4	d	216	83% 85% 15%
5	f	304	19% 19% 80%
6	i	277	18% 54% · 45%
7	j	120	71% 98% ·
8	k	337	5% 61% · 38%

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Mol	Chain	Length	Quality of chain
9	l	270	49% 50% 50%
10	m	183	19% 95%
11	n	312	22% 54% 45%
12	o	115	96%
13	p	370	7% 53% 45%
14	q	377	5% 43% 57%
15	r	226	11% 69% 30%
16	s	309	18% 67% 32%
17	t	366	35% 52% 48%
18	u	173	10% 76% 23%
19	v	153	57% 78% 22%
20	w	127	14% 93% 6%
21	x	214	78% 22%
22	y	123	8% 58% 42%
23	z	59	22% 88% 10%
24	A	280	18% 82%
25	B	151	15% 83% 15%
26	e	207	79% 79% 21%
27	D	172	54% 54% 45%
28	E	112	11% 71% 29%
29	F	141	91% 9%
30	G	259	76% 76% 23%
31	I	132	12% 72% 27%
32	J	134	42% 85% 15%
33	K	249	20% 77% 22%

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Mol	Chain	Length	Quality of chain
34	L	206	6% 67% 33%
35	C	36	100% 100%
36	M	876	26% 49% 51%
37	N	455	43% 61% 38%
38	O	688	56% 84% 15%
39	P	530	16% 82% 17%
40	Q	820	39% 60% 39%
41	R	653	40% 57% 42%
42	S	334	34% 72% 27%
43	X	31	26% 100%
44	Y	172	85% 87% 13%
45	Z	49	43% 100%
46	1	162	22% 67% 28% 5%
47	2	86	6% 71% 27%
48	0	75	49% 49% 45% 5%
49	3	184	82% 15%
50	4	118	8% 75% 24%
51	5	149	79% 52% 42% 5%
52	6	136	70% 25% 5%
53	7	578	41% 67% 29%
54	8	413	55% 59% 34% 7%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 103129 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal_L2_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	a	263	1993	1238	398	354	3	0	0

- Molecule 2 is a protein called uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	304	2325	1481	430	403	11	0	0

- Molecule 3 is a protein called uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	c	318	2497	1571	491	431	4	0	0

- Molecule 4 is a protein called uL5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	d	184	1382	885	242	249	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	f	60	464	289	92	81	2	0	0

- Molecule 6 is a protein called Mitochondrial ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	i	152	1234	788	230	213	3	0	0

- Molecule 7 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	120	Total	C	N	O	S	0	0
			941	604	173	161	3		

- Molecule 8 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	210	Total	C	N	O	S	0	0
			1620	1018	311	286	5		

- Molecule 9 is a protein called Ribosomal_L16 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	136	Total	C	N	O	S	0	0
			1079	689	209	176	5		

- Molecule 10 is a protein called Mitochondrial ribosomal protein L17,bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	177	Total	C	N	O	S	0	0
			1459	911	297	248	3		

- Molecule 11 is a protein called Mitochondrial ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	n	173	Total	C	N	O	S	0	0
			1406	897	262	240	7		

- Molecule 12 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	o	110	Total	C	N	O	S	0	0
			890	561	180	145	4		

- Molecule 13 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	204	Total	C	N	O	S	0	0
			1606	1022	301	281	2		

- Molecule 14 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	q	161	Total	C	N	O	S	0	0
			1270	795	246	221	8		

- Molecule 15 is a protein called Mitochondrial ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	158	Total	C	N	O	S	0	0
			1335	847	256	227	5		

- Molecule 16 is a protein called KOW domain-containing protein,uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	210	Total	C	N	O	S	0	0
			1565	983	284	294	4		

- Molecule 17 is a protein called Ribosomal_TL5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	192	Total	C	N	O	S	0	0
			1489	942	282	257	8		

- Molecule 18 is a protein called bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	u	133	Total	C	N	O	S	0	0
			1007	633	194	177	3		

- Molecule 19 is a protein called bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	v	120	Total	C	N	O	S	0	0
			997	627	196	171	3		

- Molecule 20 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	w	120	Total	C	N	O	S	0	0
			974	611	185	173	5		

- Molecule 21 is a protein called Ribosomal_L30 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	x	167	Total	C	N	O	S	0	0
			1397	882	279	232	4		

- Molecule 22 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	y	71	Total	C	N	O	S	0	0
			542	335	105	97	5		

- Molecule 23 is a protein called Mitochondrial ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	z	53	Total	C	N	O	S	0	0
			439	290	77	71	1		

- Molecule 24 is a protein called bL34m.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	A	50	Total	C	N	O	0	0
			427	259	100	68		

- Molecule 25 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	128	Total	C	N	O	S	0	0
			1058	664	218	175	1		

- Molecule 26 is a protein called Plastid ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	164	Total	C	N	O	S	0	0
			1238	785	223	226	4		

- Molecule 27 is a protein called mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	94	Total	C	N	O	S	0	0
			740	467	135	134	4		

- Molecule 28 is a protein called mL41.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	E	79	Total 636	C 409	N 119	O 108	0	0

- Molecule 29 is a protein called mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	129	Total 1036	C 650	N 199	O 182	S 5	0	0

- Molecule 30 is a protein called Mitochondrial ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	G	199	Total 1482	C 924	N 268	O 286	S 4	0	0

- Molecule 31 is a protein called mL63/57/60.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	97	Total 780	C 490	N 152	O 133	S 5	0	0

- Molecule 32 is a protein called mL59/64.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	114	Total 842	C 529	N 156	O 154	S 3	0	0

- Molecule 33 is a protein called mL80.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	195	Total 1571	C 987	N 305	O 276	S 3	0	0

- Molecule 34 is a protein called mL87.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	137	Total 1167	C 735	N 234	O 195	S 3	0	0

- Molecule 35 is a protein called bL36m.

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

- Molecule 36 is a protein called mL113.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M	430	Total	C	N	O	S	0	0
			3152	1965	617	561	9		

- Molecule 37 is a protein called mL114.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	N	283	Total	C	N	O	S	0	0
			2116	1337	397	377	5		

- Molecule 38 is a protein called mL115.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	O	584	Total	C	N	O	S	0	0
			4260	2671	792	778	19		

- Molecule 39 is a protein called mL116.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	P	438	Total	C	N	O	S	0	0
			3151	1979	602	564	6		

- Molecule 40 is a protein called mL117.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Q	498	Total	C	N	O	S	0	0
			3073	1893	581	587	12		

- Molecule 41 is a protein called mL118.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	376	Total	C	N	O	S	0	0
			2594	1616	511	461	6		

- Molecule 42 is a protein called mL119.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S	244	Total	C	N	O	S	0	0
			1967	1211	376	362	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	257	THR	GLY	conflict	UNP A0A2K3D424

- Molecule 43 is a protein called Unk1.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	X	31	Total	C	N	O	0	0
			155	93	31	31		

- Molecule 44 is a protein called PPR*.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Y	149	Total	C	N	O	0	0
			745	447	149	149		

- Molecule 45 is a protein called Unk2.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Z	49	Total	C	N	O	0	0
			245	147	49	49		

- Molecule 46 is a RNA chain called L1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	162	Total	C	N	O	P	0	0
			3440	1541	607	1130	162		

- Molecule 47 is a RNA chain called L2a rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	86	Total	C	N	O	P	0	0
			1821	816	311	608	86		

- Molecule 48 is a RNA chain called L3a rRNA (5S).

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	75	Total	C	N	O	P	0	0
			1592	713	280	524	75		

- Molecule 49 is a RNA chain called L3b rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3	184	Total	C	N	O	P	0	0
			3933	1757	709	1283	184		

- Molecule 50 is a RNA chain called L4 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	4	118	Total	C	N	O	P	0	0
			2538	1135	478	807	118		

- Molecule 51 is a RNA chain called L5 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	5	149	Total	C	N	O	P	0	0
			3156	1412	545	1050	149		

- Molecule 52 is a RNA chain called L6 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	136	Total	C	N	O	P	0	0
			2913	1306	542	929	136		

- Molecule 53 is a RNA chain called L7 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	578	Total	C	N	O	P	0	0
			12344	5521	2237	4008	578		

- Molecule 54 is a RNA chain called L8 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	8	413	Total	C	N	O	P	0	0
			8792	3931	1558	2890	413		

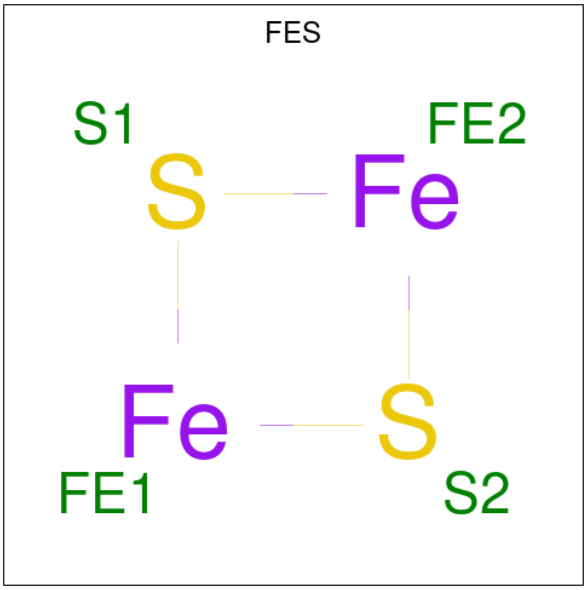
- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
55	y	1	Total Zn 1 1	0

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
56	Q	1	Total Mg 1 1	0
56	1	6	Total Mg 6 6	0
56	2	7	Total Mg 7 7	0
56	0	1	Total Mg 1 1	0
56	3	12	Total Mg 12 12	0
56	4	8	Total Mg 8 8	0
56	5	3	Total Mg 3 3	0
56	6	6	Total Mg 6 6	0
56	7	18	Total Mg 18 18	0
56	8	7	Total Mg 7 7	0

- Molecule 57 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



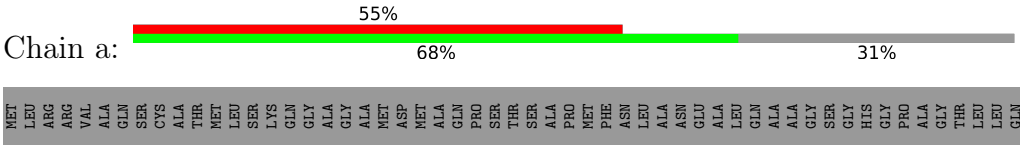
Mol	Chain	Residues	Atoms			AltConf
57	S	1	Total	Fe	S	0
			4	2	2	

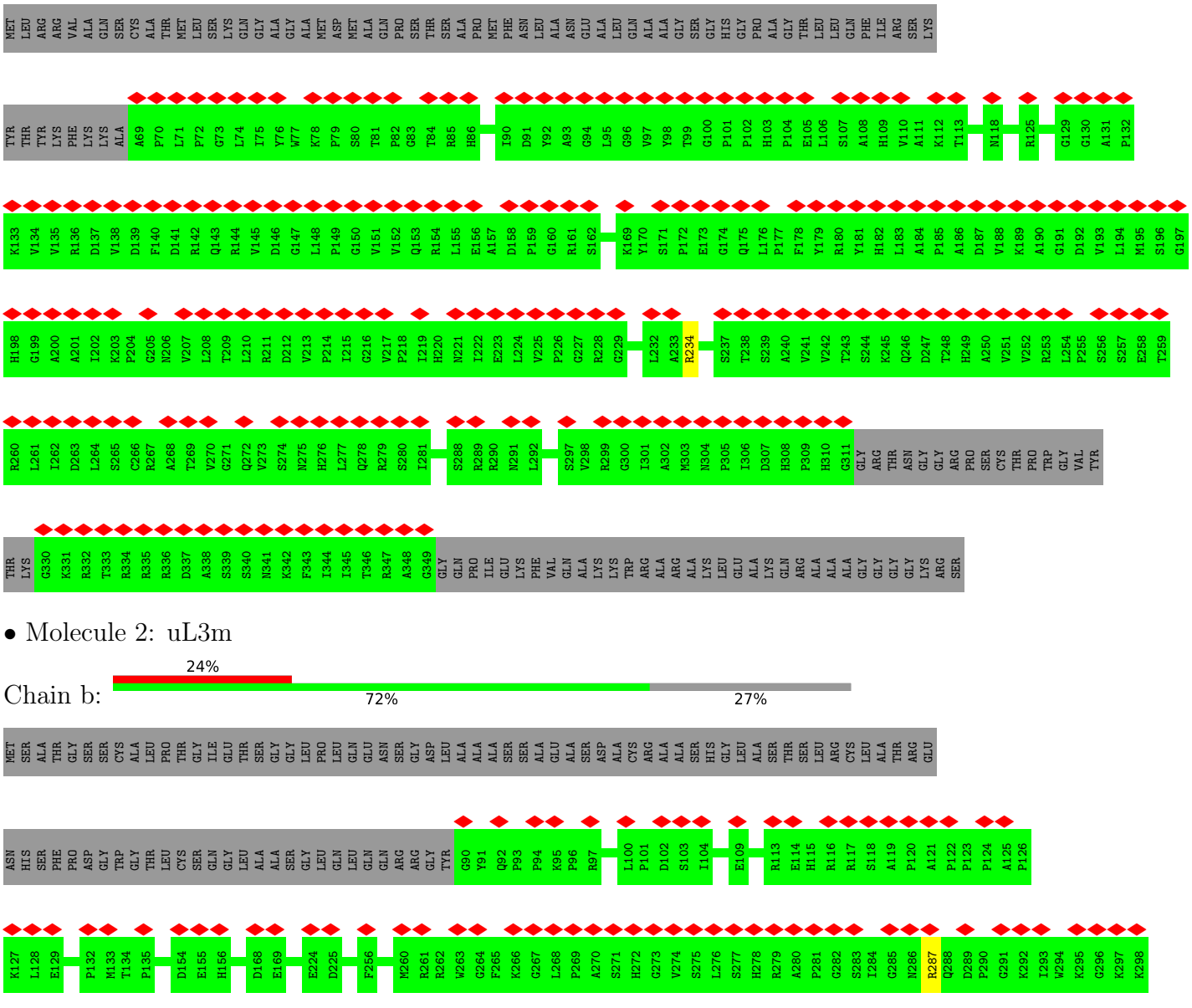
3 Residue-property plots (i)

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: Ribosomal_L2_C domain-containing protein

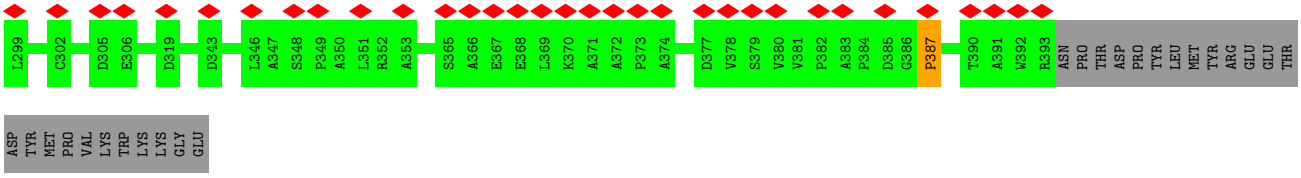
Chain a:



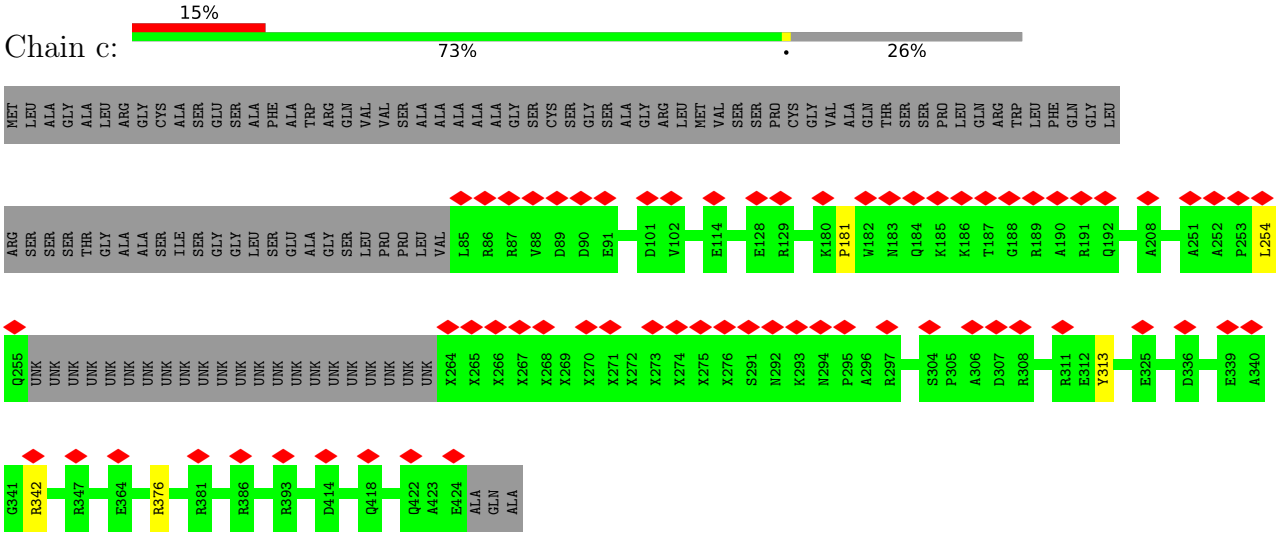


• Molecule 2: uL3m

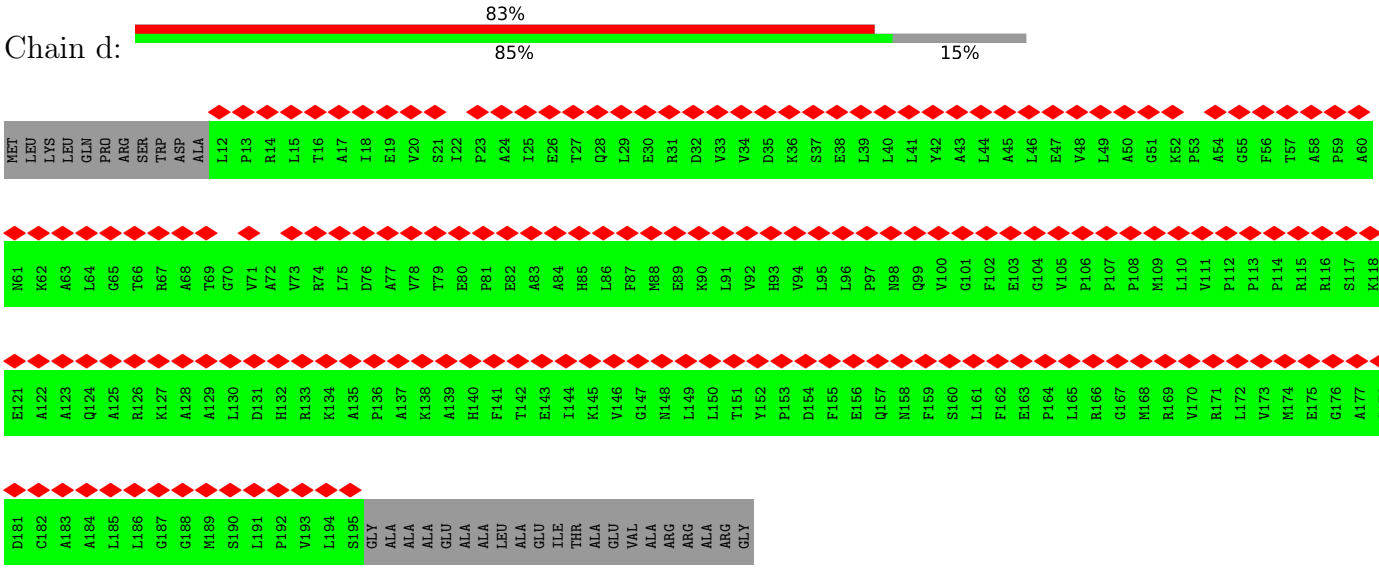
Chain b:



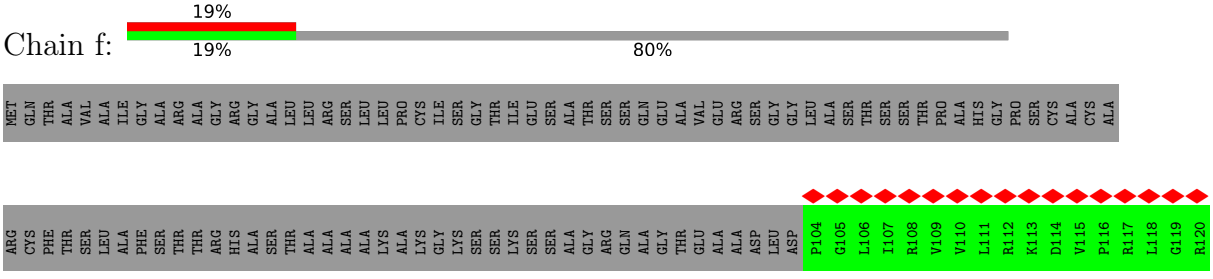
• Molecule 3: uL4m

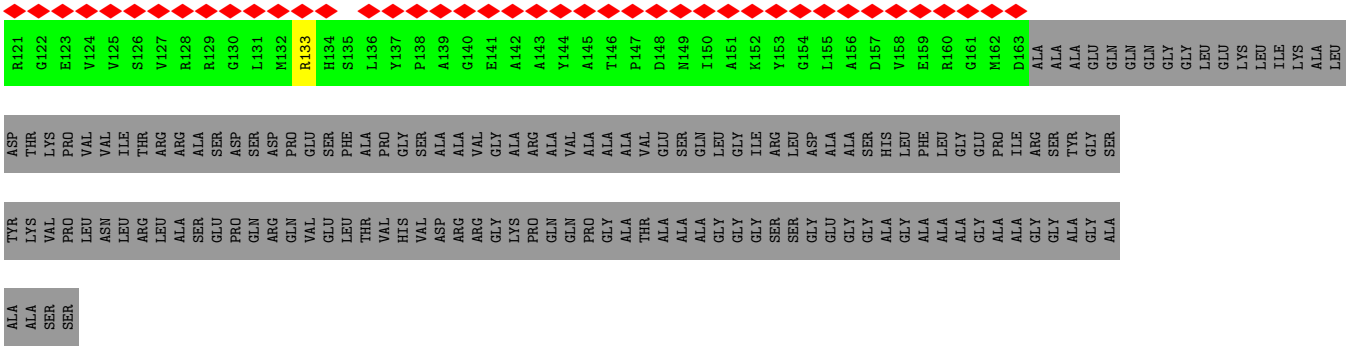


• Molecule 4: uL5m



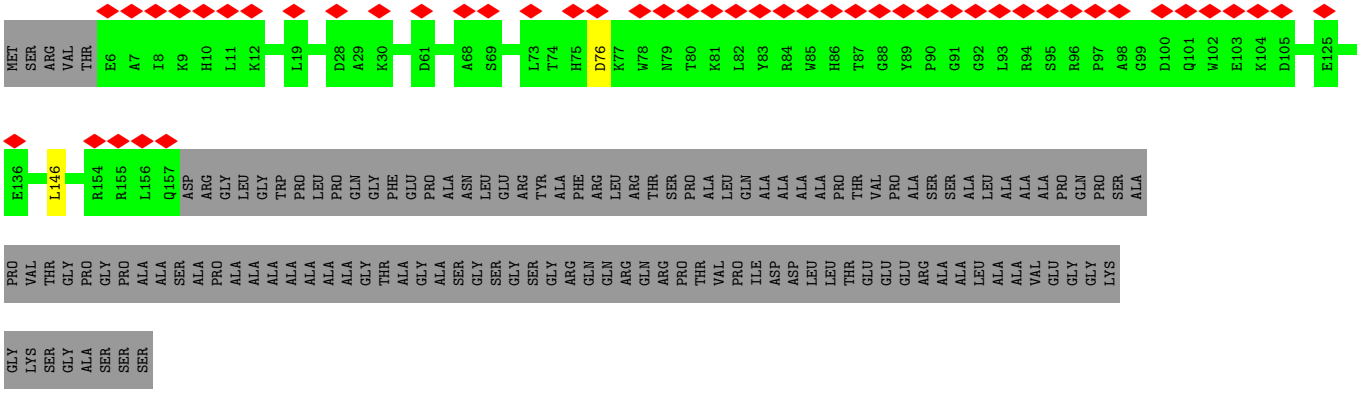
• Molecule 5: 50S ribosomal protein L9, chloroplastic





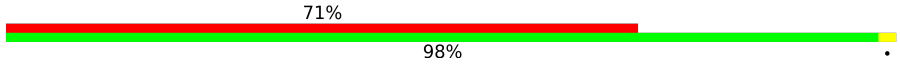
• Molecule 6: Mitochondrial ribosomal protein L13

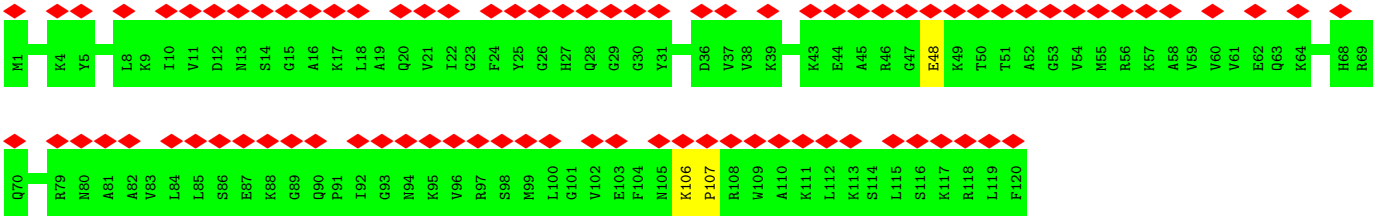
Chain i:



• Molecule 7: uL14m

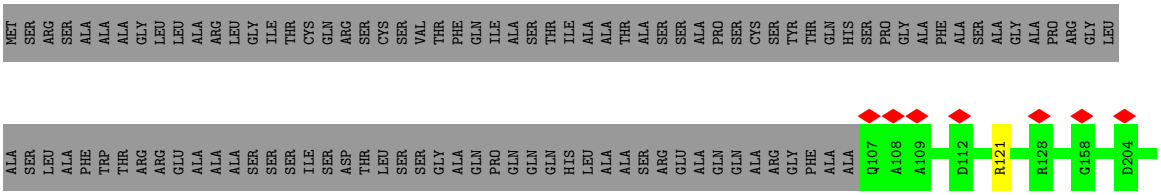
Chain j:

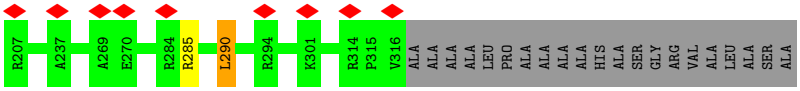




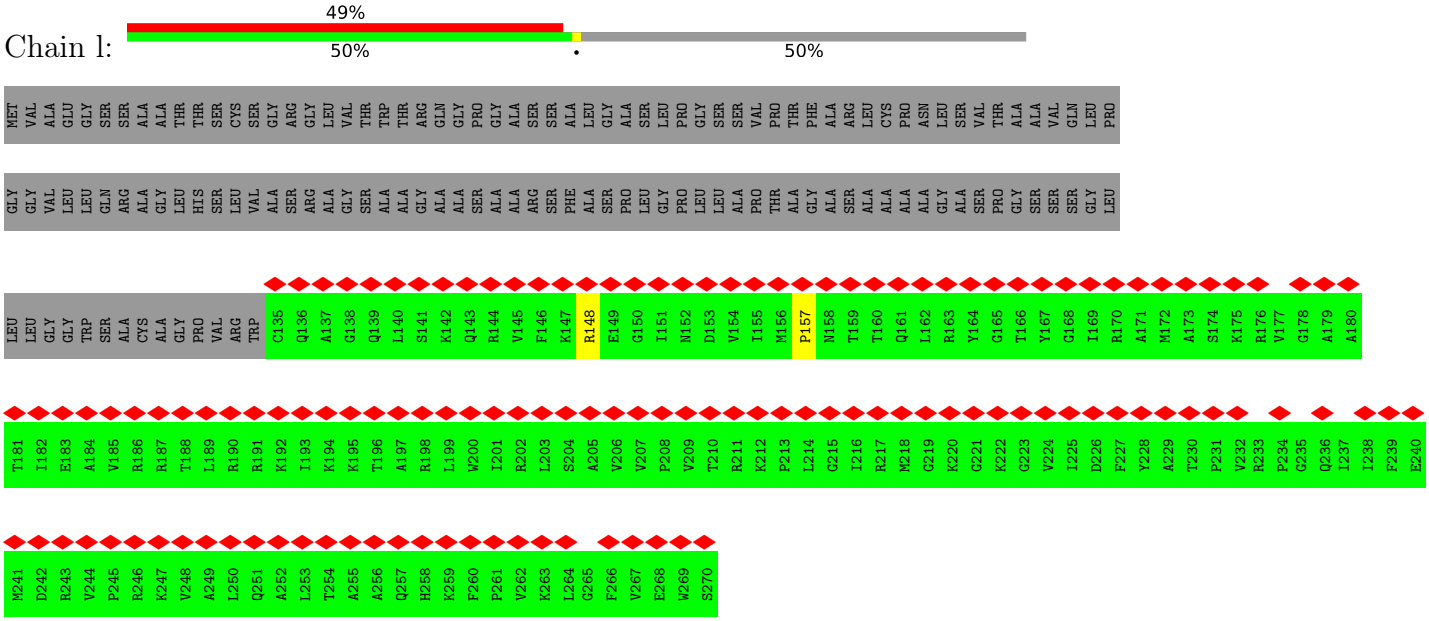
• Molecule 8: Ribosomal_L18e/L15P domain-containing protein

Chain k:

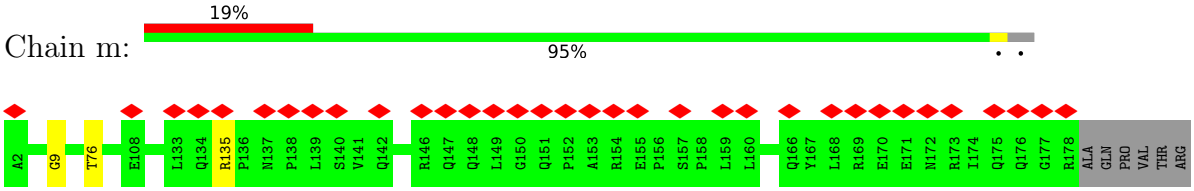




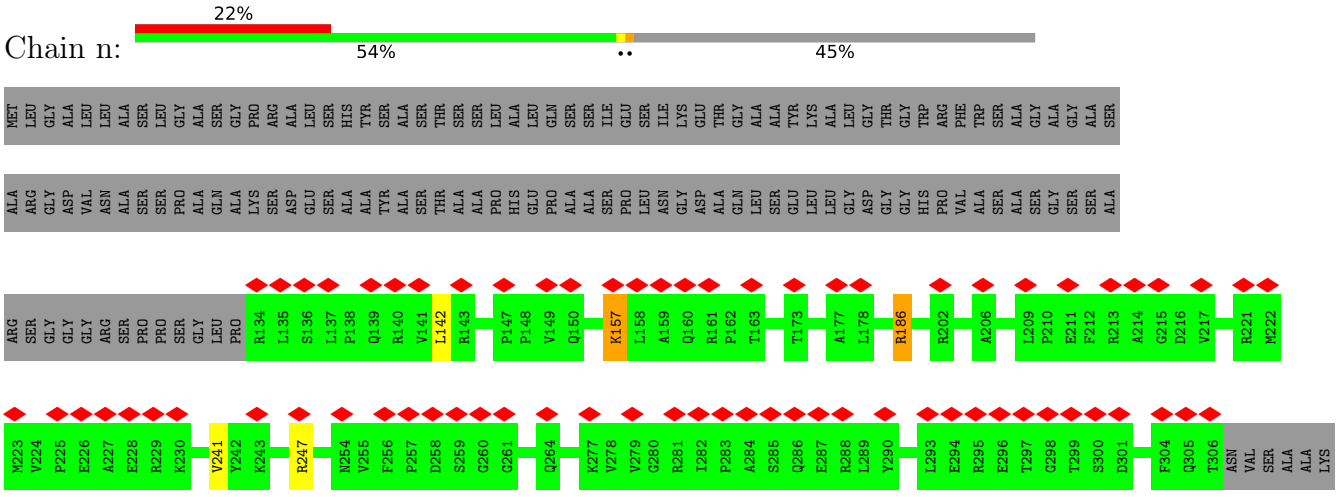
• Molecule 9: Ribosomal_L16 domain-containing protein



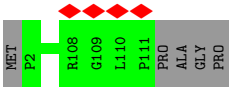
• Molecule 10: Mitochondrial ribosomal protein L17,bL17m



• Molecule 11: Mitochondrial ribosomal protein L19

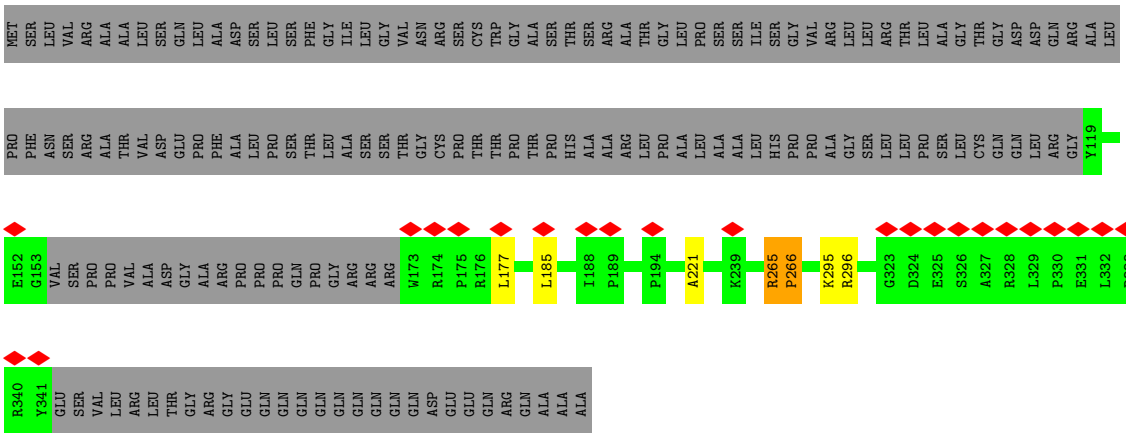


• Molecule 12: 50S ribosomal protein L20



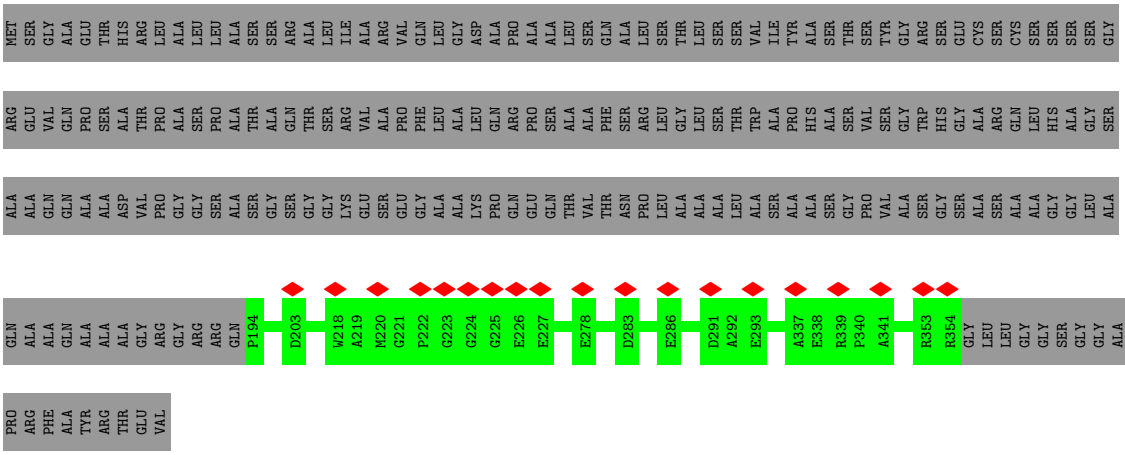
• Molecule 13: bL21m

Chain p:



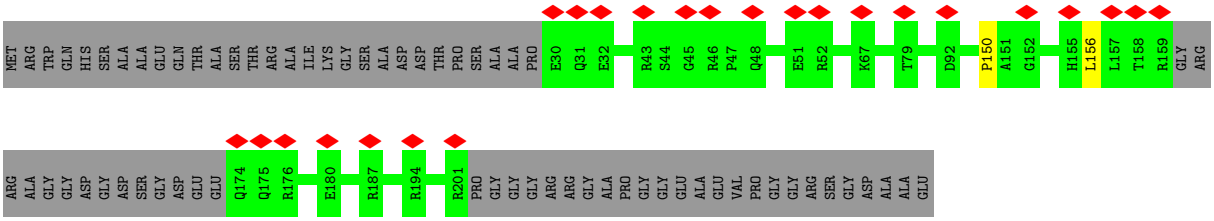
• Molecule 14: uL22m

Chain q:



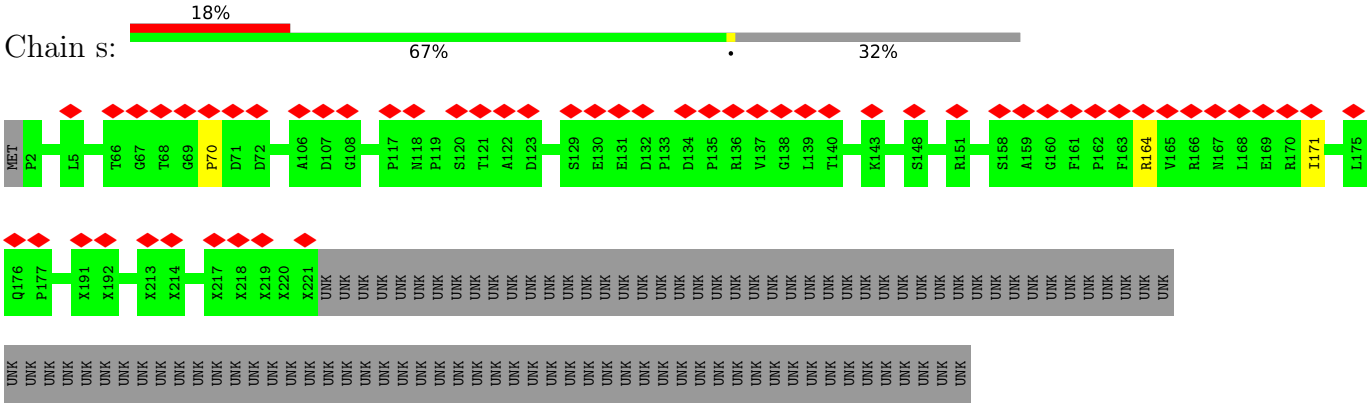
• Molecule 15: Mitochondrial ribosomal protein L23

Chain r:



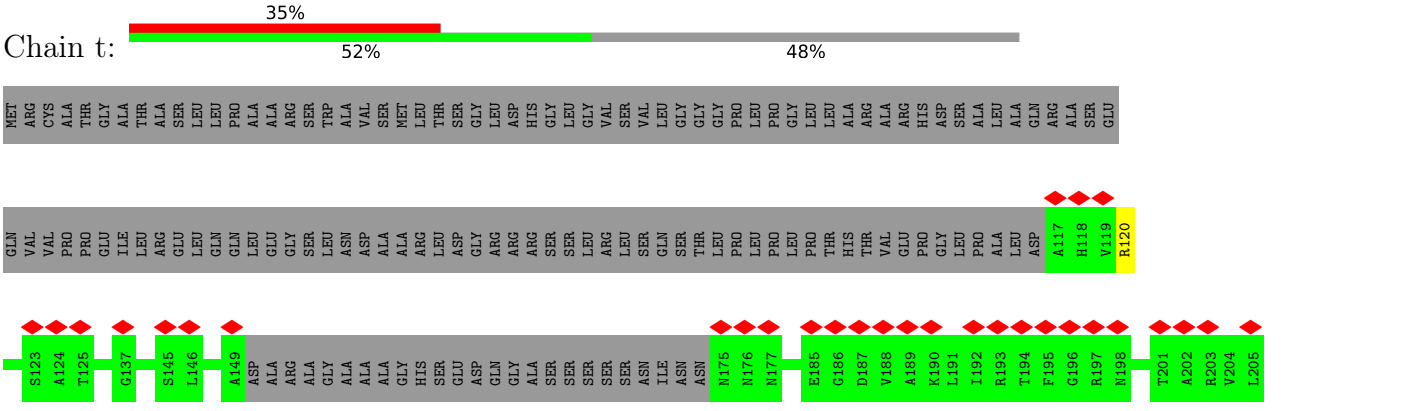
• Molecule 16: KOW domain-containing protein,uL24m

Chain s:



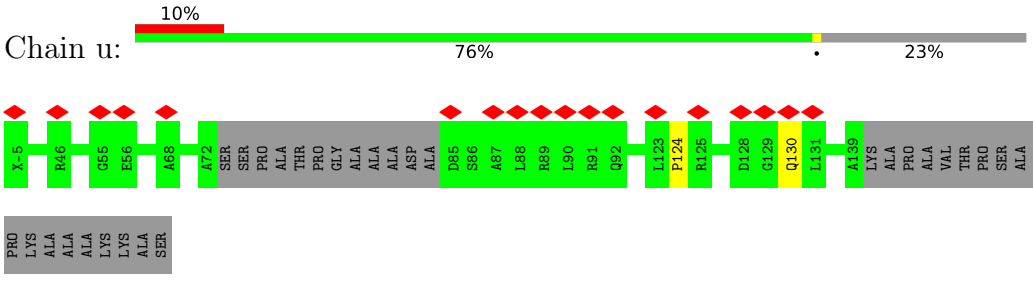
• Molecule 17: Ribosomal_TL5_C domain-containing protein

Chain t:



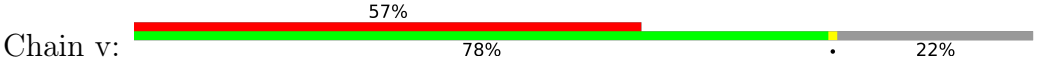
• Molecule 18: bL27m

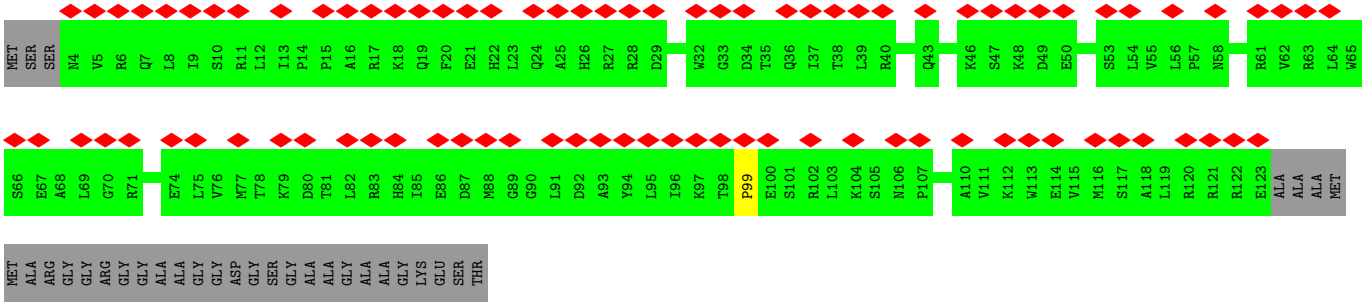
Chain u:



• Molecule 19: bL28m

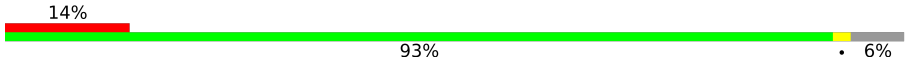
Chain v:

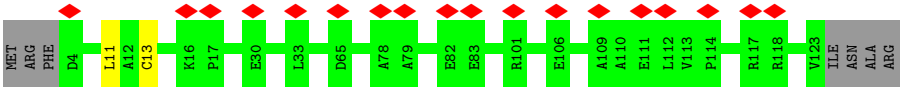




• Molecule 20: uL29m

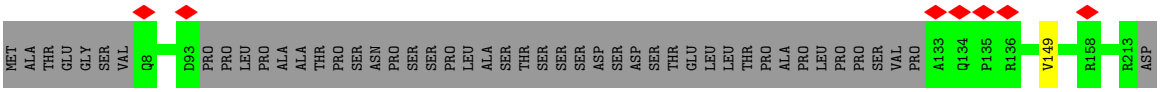
Chain w:





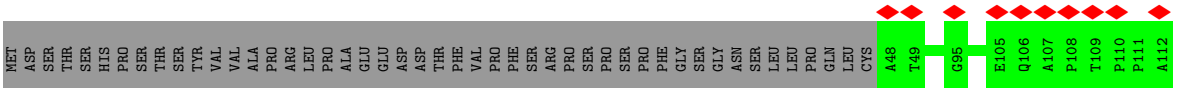
• Molecule 21: Ribosomal_L30 domain-containing protein

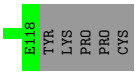
Chain x:



• Molecule 22: bL32m

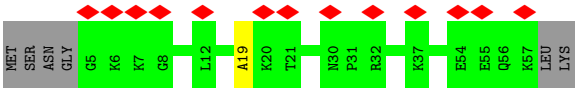
Chain y:





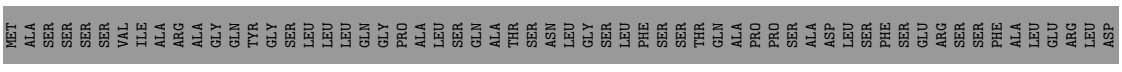
• Molecule 23: Mitochondrial ribosomal protein L33

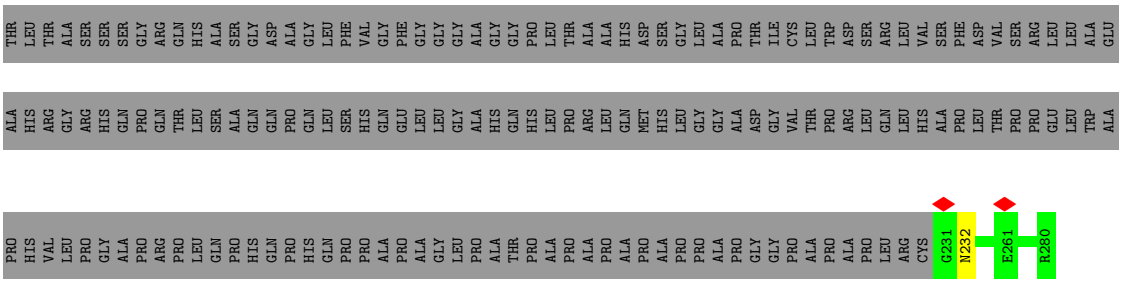
Chain z:



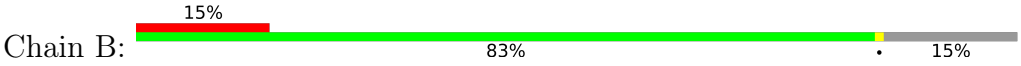
• Molecule 24: bL34m

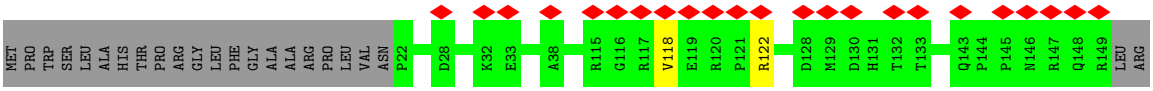
Chain A:



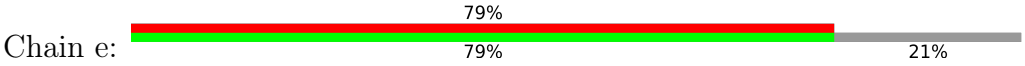


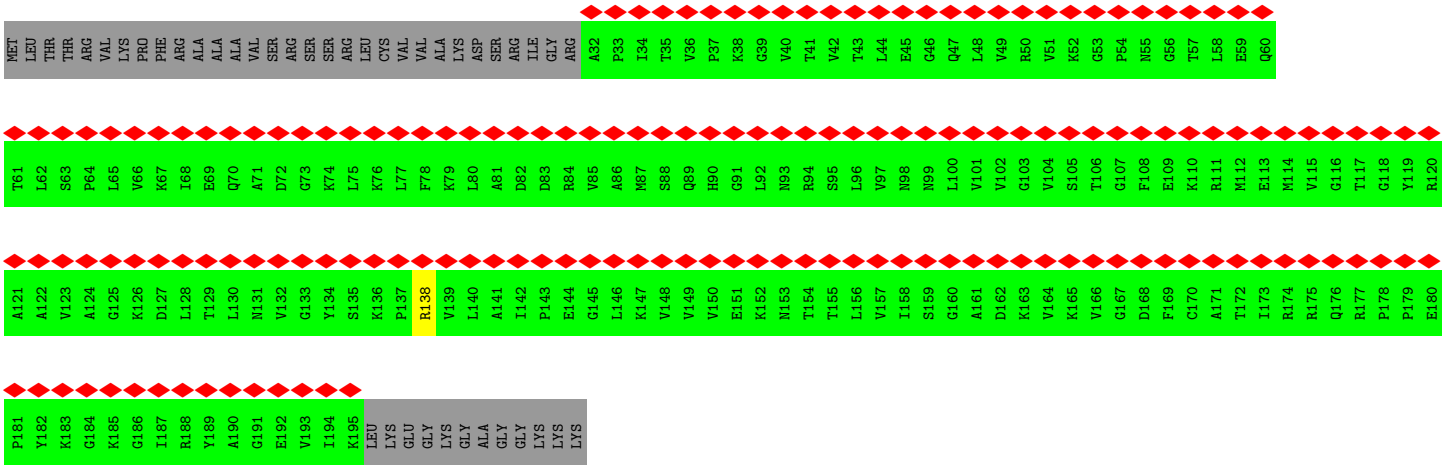
• Molecule 25: bL35m



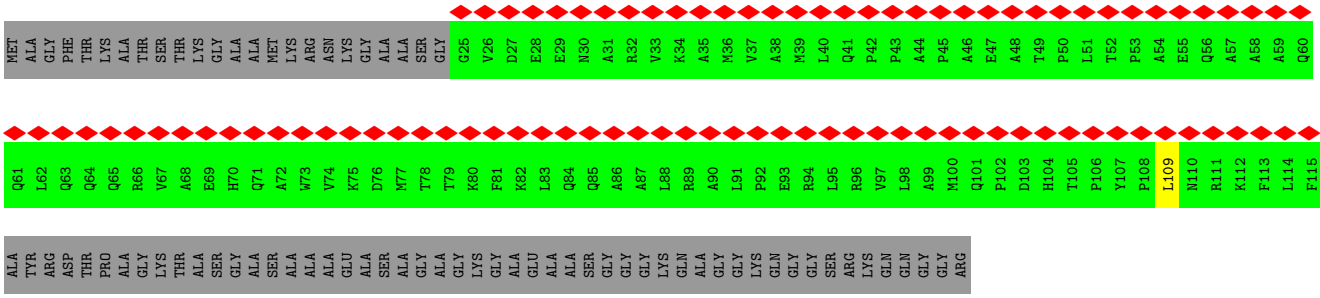


• Molecule 26: Plastid ribosomal protein L6

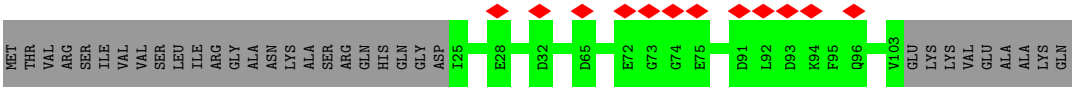




• Molecule 27: mL40

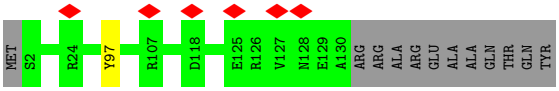


• Molecule 28: mL41



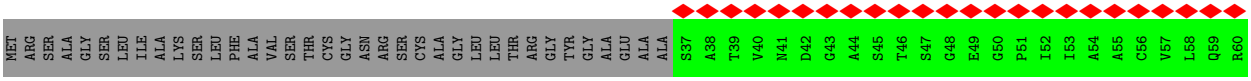
• Molecule 29: mL43

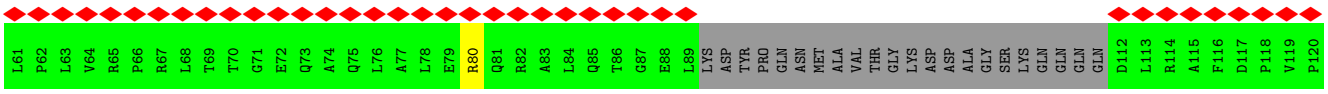
Chain F:

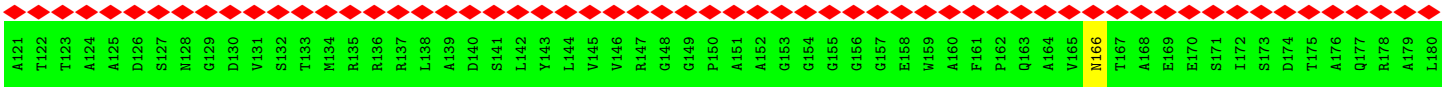


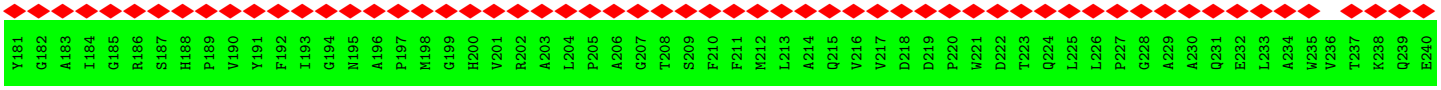
• Molecule 30: Mitochondrial ribosomal protein L17

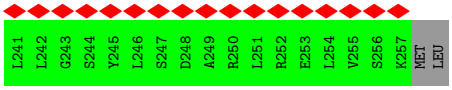
Chain G:





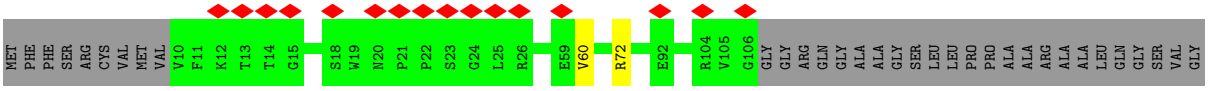






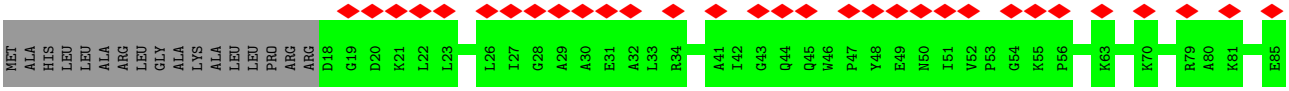
• Molecule 31: mL63/57/60

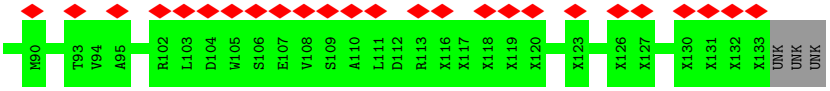
Chain I:



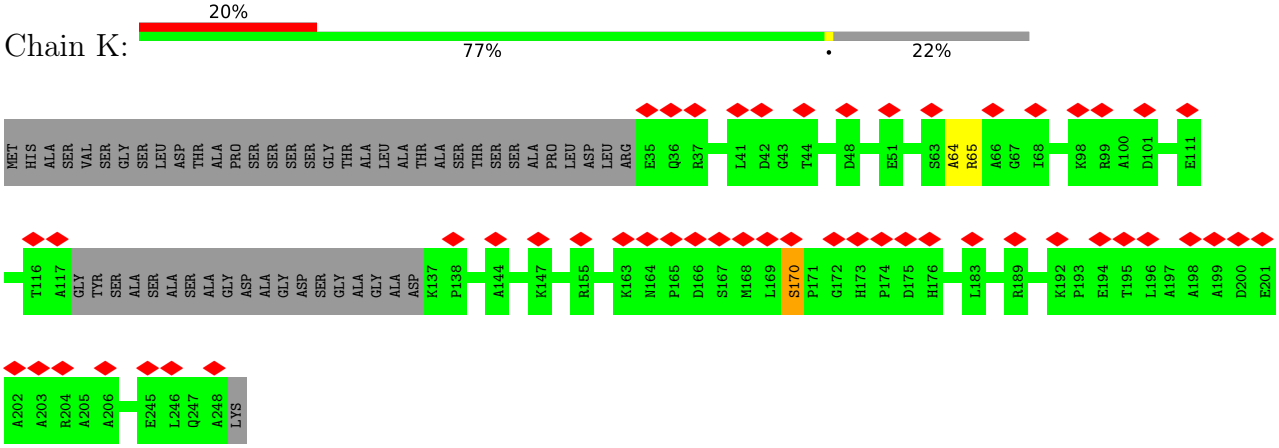
• Molecule 32: mL59/64

Chain J:

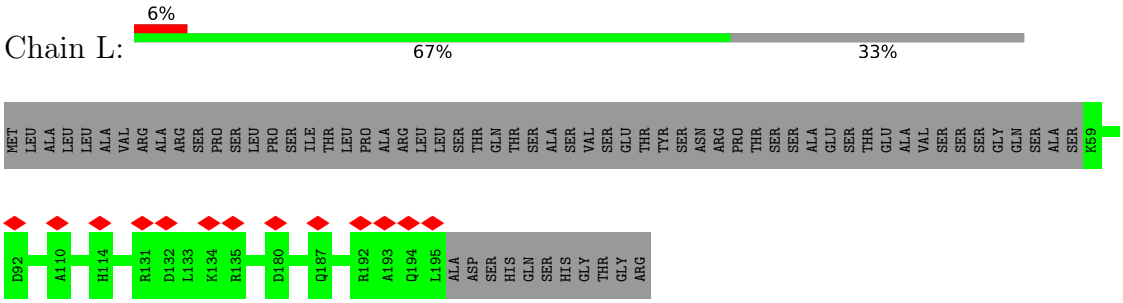




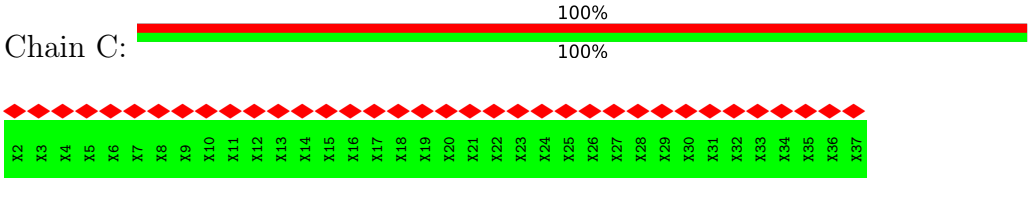
• Molecule 33: mL80



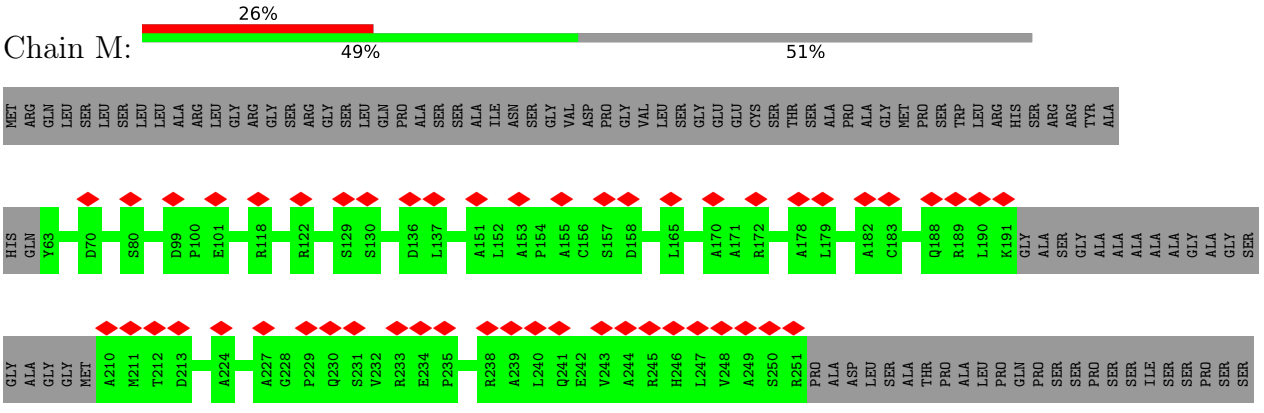
• Molecule 34: mL87

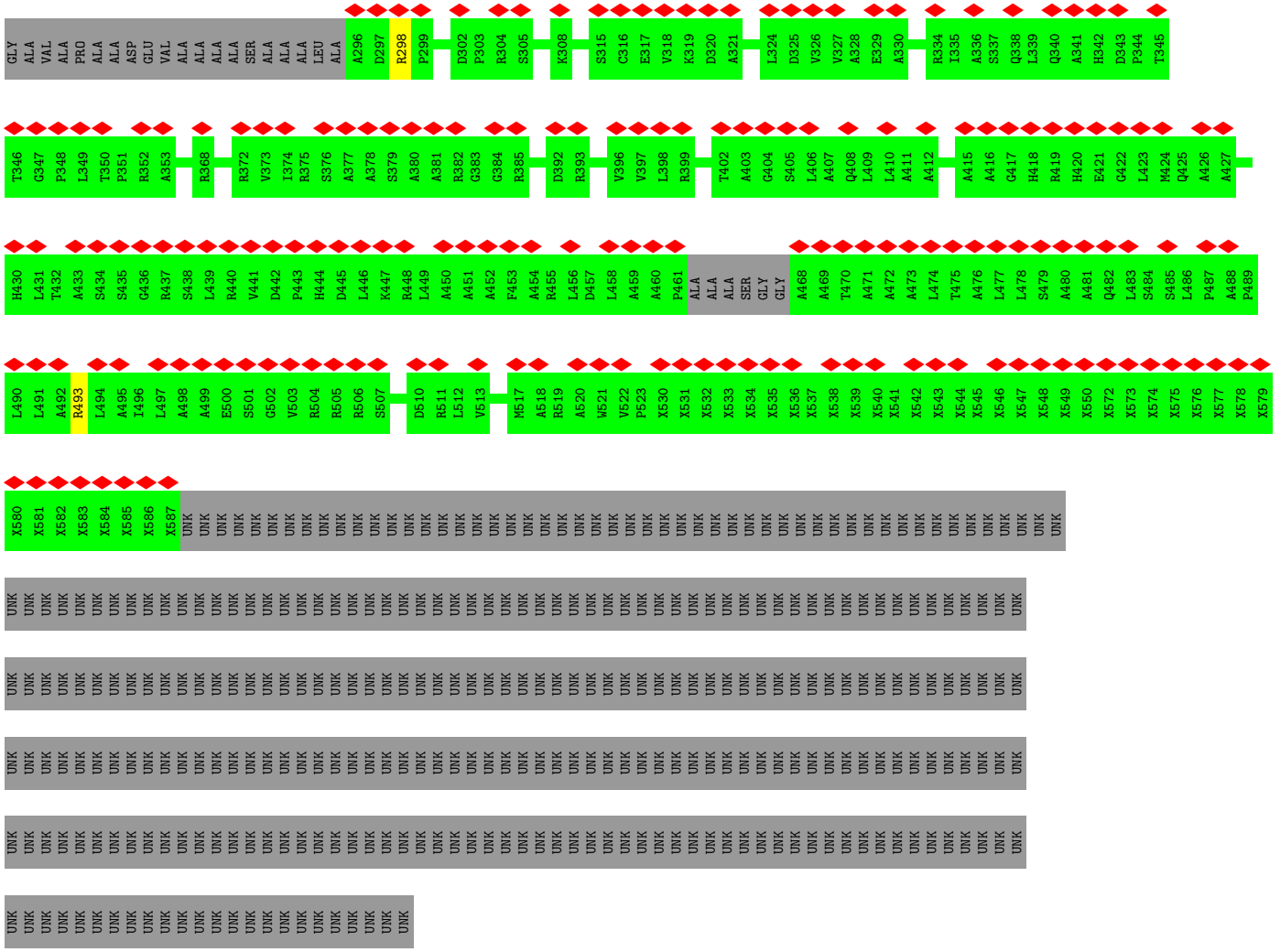


• Molecule 35: bL36m

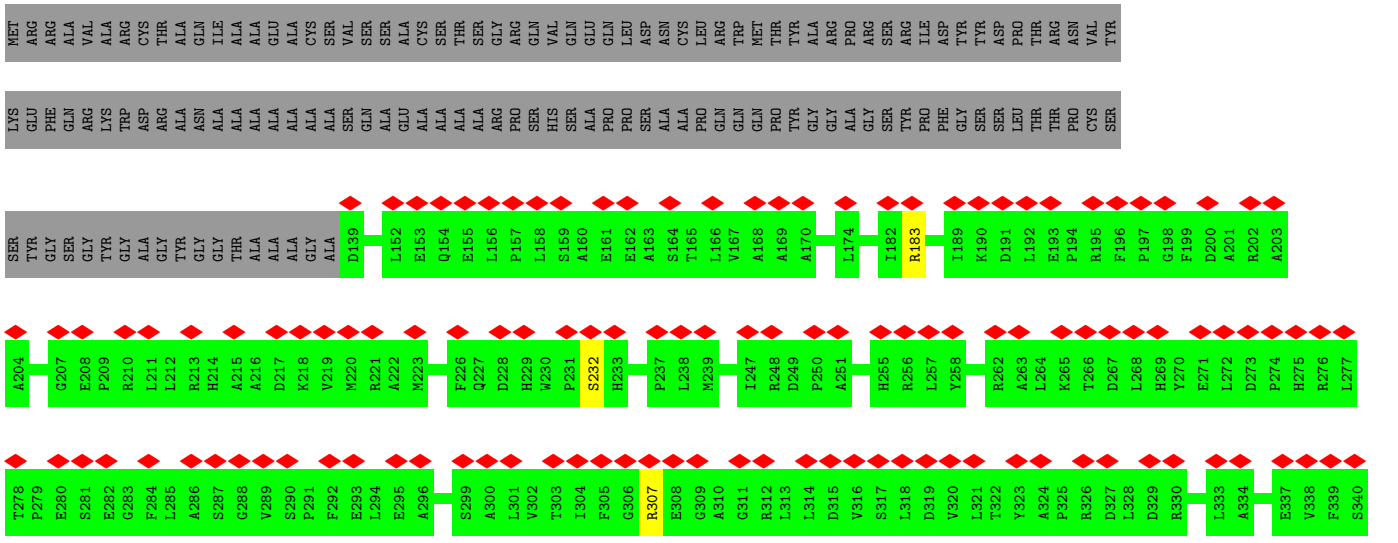


• Molecule 36: mL113





• Molecule 37: mL114



A341 A342 G343 D344 R345 G346 Y347 G348 R349 H350 S351 LEU SER THR P355 E356 G357 A358 A359 A360 A361 A362 A363 D364 R365 G366 Y367 V368 T369 D370 L371 A372 V373 A374 W375 P376 G377 V378 L379 A380 L381 P382 G383 R384 L385 G386 G387 A388 D389 G390 V391 A392 R393 L394 L395 A396 R397 V398 R399 R400

A401 G402 G403 A404 R405 Y406 R407 G408 A409 V410 G411 R412 R413 A414 L415 L416 S417 E418 V419 L420 E421 R422 P423 E424 LEU LEU GLN ALA ALA ALA GLU ALA ALA MET ARG GLY GLU GLU GLU ASP GLU GLU GLU ASP VAL GLU GLY ARG ALA GLU LEU GLU GLY LYS VAL

- Molecule 38: mL115

Chain O: 56% 84% • 15%

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

PHE ARG GLN TRP PRO ARG SER LEU GLN LEU TRP ARG GLY PHE A75 V76 N77 N78 K79 P80 S81 L82 K83 P86 V87 P88 E89 S90 Q91 H92 D93 D94 F95 T96 S97 E98 P99 T100 T101 Y102 A107 A111 A112 K113 K116 E119 D123 T124 Y125 A126 D127 R128 F129 D130

A131 V132 H133 V134 A135 A136 A137 V138 A139 R140 L141 P142 H143 L144 R148 E149 A150 V153 D154 M155 S156 A157 S158 A159 V160 V161 L162 P163 S164 G165 M166 T167 R168 T169 R170 H173 S179 A182 E183 V184 A185 A186 R187 L188 A189 A190 R191 V192 D193 A194 M195 L196 P197 Q198 H199

V200 A201 H202 F203 F204 P205 R206 Q207 A208 A209 I212 G216 E217 L218 R219 R220 H221 G222 V223 I224 E225 R226 M227 D228 S229 L230 P231 Q232 V233 L234 M235 S236 V237 T238 R239 G240 N241 L242 Q243 P244 L245 R246 V247 H248 A249 A250 G251 V252 D253 F254 A255 Q256 L257 L258 H259 A262 K263

L264 G265 H266 N267 D268 E269 P270 L271 L272 D273 A274 L275 L278 V279 T280 E281 R282 L283 G284 S285 M286 Q287 Q288 R289 E290 L298 A299 R302 R303 A304 T305 P306 E307 L308 L309 D310 E311 Q314 Q315 L316 L317 S318 T319 S320 T321 A322 F323 L324 L325 A328 C329 A330 T339

L342 A343 R344 L345 S346 P347 GLY GLY GLU GLY GLY ALA ARG VAL SER R357 R358 R359 A360 R361 V362 A363 A364 A365 R366 V367 K368 L369 Q380 A381 L382 S404 Q405 A408 D412 L415 L418 P419 N420 C421 S422 D423 A427 E431 D445 A449 G450 I451 L452 A453

E454 T459 E460 G472 A475 R476 R477 R480 D481 A489 L492 V493 R494 R495 L496 A497 R498 V499 E500 R501 L502 D503 T504 V505 A506 L507 A508 L512 G513 A514 F515 A516 Y517 D518 D519 Q520 A521 V522 L523 A524 Q525 V526 A527 A528 R529 T530 E531 Q532 L533 L534 Q535 T536 S537

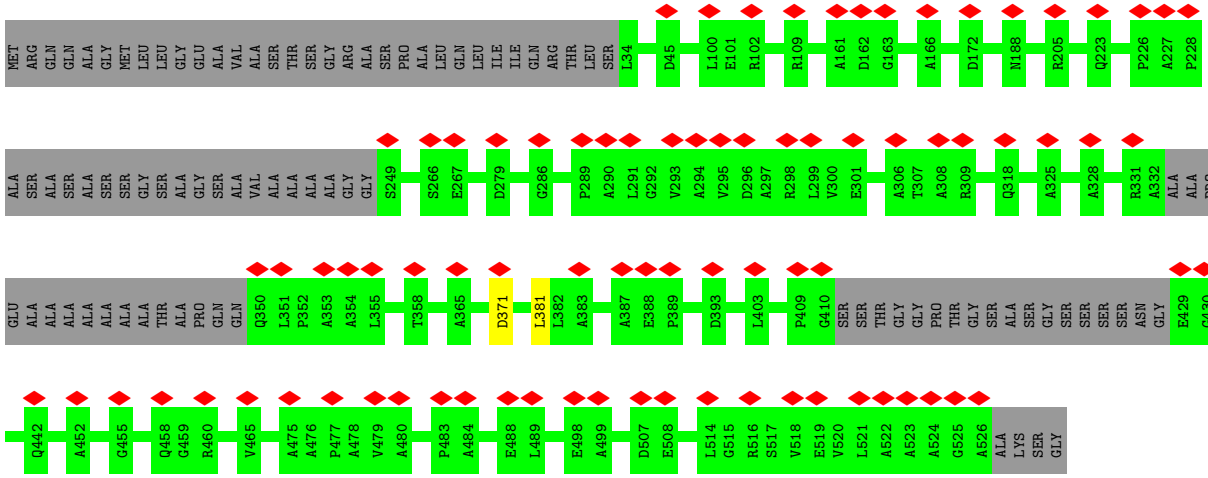
T538 T539 G540 L541 E542 Q543 L544 Q545 A546 V547 L548 R549 C550 L551 D552 A553 G554 G555 C556 S557 Y558 F559 Q560 L561 A562 V563 A564 A565 A566 R567 M568 L569 D570 D571 R572 L573 R574 A575 G576 A577 C578 R579 S580 A581 P582 L583 A584 V585 E586 V587 L588 Y589 Y590 S591 A592 R593 Q594 G595 V596 X600

X601 X602 X603 X604 X605 X606 X607 X608 X609 X610 X611 X612 X613 X614 X615 X616 X617 X618 X619 X620 X621 X622 X623 X624 X625 X626 X627 X628 X629 X630 X631 X632 X633 X634 X635 X636 X637 X638 X639 X640 X641 X642 X643 X644 X645 X646 X647 X648 X649 X650 X651 X652 X653 X654 X655 X656 X657 X658 X659 X660

X661 X662 X663 X664 X665 X666 X667 X668 X669 X670 UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK

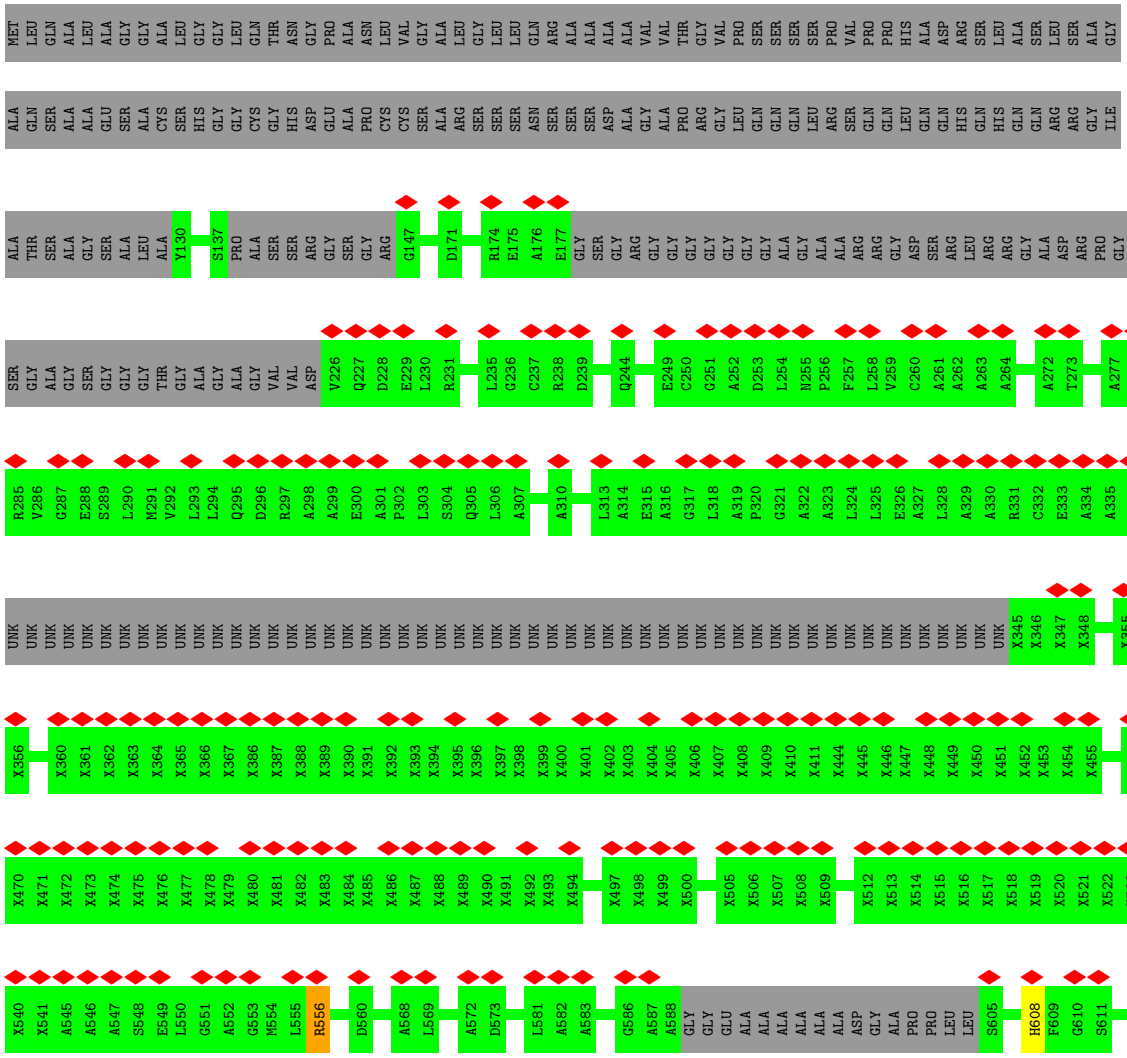
- Molecule 39: mL116

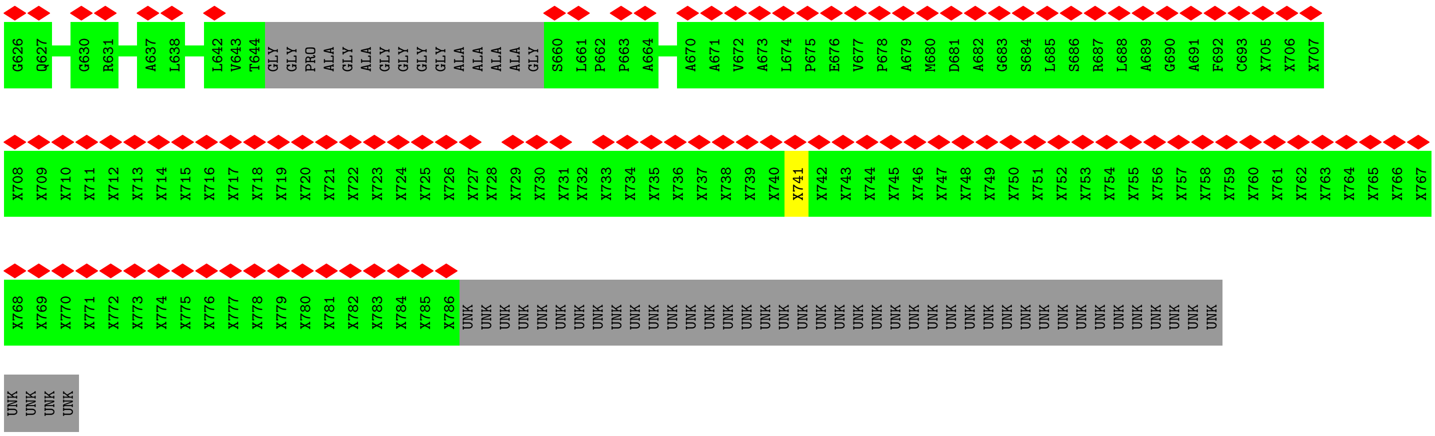
Chain P: 16% 82% 17%



- Molecule 40: mL117

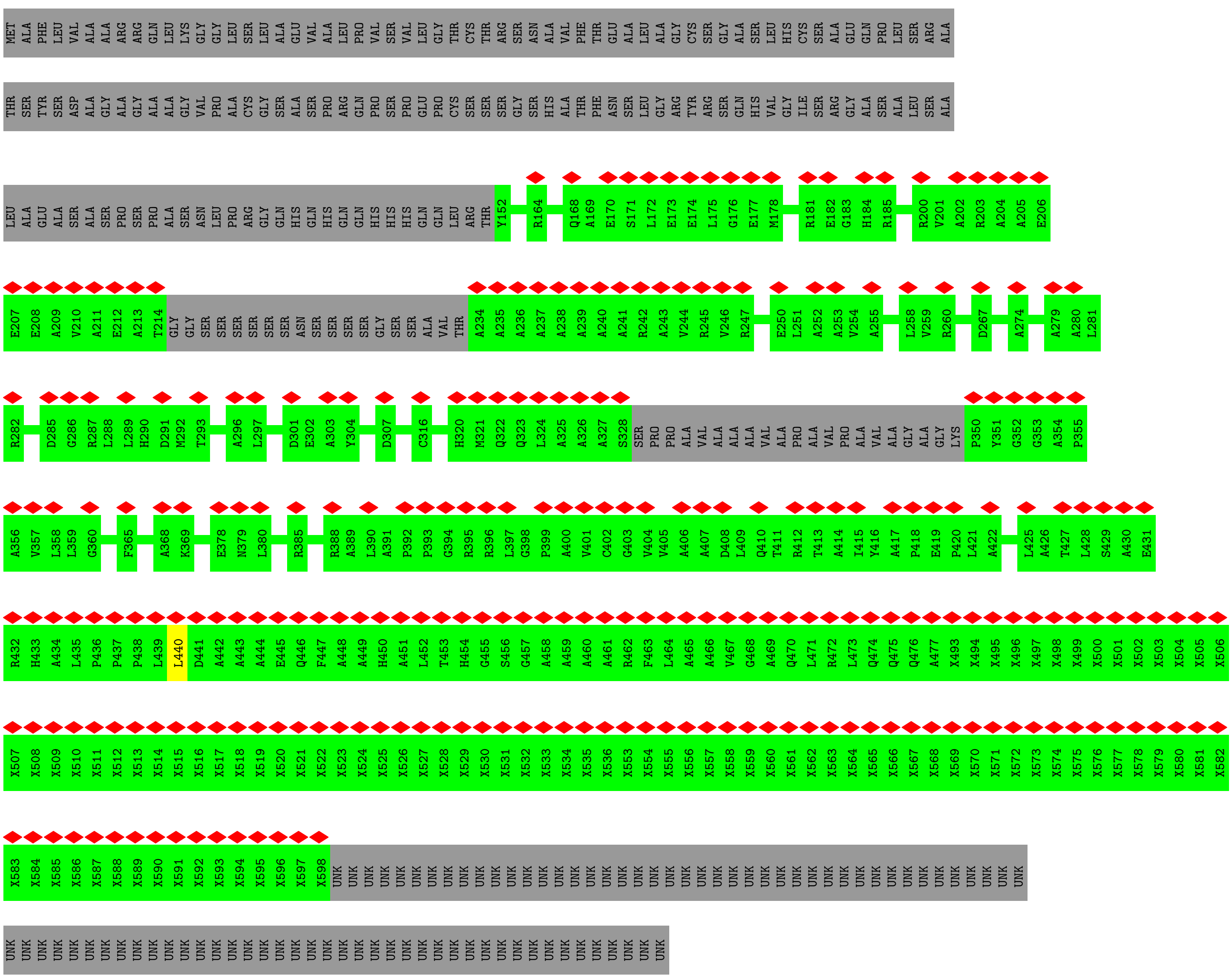
Chain Q:





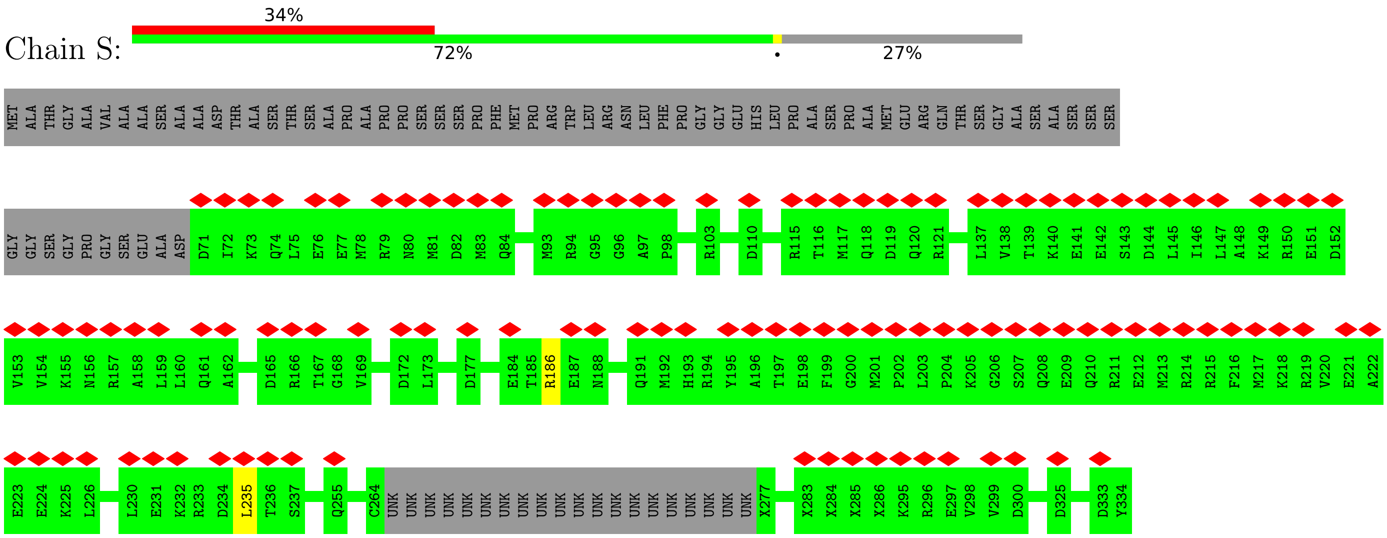
- Molecule 41: mL118

Chain R:



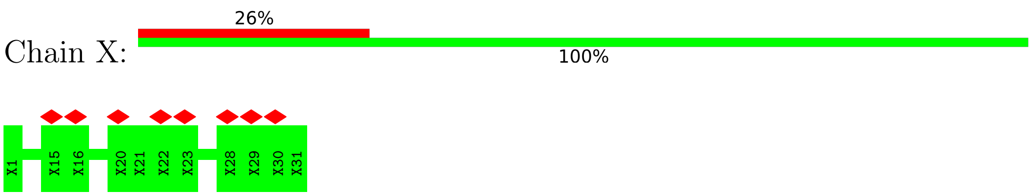
- Molecule 42: mL119

Chain S:



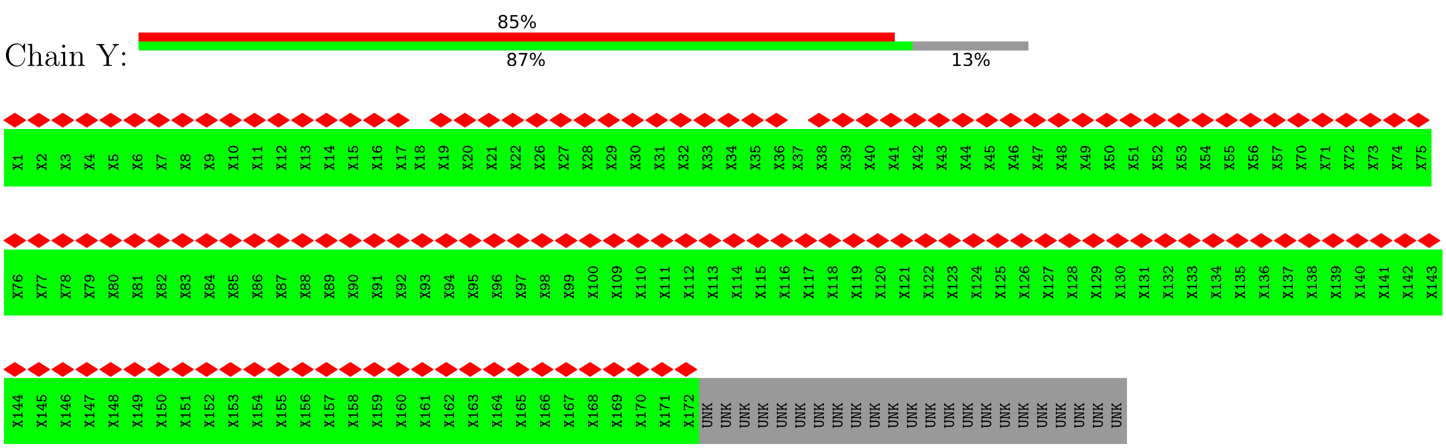
- Molecule 43: Unk1

Chain X:



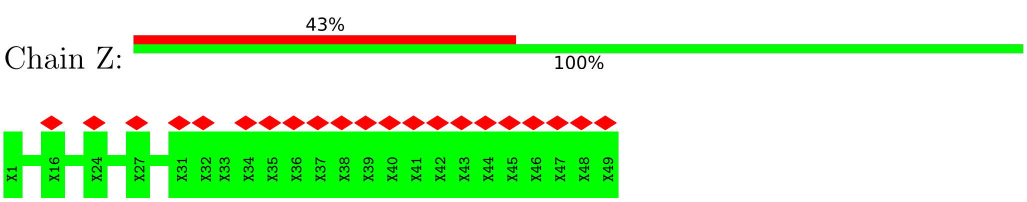
- Molecule 44: PPR*

Chain Y:



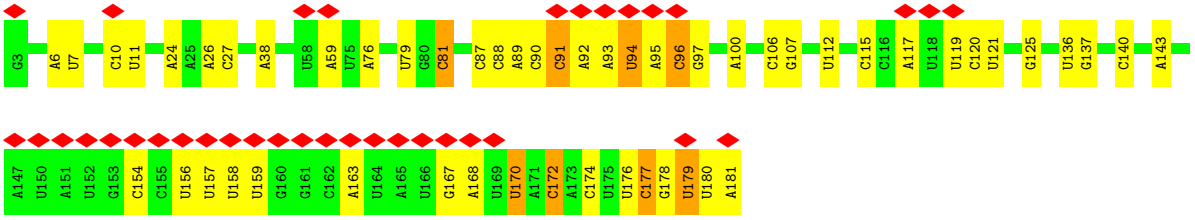
- Molecule 45: Unk2

Chain Z:



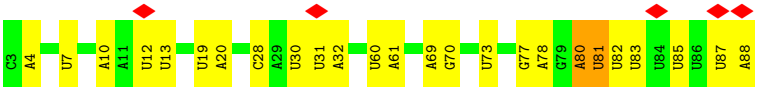
- Molecule 46: L1 rRNA

Chain 1:



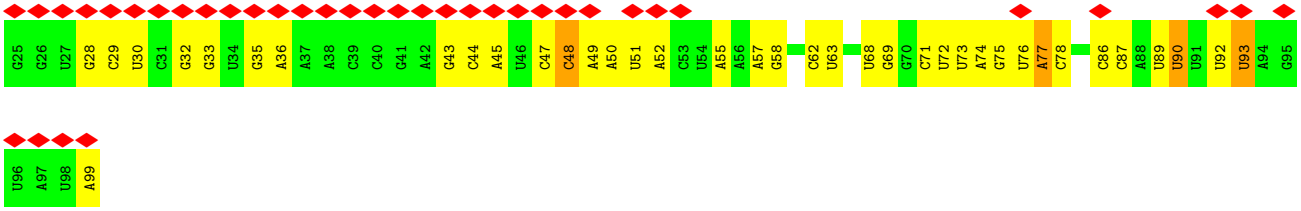
• Molecule 47: L2a rRNA

Chain 2:



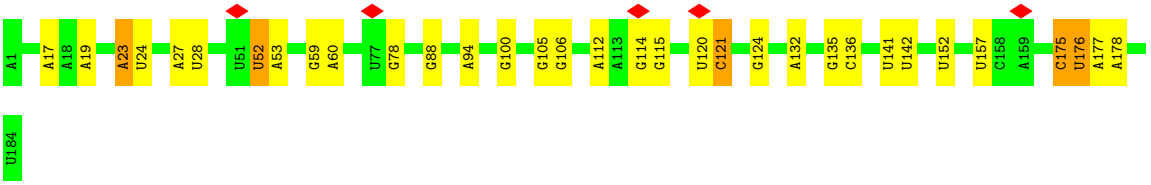
• Molecule 48: L3a rRNA (5S)

Chain 0:



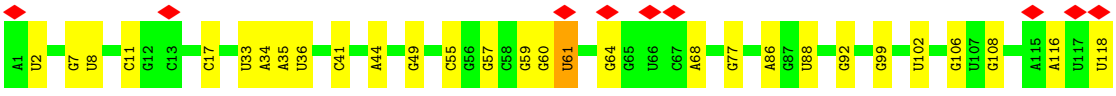
• Molecule 49: L3b rRNA

Chain 3:



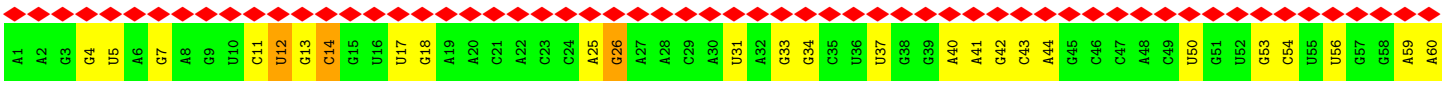
• Molecule 50: L4 rRNA

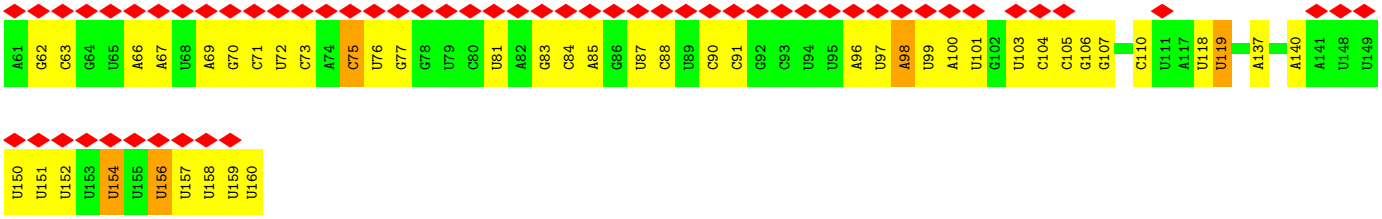
Chain 4:



• Molecule 51: L5 rRNA

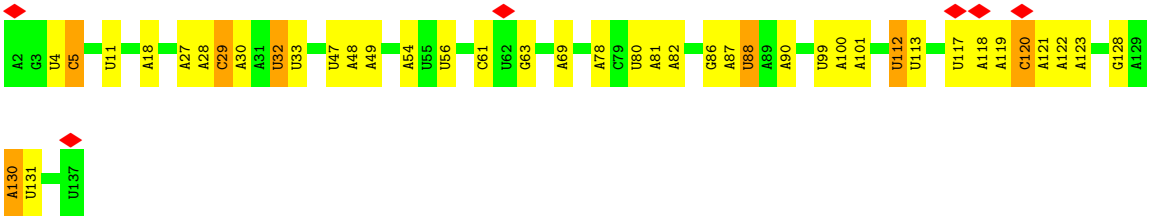
Chain 5:





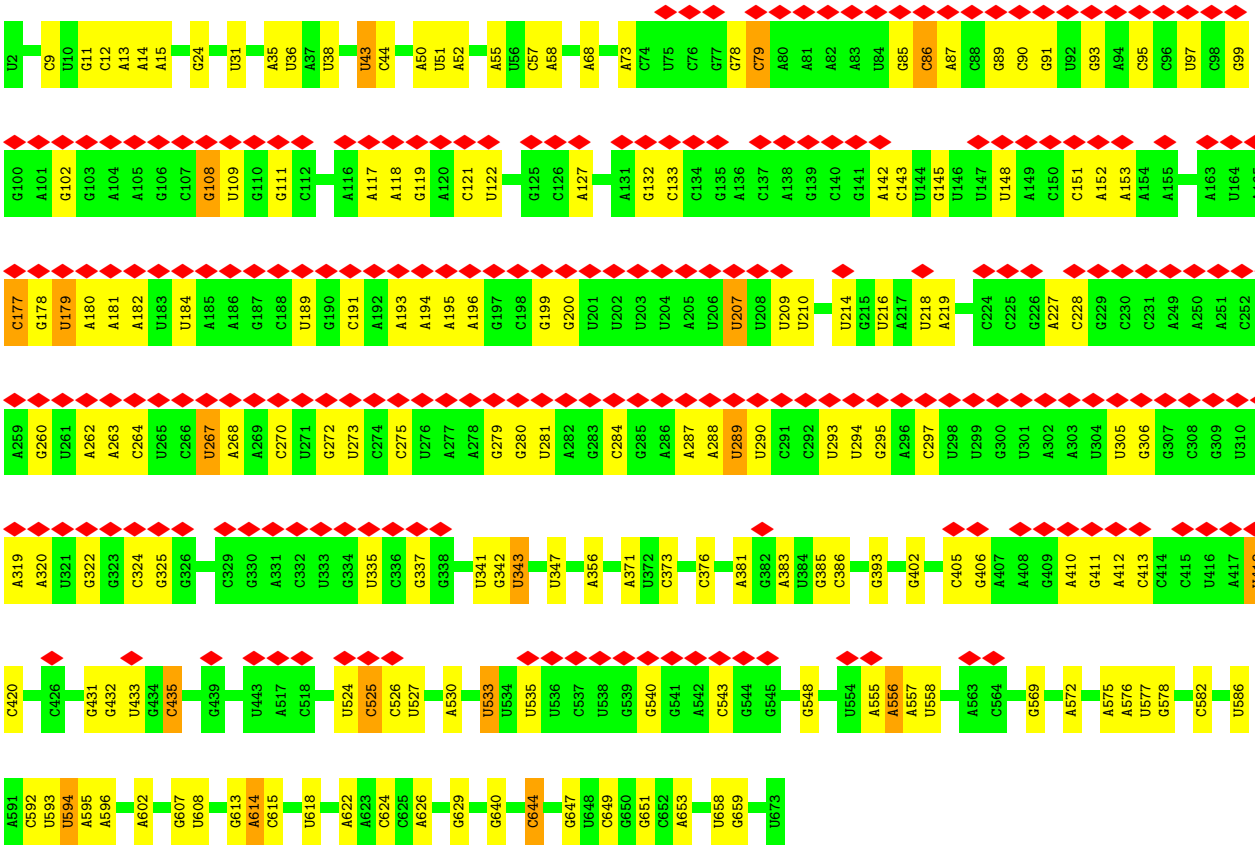
• Molecule 52: L6 rRNA

Chain 6:



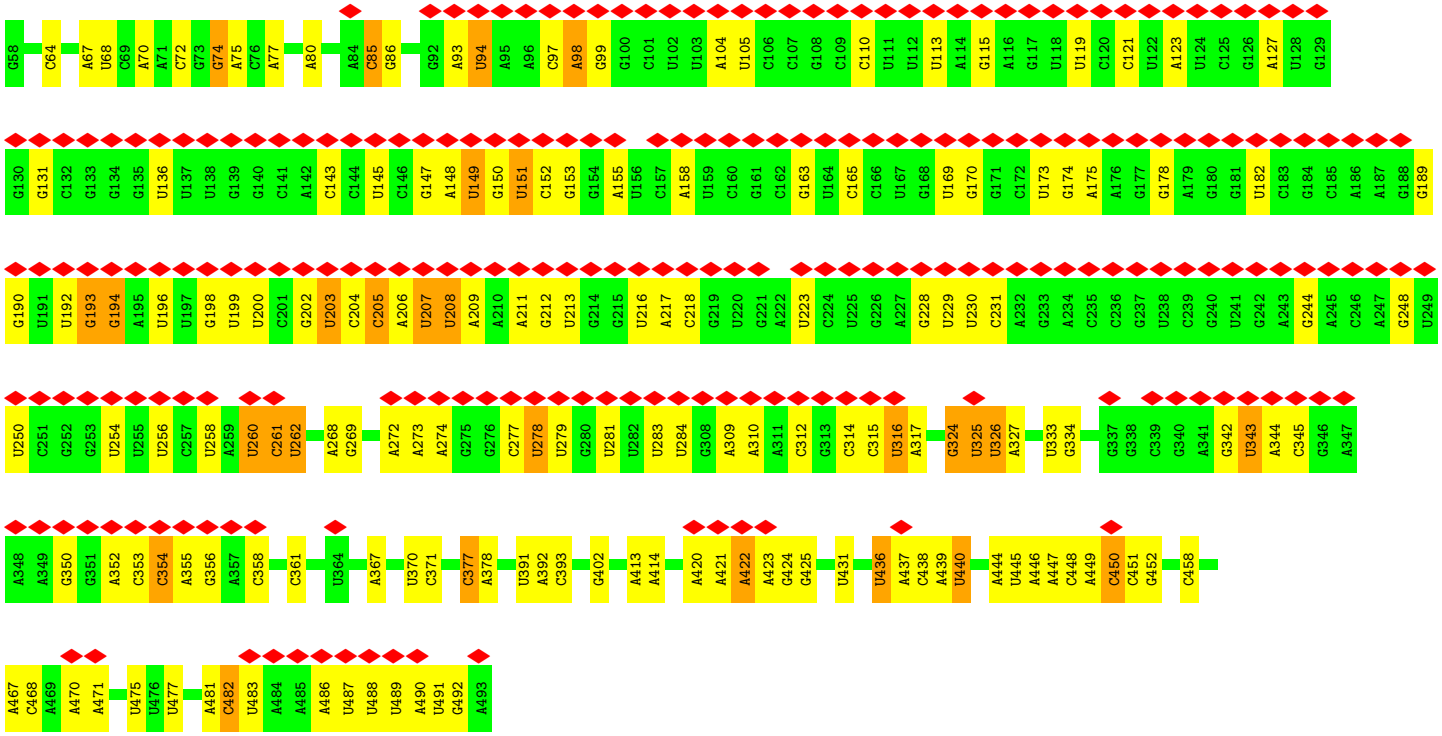
• Molecule 53: L7 rRNA

Chain 7:



• Molecule 54: L8 rRNA

Chain 8:


G58 C64 A67 U68 C69 A70 A71 C72 G73 G74 A75 C76 A77 A80 A84 C85 G86 G92 A93 U94 A95 A96 C97 A98 G99 G100 C101 U102 U103 A104 U105 C106 C107 G108 C109 C110 U111 U112 U113 A114 G115 A116 G117 U118 U119 C120 C121 U122 A123 U124 C125 G126 A127 U128 G129
G130 G131 C132 G133 G134 G135 U136 U137 U138 G139 G140 C141 A142 C143 C144 U145 C146 G147 A148 U149 G150 U151 C152 G153 G154 A155 U156 C157 A158 U159 C160 G161 C162 G163 U164 C165 C166 U167 G168 U169 G170 G171 C172 U173 G174 A175 A176 G177 G178 A179 G180 G181 U182 C183 G184 C185 A186 A187 G188 G189
G190 U191 U192 G193 G194 A195 U196 U197 G198 U199 U200 C201 G202 U203 C204 C205 A206 U207 U208 A209 A210 A211 G212 U213 G214 G215 U216 A217 C218 G219 U220 G221 A222 U223 C224 U225 G226 A227 G228 U229 U230 C231 A232 G233 A234 C235 C236 G237 U238 C239 G240 U241 G242 A243 G244 A245 C246 A247 G248 U249
U250 C251 G252 G253 U254 U255 U256 C257 U258 A259 U260 C261 U262 A268 G269 A272 A273 A274 G275 G276 C277 U278 U279 G280 U281 U282 U283 U284 G308 A309 A310 A311 C312 G313 C314 C315 U316 A317 G324 U325 U326 A327 U333 G334 G337 G338 C339 G340 A341 G342 U343 A344 C345 G346 A347
A348 A349 G350 G351 A352 C353 C354 A355 G356 A357 C358 C361 U364 A367 U370 C371 C377 A378 U391 A392 C393 G402 A413 A414 A420 A421 A422 A423 G424 G425 U431 U436 A437 C438 A439 U440 A444 U445 A446 A447 C448 A449 C450 C451 G452 C458
A467 C468 A469 A470 A471 U475 U476 U477 A481 C482 U483 A484 A485 A486 U487 U488 U489 A490 U491 G492 A493

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101291	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.092	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	432.0, 432.0, 432.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9, 0.9, 0.9	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: MG, FES, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	a	0.61	0/2039	0.73	1/2766 (0.0%)
2	b	0.59	0/2397	0.75	1/3264 (0.0%)
3	c	0.60	0/2492	0.76	1/3374 (0.0%)
4	d	0.64	0/1410	0.78	0/1918
5	f	0.63	0/471	0.82	0/633
6	i	0.32	0/1266	0.65	2/1711 (0.1%)
7	j	0.63	0/959	0.77	1/1284 (0.1%)
8	k	0.58	0/1655	0.76	0/2237
9	l	0.60	0/1098	0.71	0/1474
10	m	0.60	0/1488	0.79	1/2009 (0.0%)
11	n	0.60	0/1440	0.87	4/1954 (0.2%)
12	o	0.36	0/905	0.64	0/1211
13	p	0.58	0/1640	0.83	2/2231 (0.1%)
14	q	0.38	0/1300	0.67	0/1754
15	r	0.36	0/1370	0.69	1/1854 (0.1%)
16	s	0.61	0/1442	0.76	0/1958
17	t	0.63	0/1517	0.79	0/2057
18	u	0.59	0/994	0.75	1/1342 (0.1%)
19	v	0.30	0/1017	0.68	0/1372
20	w	0.58	0/992	0.71	0/1339
21	x	0.39	1/1434 (0.1%)	0.65	0/1933
22	y	0.63	0/555	0.81	0/748
23	z	0.35	0/449	0.78	0/600
24	A	0.34	0/433	0.73	0/575
25	B	0.57	0/1094	0.74	0/1481
26	e	0.64	0/1254	0.75	0/1692
27	D	0.29	0/757	0.69	1/1030 (0.1%)
28	E	0.57	0/650	0.71	0/877
29	F	0.36	0/1058	0.68	0/1428
30	G	0.60	0/1509	0.68	0/2054
31	I	0.33	0/795	0.73	2/1069 (0.2%)
32	J	0.60	0/769	0.78	0/1039

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	K	0.58	0/1615	0.72	0/2192
34	L	0.35	0/1205	0.63	0/1630
36	M	0.58	0/3027	0.70	0/4123
37	N	0.64	1/2163 (0.0%)	0.77	2/2937 (0.1%)
38	O	0.31	0/3974	0.71	2/5407 (0.0%)
39	P	0.31	0/3195	0.73	3/4362 (0.1%)
40	Q	3.55	6/1969 (0.3%)	0.74	2/2668 (0.1%)
41	R	0.31	0/2184	0.72	1/2967 (0.0%)
42	S	0.35	0/1947	0.74	1/2603 (0.0%)
46	1	0.59	0/3844	1.29	61/5979 (1.0%)
47	2	0.60	0/2034	0.99	4/3164 (0.1%)
48	0	0.44	0/1779	1.28	18/2768 (0.7%)
49	3	0.58	0/4401	1.10	17/6859 (0.2%)
50	4	0.64	0/2846	1.16	24/4437 (0.5%)
51	5	0.44	0/3522	1.24	36/5477 (0.7%)
52	6	0.66	0/3266	1.16	29/5088 (0.6%)
53	7	0.45	0/13815	1.12	110/21523 (0.5%)
54	8	0.43	0/9830	1.21	117/15312 (0.8%)
All	All	0.70	8/105265 (0.0%)	0.96	445/151764 (0.3%)

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
8	k	0	1
13	p	0	1
19	v	0	1
23	z	0	1
29	F	0	1
33	K	0	2
38	O	0	2
40	Q	0	2
42	S	0	1
All	All	0	12

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	Q	556	ARG	CZ-NH2	151.26	3.29	1.33
40	Q	608	HIS	CG-CD2	22.03	1.73	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	Q	608	HIS	CG-ND1	20.18	1.83	1.38
40	Q	608	HIS	CD2-NE2	18.87	1.81	1.42
40	Q	608	HIS	CE1-NE2	15.09	1.67	1.32

The worst 5 of 445 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	8	450	C	N1-C2-O2	13.02	126.71	118.90
40	Q	556	ARG	NE-CZ-NH1	-12.68	113.96	120.30
54	8	450	C	C2-N1-C1'	12.01	132.01	118.80
54	8	325	U	C2-N1-C1'	11.43	131.42	117.70
49	3	175	C	N1-C2-O2	11.37	125.72	118.90

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	F	97	TYR	Peptide
8	k	290	LEU	Mainchain
13	p	265	ARG	Mainchain
19	v	99	PRO	Peptide
23	z	19	ALA	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
1	a	259/383 (68%)	251 (97%)	8 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	302/417 (72%)	284 (94%)	16 (5%)	2 (1%)	22	60
3	c	301/427 (70%)	288 (96%)	11 (4%)	2 (1%)	22	60
4	d	182/216 (84%)	168 (92%)	14 (8%)	0	100	100
5	f	58/304 (19%)	54 (93%)	4 (7%)	0	100	100
6	i	150/277 (54%)	139 (93%)	11 (7%)	0	100	100
7	j	118/120 (98%)	109 (92%)	8 (7%)	1 (1%)	19	57
8	k	208/337 (62%)	198 (95%)	8 (4%)	2 (1%)	15	53
9	l	134/270 (50%)	127 (95%)	6 (4%)	1 (1%)	22	60
10	m	175/183 (96%)	169 (97%)	5 (3%)	1 (1%)	25	64
11	n	171/312 (55%)	163 (95%)	6 (4%)	2 (1%)	13	48
12	o	108/115 (94%)	107 (99%)	1 (1%)	0	100	100
13	p	200/370 (54%)	187 (94%)	11 (6%)	2 (1%)	15	53
14	q	159/377 (42%)	150 (94%)	9 (6%)	0	100	100
15	r	154/226 (68%)	142 (92%)	11 (7%)	1 (1%)	25	64
16	s	177/309 (57%)	159 (90%)	16 (9%)	2 (1%)	14	50
17	t	186/366 (51%)	172 (92%)	14 (8%)	0	100	100
18	u	124/173 (72%)	121 (98%)	2 (2%)	1 (1%)	19	57
19	v	118/153 (77%)	107 (91%)	11 (9%)	0	100	100
20	w	118/127 (93%)	110 (93%)	8 (7%)	0	100	100
21	x	163/214 (76%)	157 (96%)	6 (4%)	0	100	100
22	y	69/123 (56%)	63 (91%)	6 (9%)	0	100	100
23	z	51/59 (86%)	48 (94%)	3 (6%)	0	100	100
24	A	48/280 (17%)	46 (96%)	2 (4%)	0	100	100
25	B	126/151 (83%)	116 (92%)	9 (7%)	1 (1%)	19	57
26	e	162/207 (78%)	150 (93%)	12 (7%)	0	100	100
27	D	92/172 (54%)	80 (87%)	12 (13%)	0	100	100
28	E	77/112 (69%)	74 (96%)	3 (4%)	0	100	100
29	F	127/141 (90%)	116 (91%)	11 (9%)	0	100	100
30	G	195/259 (75%)	184 (94%)	11 (6%)	0	100	100
31	I	95/132 (72%)	93 (98%)	2 (2%)	0	100	100
32	J	94/134 (70%)	84 (89%)	10 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
33	K	191/249 (77%)	184 (96%)	6 (3%)	1 (0%)	29 68
34	L	135/206 (66%)	126 (93%)	9 (7%)	0	100 100
36	M	385/876 (44%)	368 (96%)	17 (4%)	0	100 100
37	N	279/455 (61%)	262 (94%)	16 (6%)	1 (0%)	34 72
38	O	509/688 (74%)	459 (90%)	50 (10%)	0	100 100
39	P	430/530 (81%)	400 (93%)	30 (7%)	0	100 100
40	Q	260/820 (32%)	237 (91%)	23 (9%)	0	100 100
41	R	280/653 (43%)	264 (94%)	16 (6%)	0	100 100
42	S	230/334 (69%)	210 (91%)	20 (9%)	0	100 100
All	All	7400/12257 (60%)	6926 (94%)	454 (6%)	20 (0%)	44 76

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	p	221	ALA
13	p	266	PRO
2	b	287	ARG
3	c	181	PRO
10	m	9	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
1	a	209/295 (71%)	209 (100%)	0	100 100
2	b	244/331 (74%)	244 (100%)	0	100 100
3	c	254/313 (81%)	252 (99%)	2 (1%)	81 93
4	d	144/164 (88%)	144 (100%)	0	100 100
5	f	47/209 (22%)	46 (98%)	1 (2%)	53 82
6	i	133/214 (62%)	133 (100%)	0	100 100
7	j	99/99 (100%)	98 (99%)	1 (1%)	76 91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	k	165/247 (67%)	164 (99%)	1 (1%)	86 95
9	l	112/197 (57%)	111 (99%)	1 (1%)	78 92
10	m	152/157 (97%)	151 (99%)	1 (1%)	84 94
11	n	153/245 (62%)	151 (99%)	2 (1%)	69 89
12	o	93/96 (97%)	93 (100%)	0	100 100
13	p	172/303 (57%)	168 (98%)	4 (2%)	50 80
14	q	128/269 (48%)	128 (100%)	0	100 100
15	r	143/184 (78%)	143 (100%)	0	100 100
16	s	156/157 (99%)	155 (99%)	1 (1%)	86 95
17	t	161/287 (56%)	160 (99%)	1 (1%)	86 95
18	u	100/122 (82%)	100 (100%)	0	100 100
19	v	109/122 (89%)	109 (100%)	0	100 100
20	w	106/112 (95%)	104 (98%)	2 (2%)	57 84
21	x	148/189 (78%)	148 (100%)	0	100 100
22	y	56/104 (54%)	56 (100%)	0	100 100
23	z	49/54 (91%)	49 (100%)	0	100 100
24	A	45/219 (20%)	44 (98%)	1 (2%)	52 81
25	B	108/126 (86%)	107 (99%)	1 (1%)	78 92
26	e	135/168 (80%)	134 (99%)	1 (1%)	84 94
27	D	77/116 (66%)	77 (100%)	0	100 100
28	E	66/93 (71%)	66 (100%)	0	100 100
29	F	112/121 (93%)	112 (100%)	0	100 100
30	G	151/195 (77%)	149 (99%)	2 (1%)	69 89
31	I	82/105 (78%)	82 (100%)	0	100 100
32	J	75/87 (86%)	75 (100%)	0	100 100
33	K	158/193 (82%)	157 (99%)	1 (1%)	86 95
34	L	115/172 (67%)	115 (100%)	0	100 100
36	M	287/369 (78%)	285 (99%)	2 (1%)	84 94
37	N	201/335 (60%)	199 (99%)	2 (1%)	76 91
38	O	403/466 (86%)	402 (100%)	1 (0%)	93 98
39	P	301/353 (85%)	301 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	Q	191/313 (61%)	191 (100%)	0	100 100
41	R	199/336 (59%)	199 (100%)	0	100 100
42	S	206/254 (81%)	206 (100%)	0	100 100
All	All	6045/8491 (71%)	6017 (100%)	28 (0%)	89 96

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	t	120	ARG
38	O	494	ARG
24	A	232	ASN
36	M	493	ARG
20	w	13	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
20	w	94	GLN
26	e	93	ASN
38	O	315	GLN
33	K	173	HIS
38	O	256	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	1	159/162 (98%)	43 (27%)	1 (0%)
47	2	85/86 (98%)	24 (28%)	2 (2%)
48	0	74/75 (98%)	31 (41%)	0
49	3	183/184 (99%)	32 (17%)	1 (0%)
50	4	117/118 (99%)	22 (18%)	0
51	5	146/149 (97%)	62 (42%)	1 (0%)
52	6	135/136 (99%)	35 (25%)	3 (2%)
53	7	574/578 (99%)	158 (27%)	5 (0%)
54	8	411/413 (99%)	153 (37%)	9 (2%)
All	All	1884/1901 (99%)	560 (29%)	22 (1%)

5 of 560 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	1	6	A
46	1	7	U
46	1	10	C
46	1	24	A
46	1	26	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	8	212	G
54	8	316	U
54	8	309	A
54	8	324	G
52	6	120	C

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 71 ligands modelled in this entry, 70 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
57	FES	S	401	42	0,4,4	-	-	-		

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
57	FES	S	401	42	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
40	Q	6
53	7	3
44	Y	3
46	1	2
41	R	2
51	5	2
36	M	2
3	c	1
54	8	1
38	O	1
42	S	1
16	s	1
32	J	1

The worst 5 of 26 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	59:A	O3'	75:U	P	56.66
1	R	536:UNK	C	553:UNK	N	27.93
1	c	276:UNK	C	291:SER	N	25.05

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	111:U	O3'	117:A	P	21.41
1	R	477:ALA	C	493:UNK	N	21.21

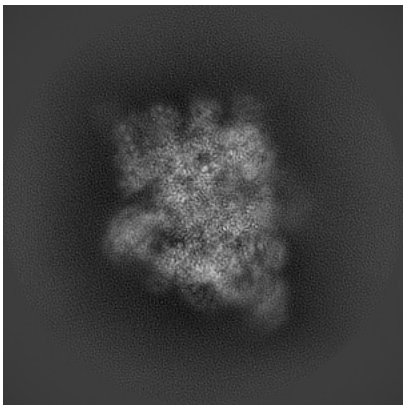
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13480. These allow visual inspection of the internal detail of the map and identification of artifacts.

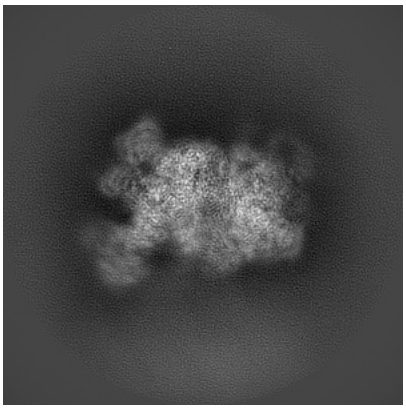
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

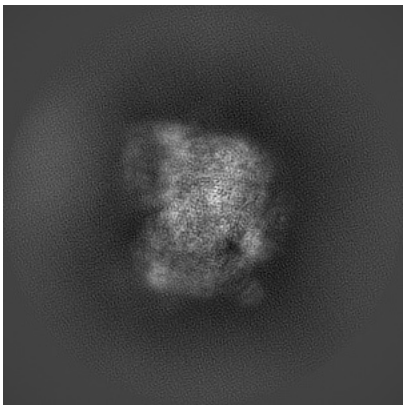
6.1.1 Primary map



X

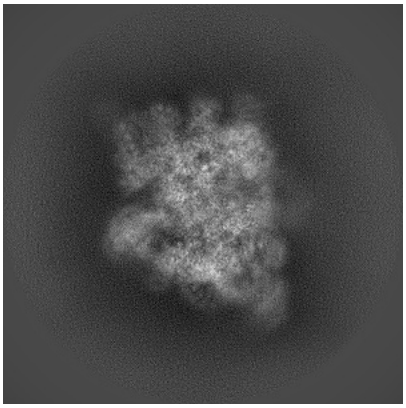


Y

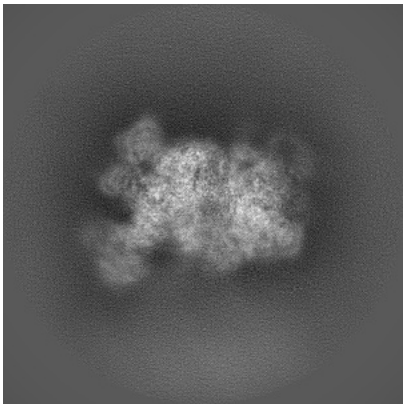


Z

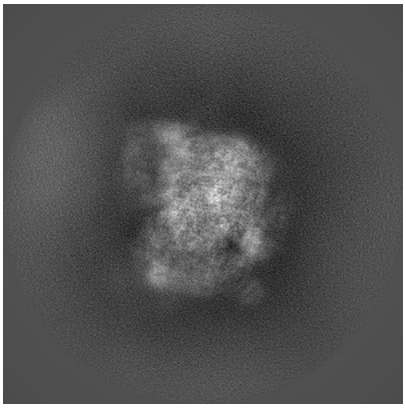
6.1.2 Raw map



X



Y

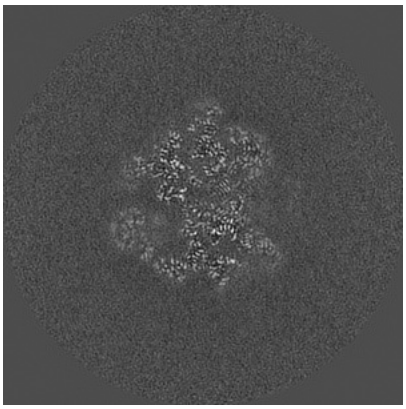


Z

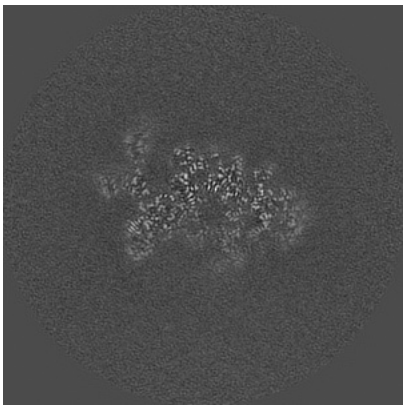
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

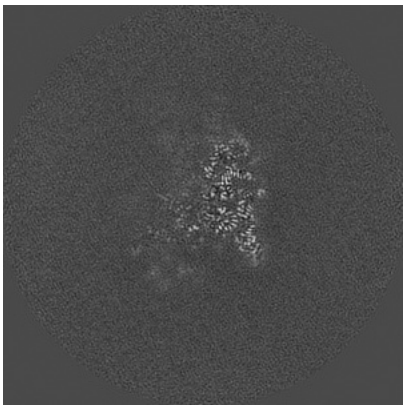
6.2.1 Primary map



X Index: 240

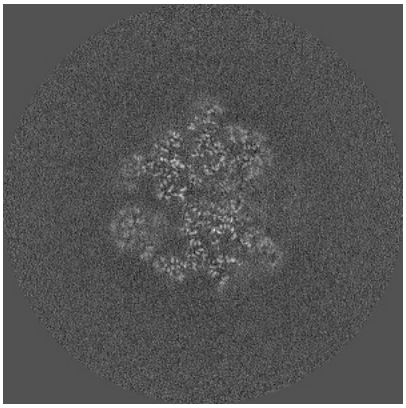


Y Index: 240

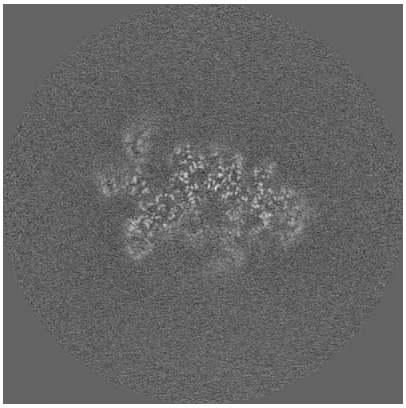


Z Index: 240

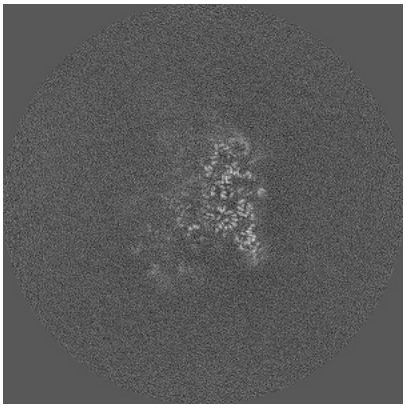
6.2.2 Raw map



X Index: 240



Y Index: 240

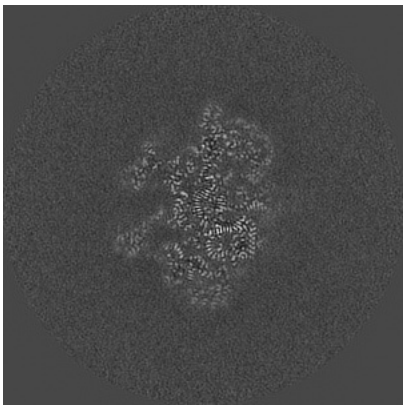


Z Index: 240

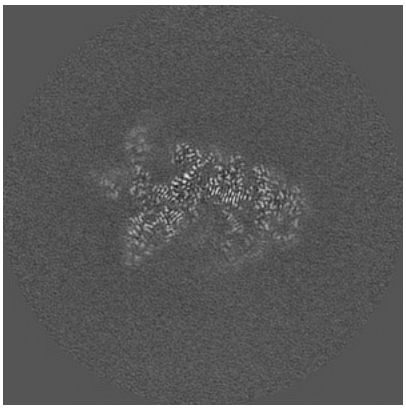
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

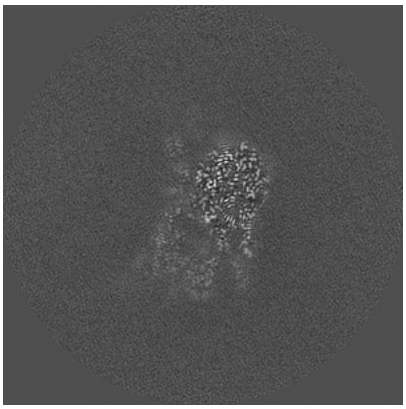
6.3.1 Primary map



X Index: 256

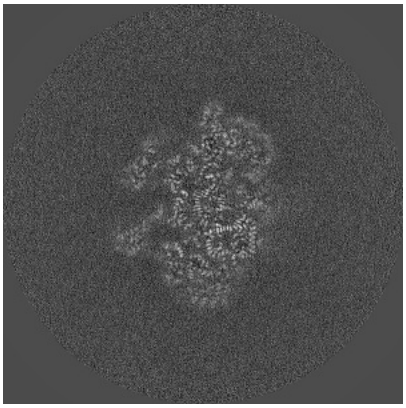


Y Index: 245

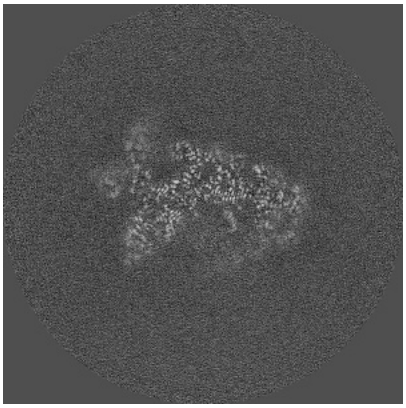


Z Index: 217

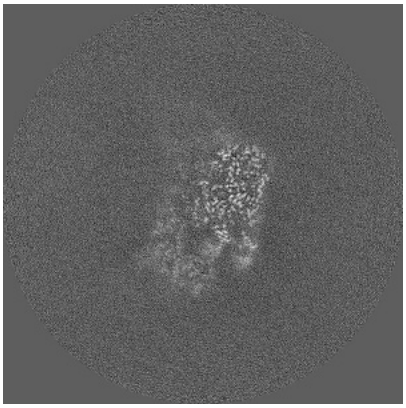
6.3.2 Raw map



X Index: 256



Y Index: 246



Z Index: 225

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

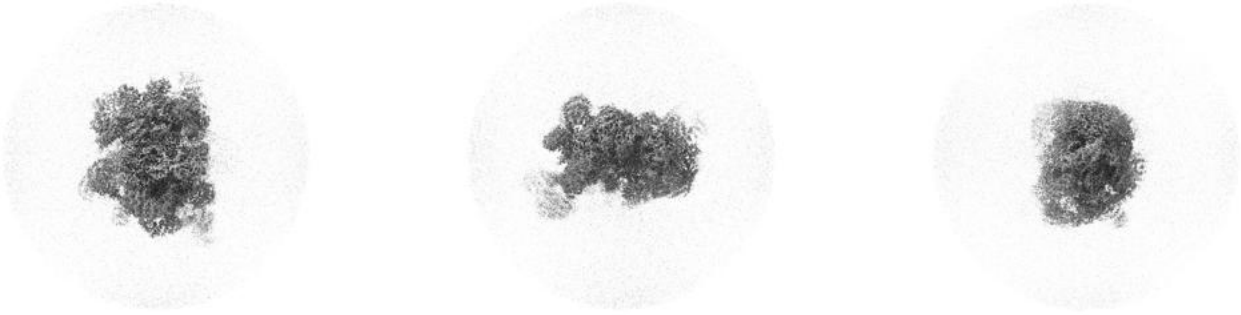
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X Y Z

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

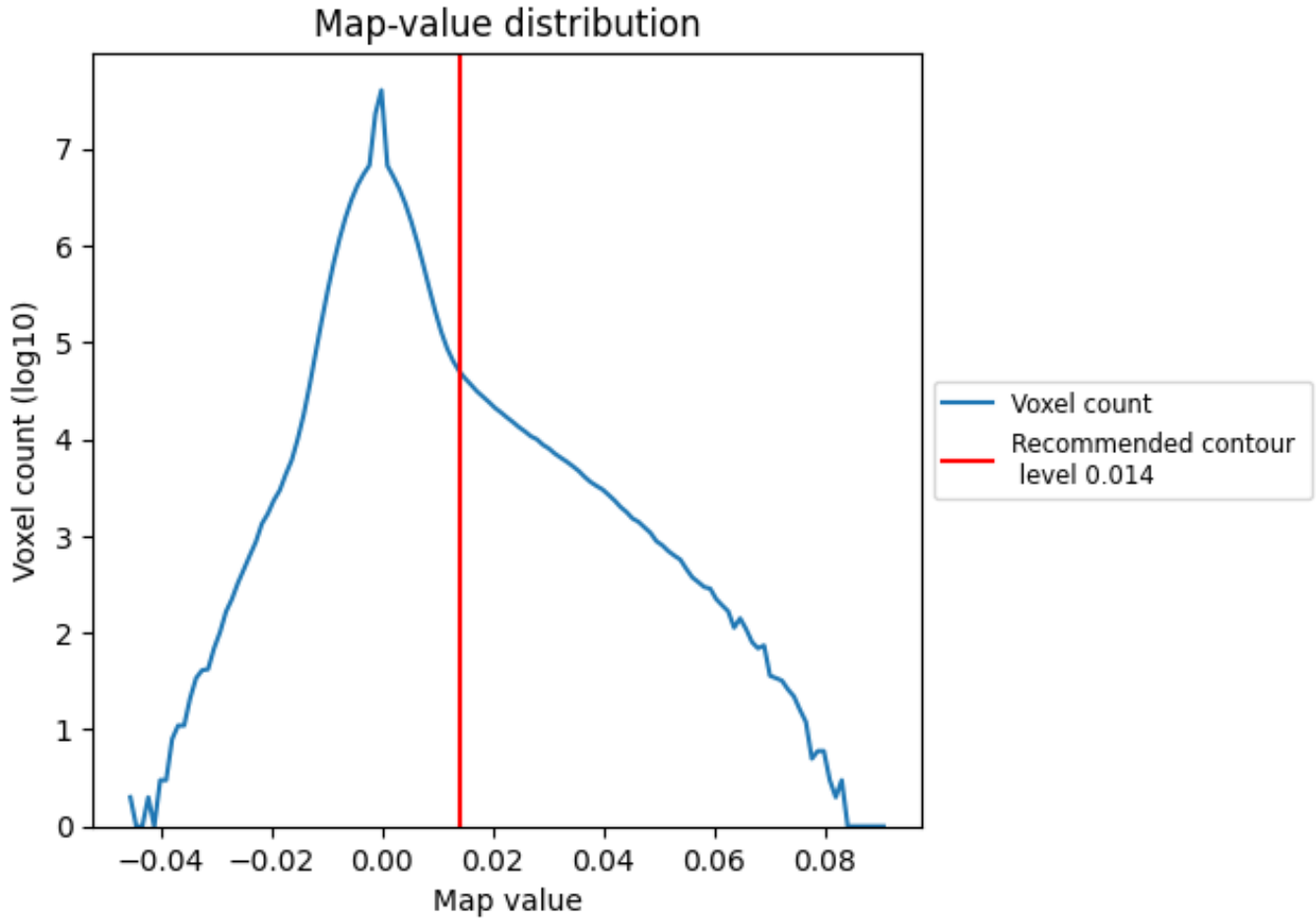
6.5 Mask visualisation (i)

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

7 Map analysis

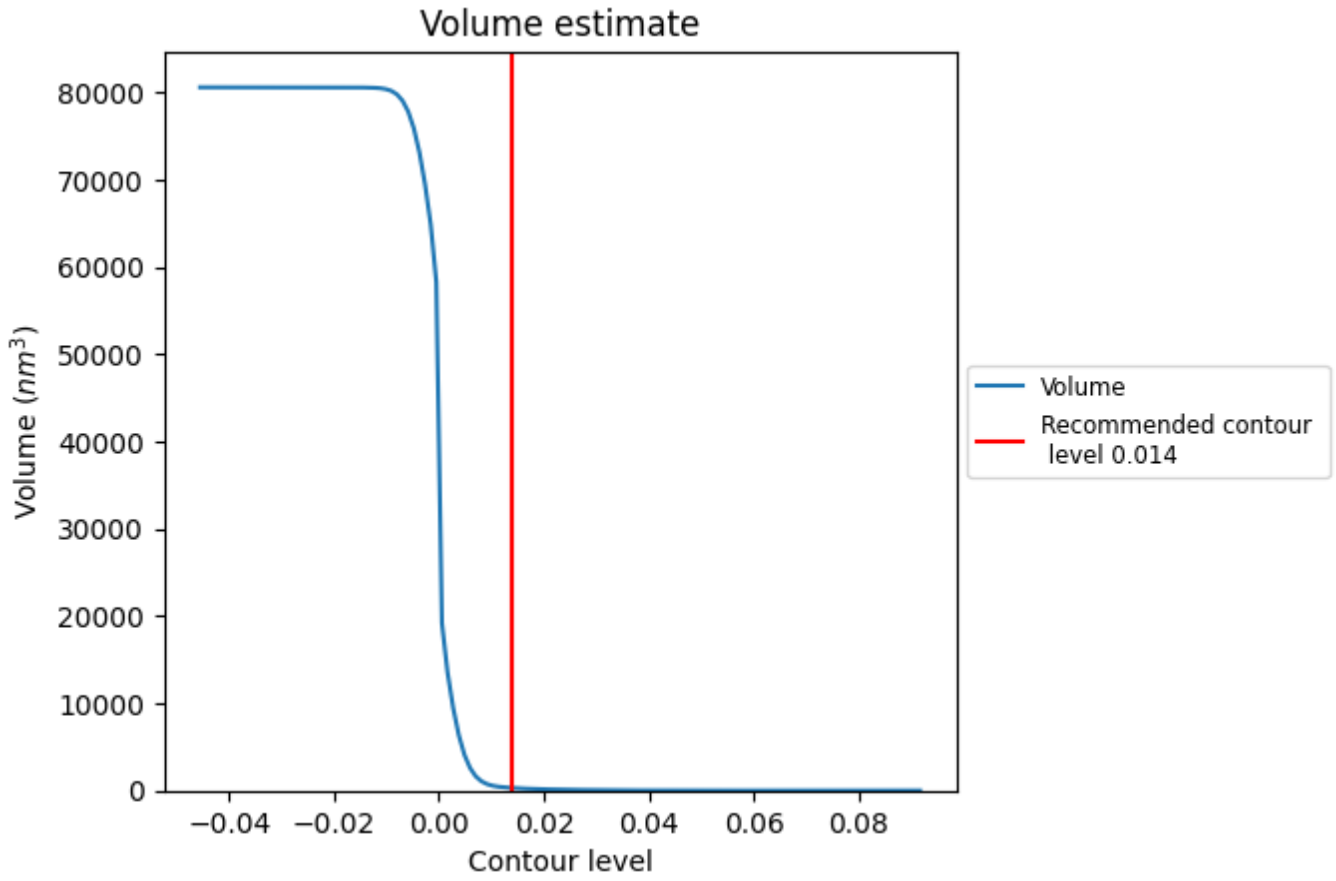
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

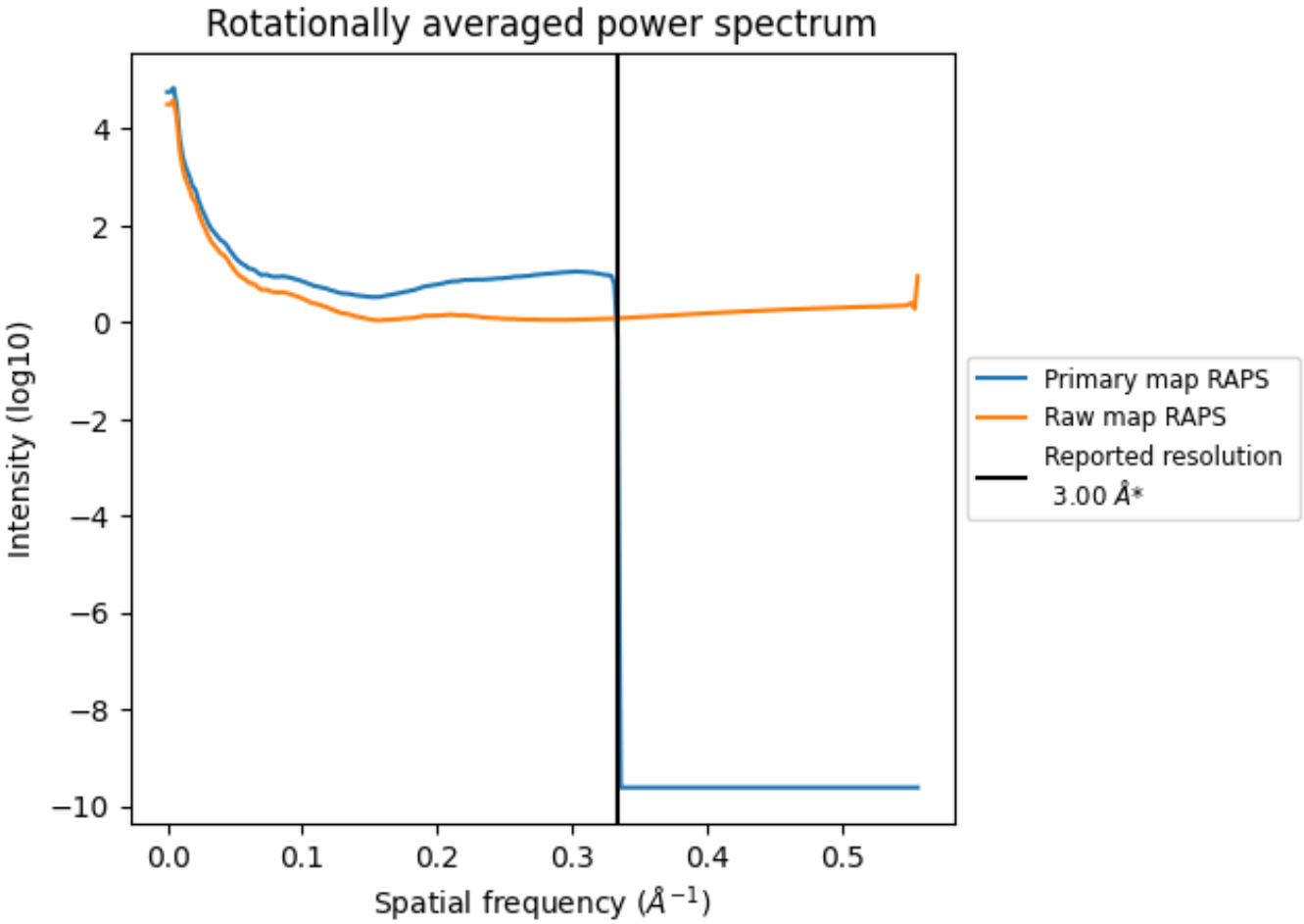
7.2 Volume estimate (i)



The volume at the recommended contour level is 297 nm^3; this corresponds to an approximate mass of 268 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)

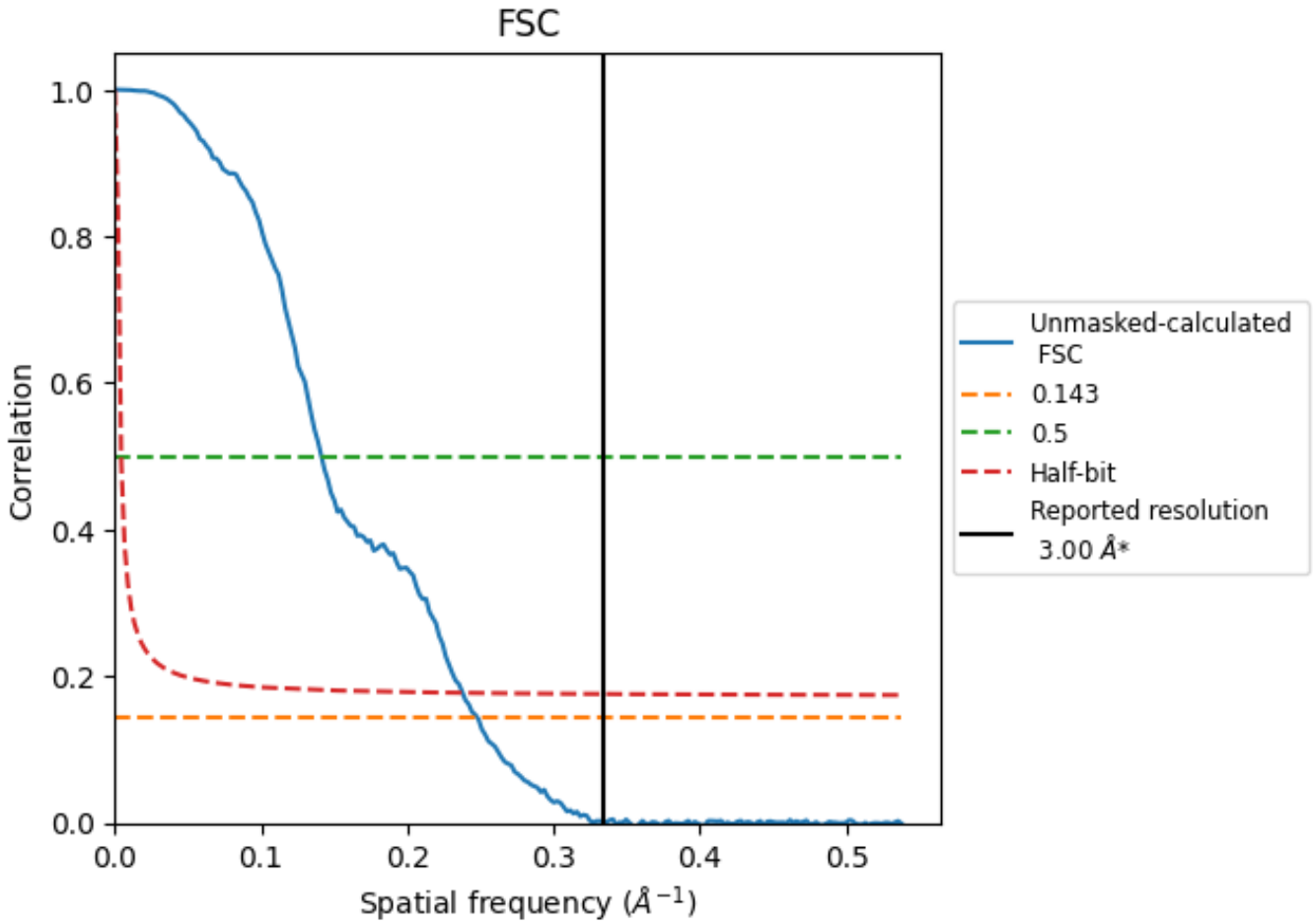


*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

8.2 Resolution estimates (i)

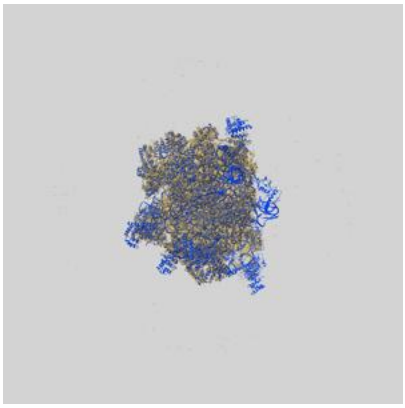
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.03	7.08	4.21

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 3.0 by more than 10 %

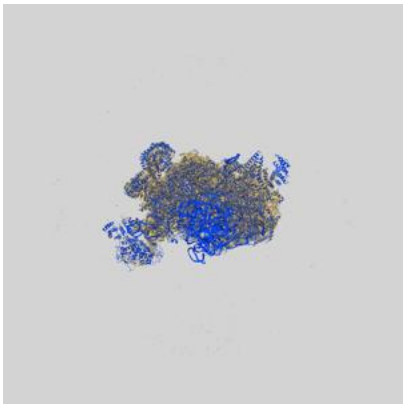
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13480 and PDB model 7PKT. Per-residue inclusion information can be found in section 3 on page 15.

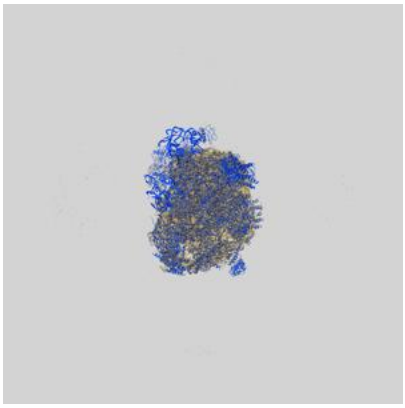
9.1 Map-model overlay



X



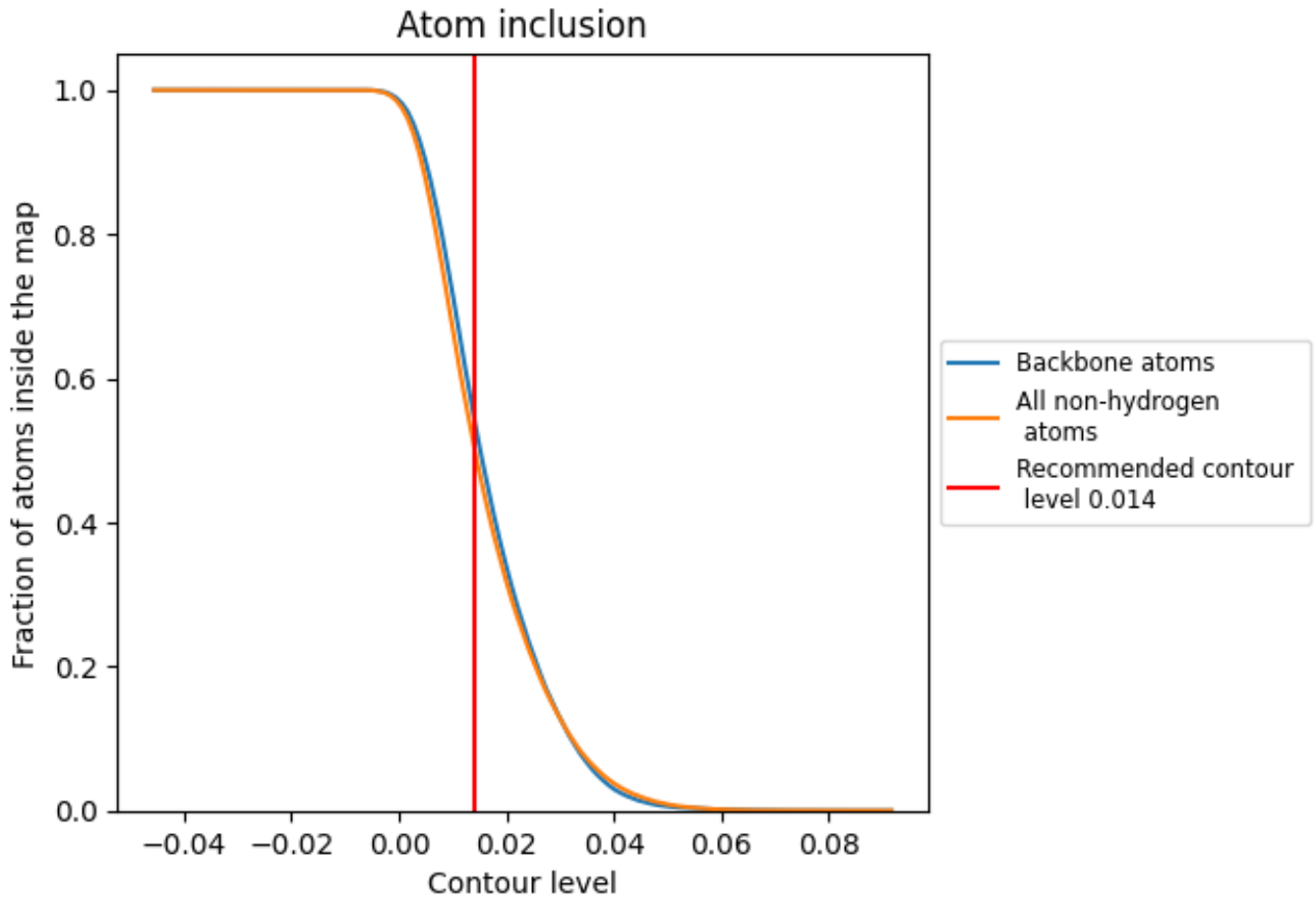
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014 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 Atom inclusion (i)



At the recommended contour level, 55% of all backbone atoms, 51% of all non-hydrogen atoms, are inside the map.