wwPDB EM Validation Summary Report (i)

Aug 27, 2026 – 08:56 am BST

PDB ID	:	9HCC / pdb_00009hcc
EMDB ID	:	EMD-52044
Title	:	Mouse mitoribosome large subunit assembly intermediate (without uL16m) bound to MRM3-dimer, DDX28 and the MALSU-L0R8F8-mt-ACP complex, State A1 (SAMC knock-out)
Authors	:	Singh, V.; Rorbach, J.; Freyer, C.; Amunts, A.; Wredenberg, A.
Deposited on	:	2024-11-08
Resolution	:	5.67 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:

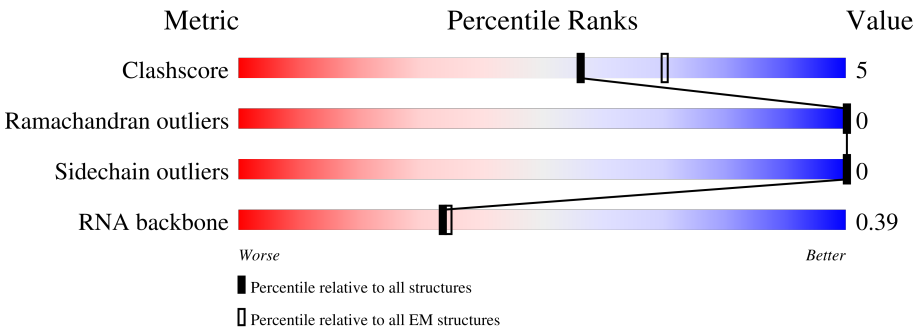
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

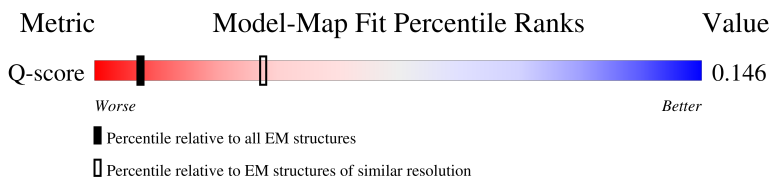
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.67 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	467 (5.18 - 6.17)

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	1584	11% 41% 23% 7% 29%
2	B	68	21% 43% 38% 9% 10%
3	D	246	50% 60% 10% 30%

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Mol	Chain	Length	Quality of chain
4	E	348	6% 70% 6% 24%
5	F	294	8% 63% 10% 27%
6	H	268	15% 27% 9% 65%
7	I	262	43% 50% 8% 41%
8	J	192	70% 64% 10% 26%
9	K	178	6% 88% 8%
10	L	145	50% 72% 8% 21%
11	M	295	7% 72% 13% 16%
12	O	176	73% 12% 15%
13	P	180	10% 64% 14% 22%
14	Q	292	7% 66% 9% 26%
15	R	149	6% 83% 5% 12%
16	S	209	5% 69% 7% 24%
17	T	206	7% 72% 8% 19%
18	U	146	23% 77% 9% 14%
19	V	216	59% 78% 13% 8%
20	X	294	28% 73% 10% 18%
21	Y	252	19% 65% 5% 30%
22	Z	160	6% 68% 28%
23	0	187	49% 9% 42%
24	5	423	51% 85% 6% 9%
25	6	380	29% 62% 17% 22%
26	7	336	7% 79% 7% 13%
27	8	206	23% 26% 71%
28	9	135	23% 66% 5% 29%

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Mol	Chain	Length	Quality of chain
29	a	142	15% 65% 7% 27%
30	b	159	• 84% 9% 7%
31	c	308	5% 81% 9% 9%
32	d	306	21% 55% 12% 33%
33	e	283	59% 53% 10% 37%
34	f	211	38% 35% 7% 58%
35	g	166	5% 70% 9% 20%
36	h	159	8% 61% 8% 31%
37	i	128	12% 62% 10% 27%
38	j	121	6% 66% • 30%
39	k	118	36% 56% 12% 32%
40	l	135	44% 47% 9% 44%
41	o	102	5% 73% • 24%
42	p	206	11% 53% 11% 36%
43	q	222	• 39% 5% 56%
44	r	196	8% 71% 9% 20%
45	s	442	16% 74% 12% 15%
46	u	228	29% 47% 8% 45%
47	v	70	77% 90% 9% •
48	w	156	49% 46% 5% 49%
49	x	418	35% 56% 14% 29%
49	y	418	31% 52% 18% 30%
50	z	540	36% 79% 6% 15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
52	FES	r	301	-	-	X	-

2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 174926 atoms, of which 81656 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 16S rRNA (1584-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	1129	36145	10796	12126	4363	7731	1129	0	0

- Molecule 2 is a RNA chain called tRNA-Phe (68-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	B	61	1960	585	657	240	417	61	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	D	172	2708	835	1373	253	240	7	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	264	4219	1367	2097	361	388	6	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	F	214	3483	1113	1755	305	304	6	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
6	H	95	1593	492	814	150	137	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL10m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	I	154	2575	810	1330	222	207	6	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL11m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	J	142	2220	690	1145	191	191	3	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	K	171	2794	894	1398	253	243	6	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein uL14m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	L	115	1837	560	944	174	155	4	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL15m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	M	249	4090	1285	2080	365	355	5	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein bL17m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	O	149	2476	774	1254	230	213	5	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL18m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	P	141	2302	725	1148	221	203	5	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	Q	217	3612	1150	1822	309	322	9	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein bL20m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	R	131	2214	685	1137	214	175	3	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	S	159	2673	840	1372	233	226	2	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein uL22m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	T	166	2771	871	1402	256	234	8	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	U	125	2072	664	1038	193	174	3	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	V	198	3250	1026	1622	302	294	6	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein bL28m,Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	X	242	4072	1304	2051	358	355	4	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
21	Y	176	3076	973	1553	290	255	5	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
22	Z	115	1913	598	979	171	162	3	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
23	0	108	1789	546	908	174	155	6	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein mL37.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
24	5	387	6355	2045	3187	554	560	9	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
25	6	297	4954	1630	2420	462	437	5	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein mL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
26	7	292	4757	1517	2378	409	438	15	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein mL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
27	8	59	977	306	484	87	98	2	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein mL41.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
28	9	96	1550	510	772	123	144	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein mL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
29	a	103	1703	542	843	156	159	3	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
30	b	148	2376	731	1195	234	214	2	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
31	c	279	4502	1440	2256	389	409	8	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein mL45.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
32	d	204	3358	1085	1670	299	293	11	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein mL46.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
33	e	177	2911	922	1474	258	252	5	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein mL48.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
34	f	89	1418	452	704	120	138	4	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
35	g	132	2184	709	1094	187	192	2	0	0

- Molecule 36 is a protein called Large ribosomal subunit protein mL50.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
36	h	110	1740	552	868	156	160	4	0	0

- Molecule 37 is a protein called Large ribosomal subunit protein mL51.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
37	i	93	1611	517	816	153	123	2	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein mL52.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
38	j	85	1376	426	692	135	121	2	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein mL53.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
39	k	80	1268	393	639	114	117	5	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein mL54.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
40	l	76	1266	403	631	114	116	2	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein mL63.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
41	o	78	1263	402	623	118	116	4	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein mL62.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
42	p	132	2201	682	1112	205	198	4	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein mL64.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
43	q	97	1584	501	785	155	142	1	0	0

- Molecule 44 is a protein called Large ribosomal subunit protein mL66.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
44	r	156	2586	806	1319	241	209	11	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein mL65.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
45	s	377	6102	1938	3057	555	540	12	0	0

- Molecule 46 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	u	125	2041	659	1012	170	191	9	0	0

- Molecule 47 is a protein called Predicted gene, 55359.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
47	v	69	1189	374	603	112	99	1	0	0

- Molecule 48 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
48	w	79	1277	410	640	95	127	5	0	0

- Molecule 49 is a protein called rRNA methyltransferase 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
49	x	295	4661	1478	2356	399	420	8	0	0
49	y	293	4631	1469	2340	397	417	8	0	0

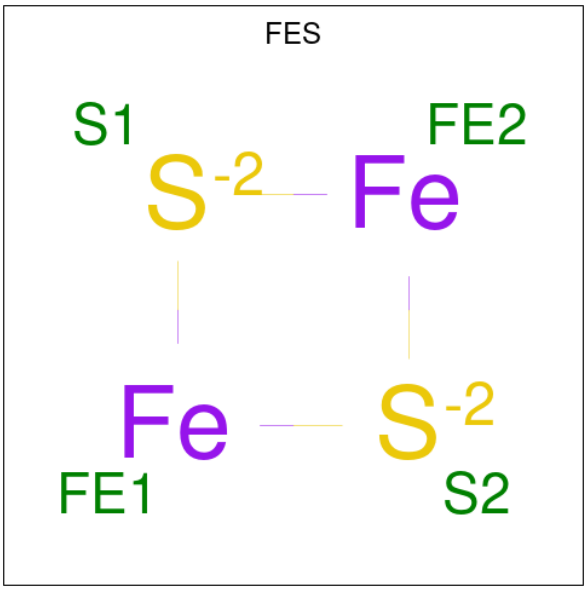
- Molecule 50 is a protein called Probable ATP-dependent RNA helicase DDX28.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
50	z	458	7236	2259	3681	643	644	9	0	0

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
51	0	1	1	1	0

- Molecule 52 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



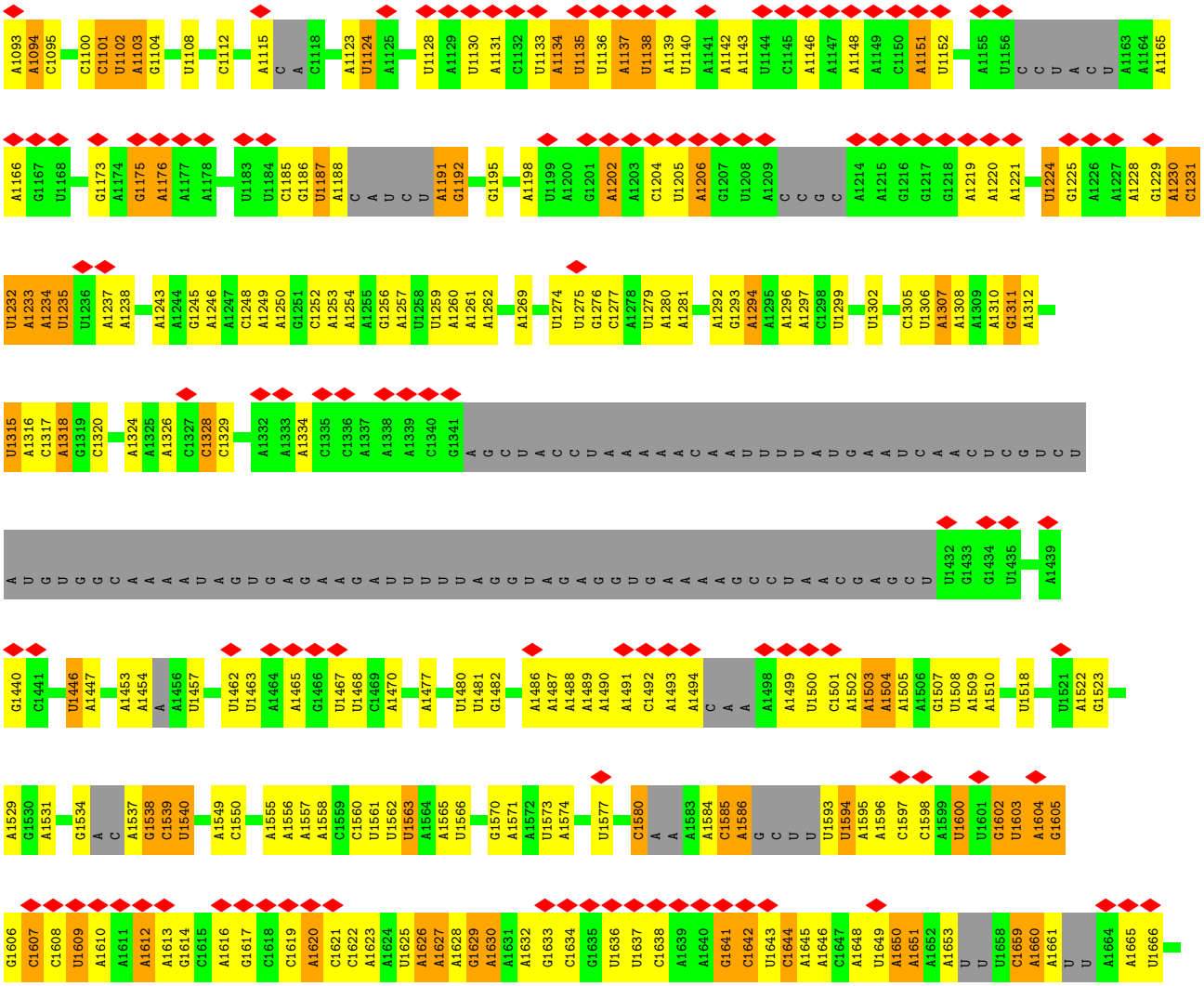
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
52	r	1	4	2	2	0

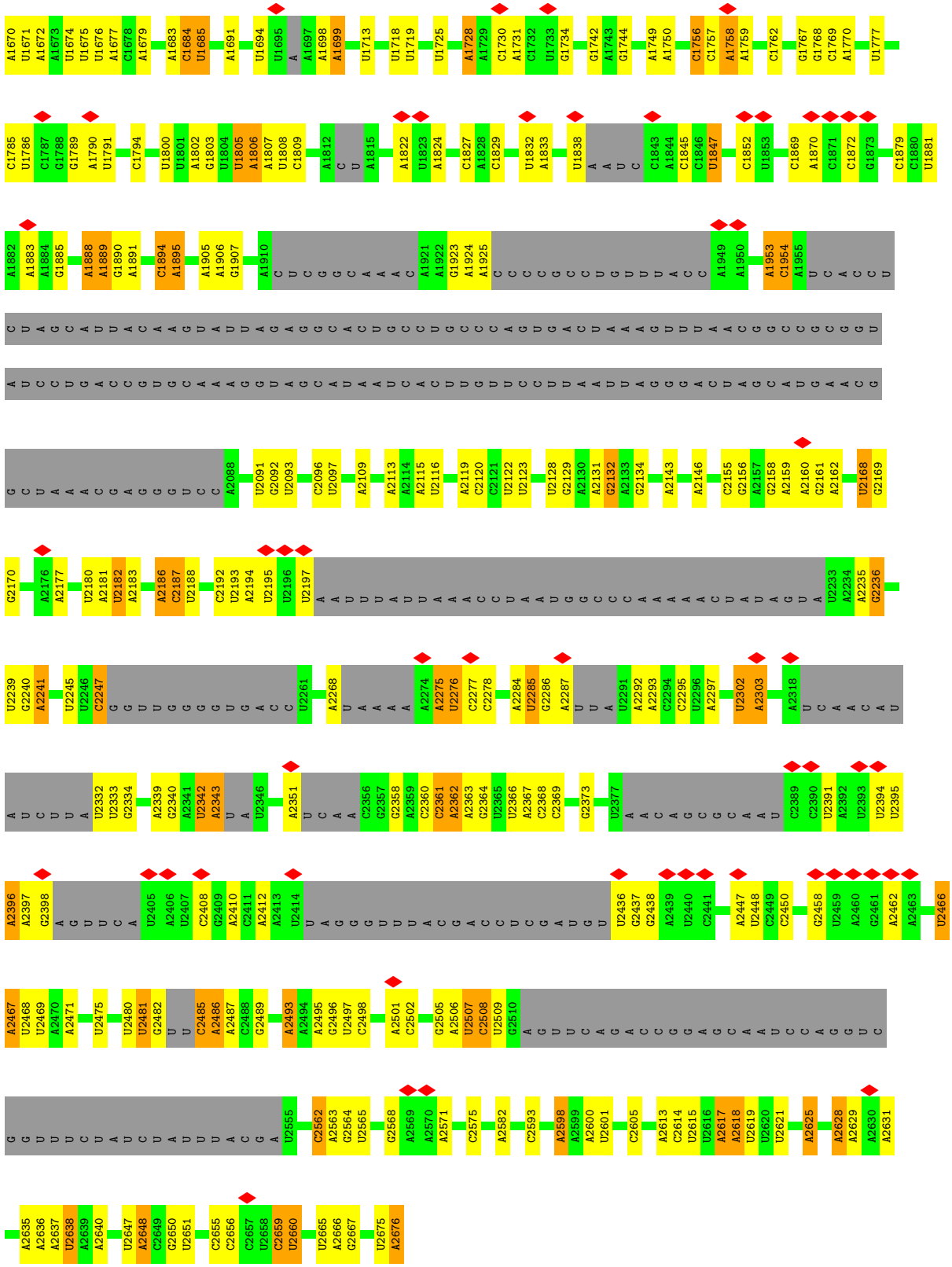
3 Residue-property plots (i)

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: 16S rRNA (1584-MER)

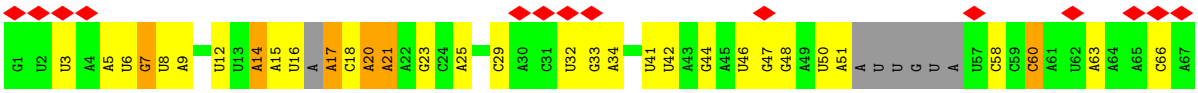
Chain A: 11% 41% 23% 7% 29%





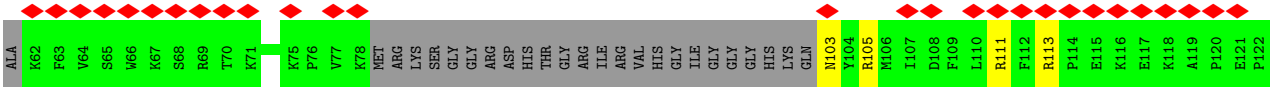
- Molecule 2: tRNA-Phe (68-MER)

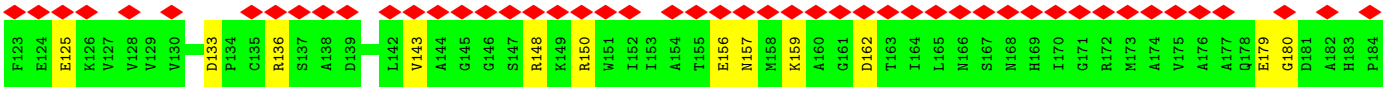
Chain B:

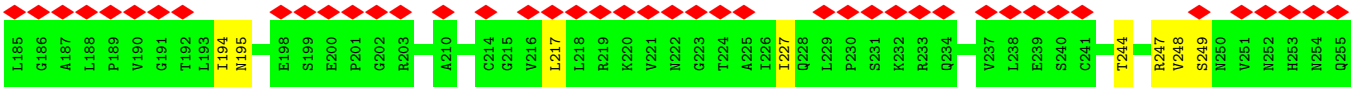


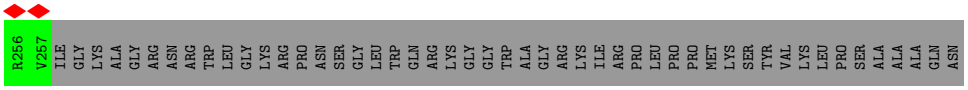
• Molecule 3: Large ribosomal subunit protein uL2m

Chain D:



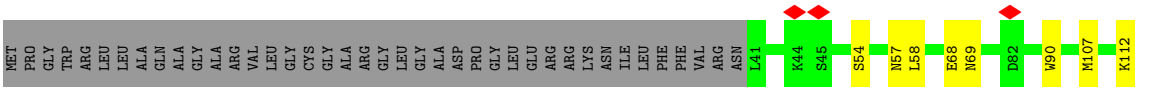


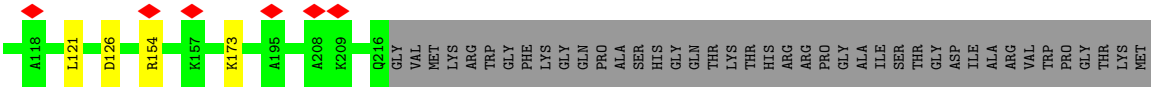


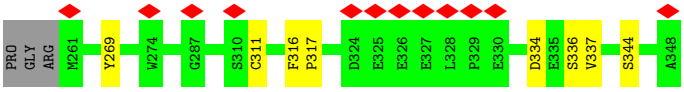


• Molecule 4: Large ribosomal subunit protein uL3m

Chain E:

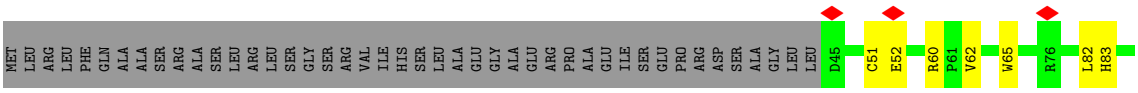


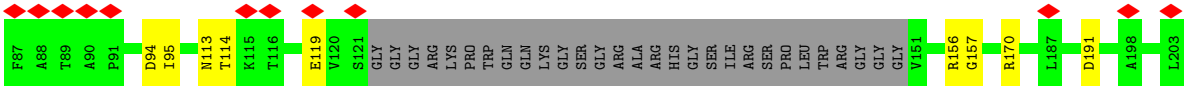


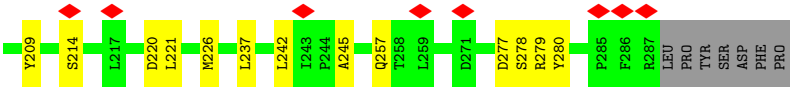


• Molecule 5: Large ribosomal subunit protein uL4m

Chain F:

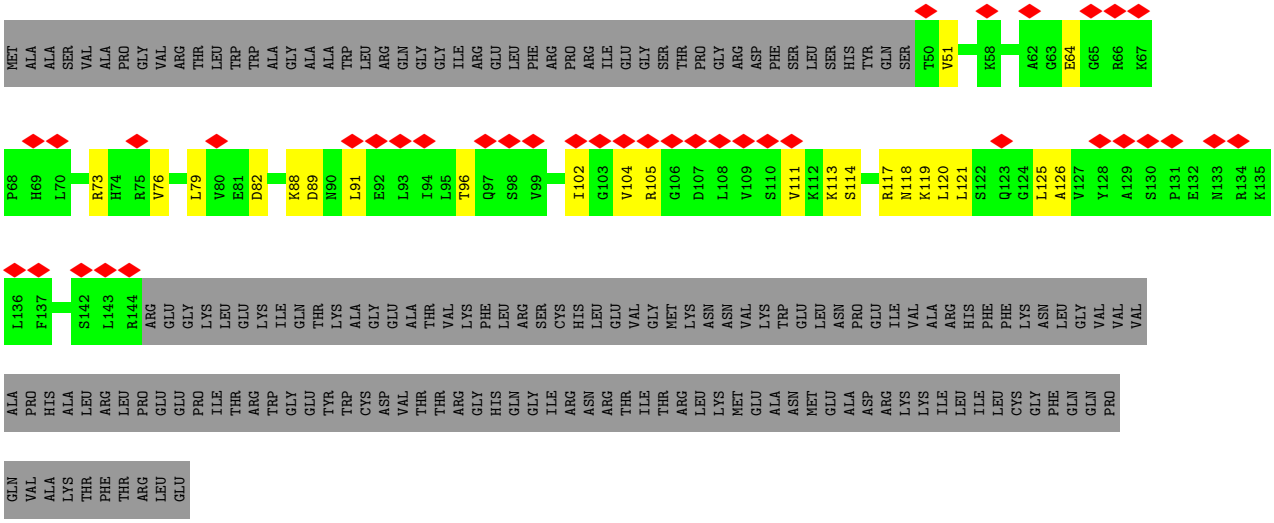






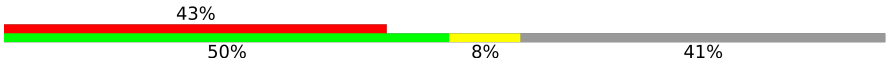
• Molecule 6: Large ribosomal subunit protein bL9m

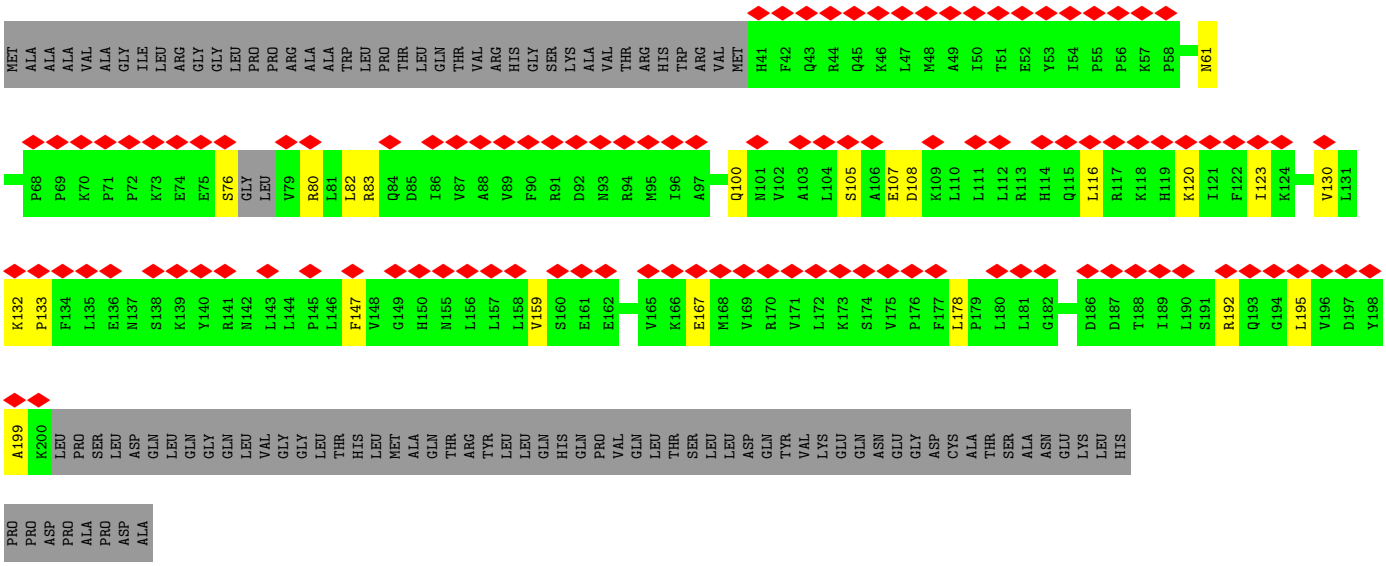
Chain H:



• Molecule 7: Large ribosomal subunit protein uL10m

Chain I:



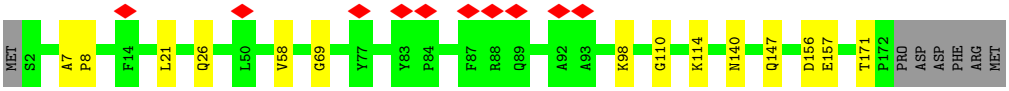


• Molecule 8: Large ribosomal subunit protein uL11m

Chain J:

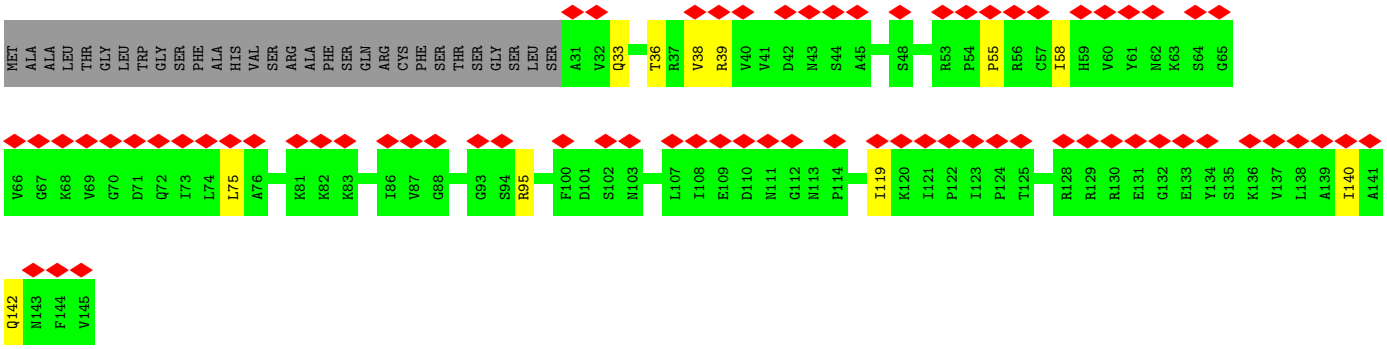
• Molecule 9: Large ribosomal subunit protein uL13m

Chain K:



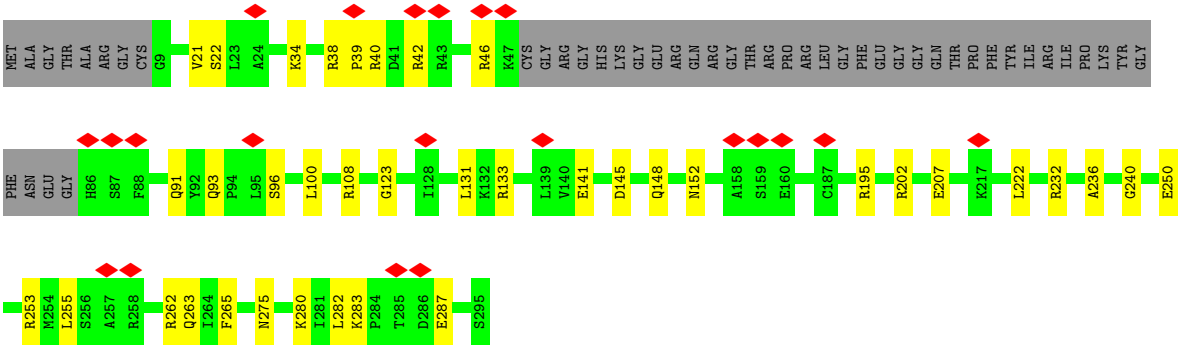
• Molecule 10: Large ribosomal subunit protein uL14m

Chain L:



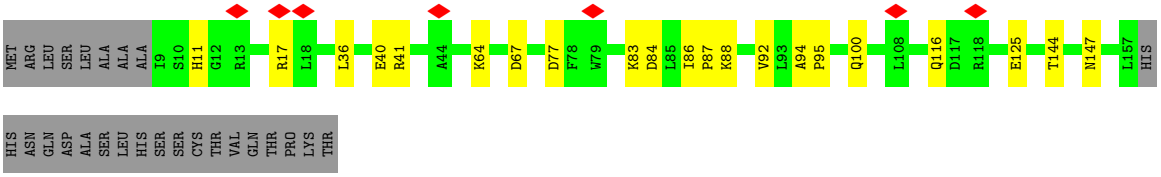
• Molecule 11: Large ribosomal subunit protein uL15m

Chain M:



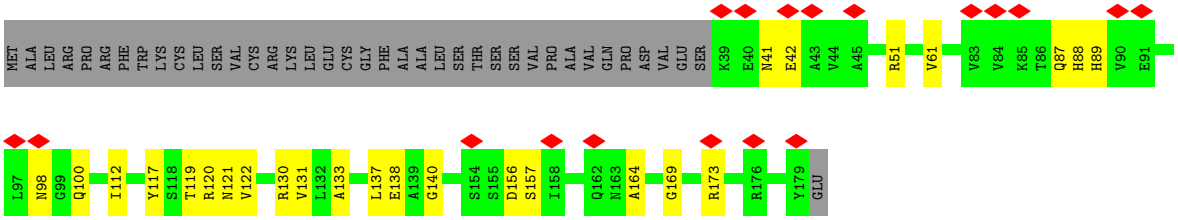
- Molecule 12: Large ribosomal subunit protein bL17m

Chain O:



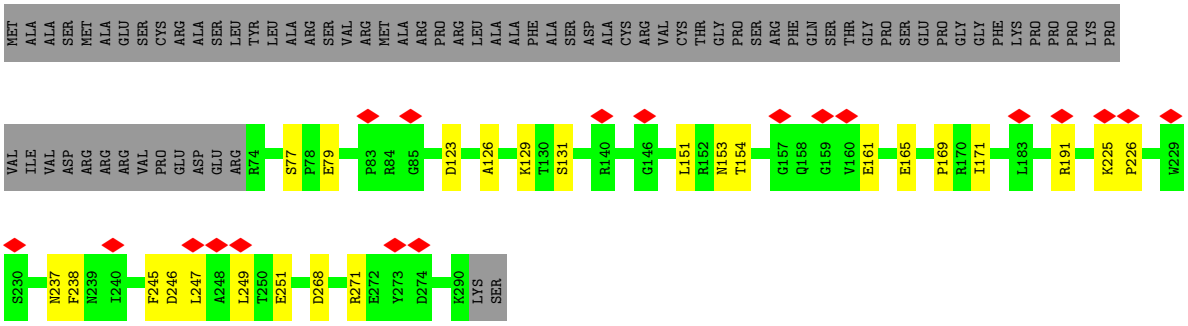
- Molecule 13: Large ribosomal subunit protein uL18m

Chain P:



- Molecule 14: Large ribosomal subunit protein bL19m

Chain Q:



- Molecule 15: Large ribosomal subunit protein bL20m

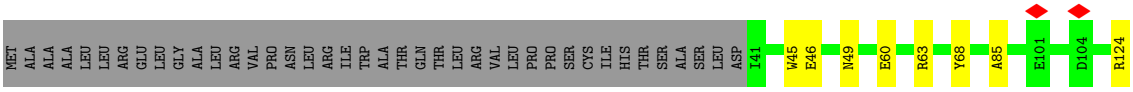
Chain R:

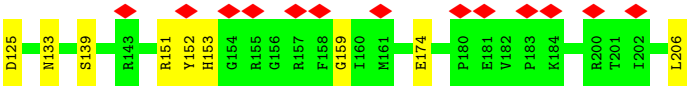
- Molecule 16: Large ribosomal subunit protein bL21m

Chain S:

• Molecule 17: Large ribosomal subunit protein uL22m

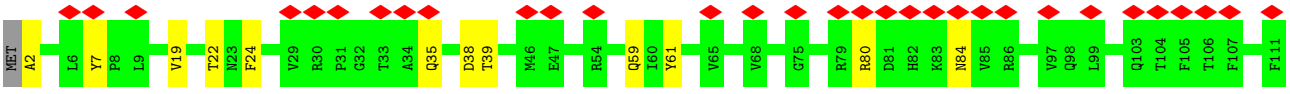
Chain T:

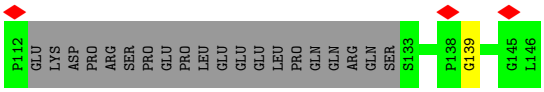




• Molecule 18: Large ribosomal subunit protein uL23m

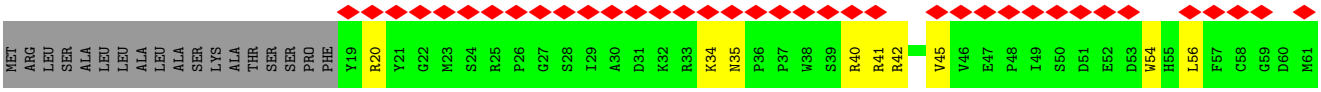
Chain U:

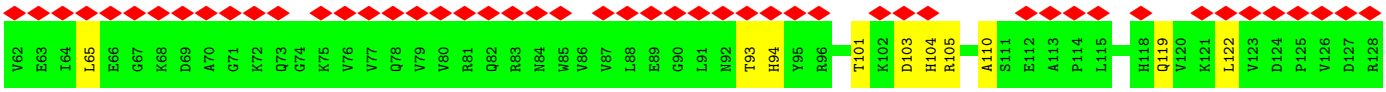


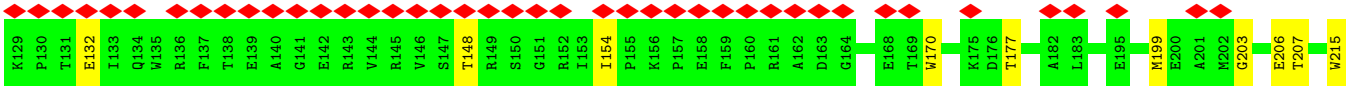


• Molecule 19: Large ribosomal subunit protein uL24m

Chain V:

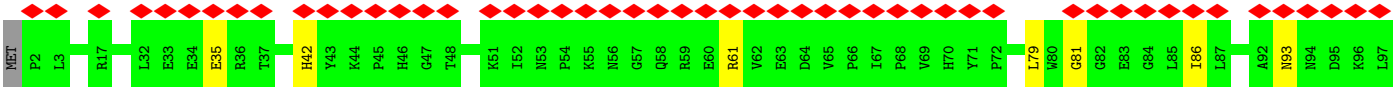


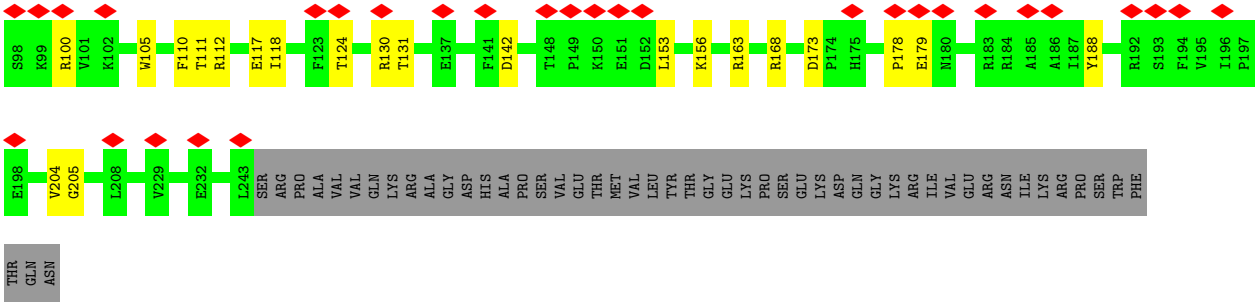




• Molecule 20: Large ribosomal subunit protein bL28m,Large ribosomal subunit protein bL32m

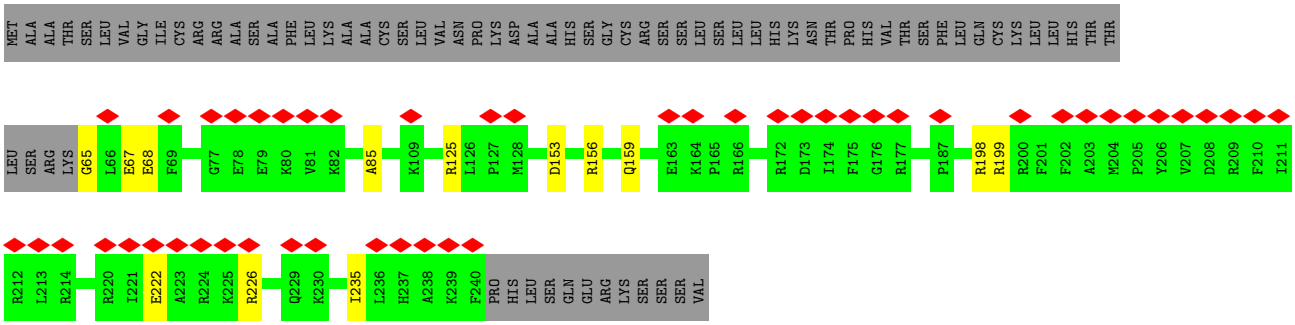
Chain X:





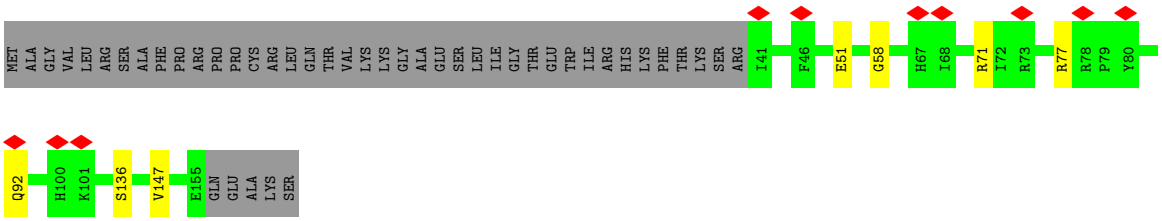
- Molecule 21: Large ribosomal subunit protein uL29m

Chain Y:



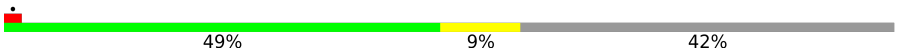
- Molecule 22: Large ribosomal subunit protein uL30m

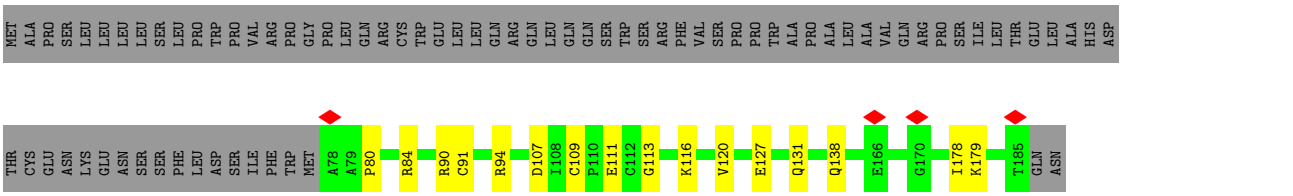
Chain Z:



- Molecule 23: Large ribosomal subunit protein bL32m

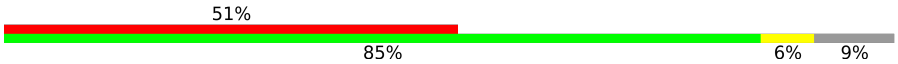
Chain 0:





- Molecule 24: Large ribosomal subunit protein mL37

Chain 5:



MET ALA LEU ALA SER GLY PRO ALA LEU ARG ALA LEU ALA GLY SER GLY ARG LEU GLY LEU GLY GLY TYR GLY THR PRO LYS ARG GLY A30 Y31 E32 W33 G34 V35 R36 S37 T38 R39 K40 PRO GLU PRO ARG PRO LEU ASP R48 V49 Y50 E51 I52 P53 G54 L55 E56 P57 I58 T59 Y60

E61 G62 K63 K64 H65 F66 V67 P68 W69 L70 A71 R72 P73 I74 F75 P76 P77 W78 E79 R80 G81 W82 N83 D84 P85 R86 F87 H88 R89 A90 A91 P92 I93 H94 E95 Q96 T97 L98 Y99 K100 E101 E102 P103 C104 Y105 I106 R112 L113 L114 E115 G116 M117 K118 K125 L128 I129 E130

G131 L132 P133 K134 K135 V136 L139 V140 D141 D142 P143 A144 N145 H146 I147 E148 E151 Q152 T167 E168 D169 I170 P171 K172 R173 E174 P178 L179 I180 V181 D182 S183 L184 I185 Q186 L187 C188 K189 S190 Q191 I192 L193 K194 H195 R200 N206 C207 A210 W213 N214 R215 E216

S217 L218 L219 L220 Q221 V222 R223 G224 T225 S226 I229 D234 P235 V238 I239 A240 S241 R242 E243 E244 V245 R249 S250 H251 V252 L253 E254 T255 F256 Y257 P258 I259 D264 L265 Q266 E267 C268 H269 E272 V273 K274 D275 Q280 E281 Y292 F293 L294 E295 K296 A297 N298

Q302 R303 F304 L305 P306 E307 Q308 L309 R310 A311 A317 F318 A319 N320 A323 Q324 A325 R326 L327 L328 Y329 G330 N331 V341 V342 Q343 S344 V345 D348 V351 F354 L355 V356 L357 Q358 T362 D363 L364 A365 S366 S367 E368 G369 V370 K371 N372 L373 T376 D377 S378 D379 Q380

L381 H385 R389 I392 K393 K394 K395 V396 V397 V398 E399 V404 F411 L417 Y418 L419 H420 G421 V422 V423

- Molecule 25: Large ribosomal subunit protein mL38

Chain 6:

MET ALA ALA PRO TRP TRP ARG ALA ALA PHE PHE GLY ILE GLY ARG CYS ARG GLY PHE SER THR SER ALA PHE LEU SER ARG ARG THR PRO PRO LEU GLY PRO MET PRO ASN GLU ASP ILE ASP VAL SER ASN LEU GLU ARG LEU E49 R60 A61 E62 Q63 E64 A65 R66 A67 P68 H69

W70 V71 R72 R75 F78 V79 LYS GLU THR ASP PRO LYS ASP LYS ILE ASP ILE GLY LEU PRO PRO PRO ARG VAL SER R99 T100 Q101 K102 L103 L104 E105 R106 K107 H108 F109 L110 R111 E112 L113 R114 A115 N116 V117 E118 E119 E120 R121 A122 A123 R124 L125 R126 T127 A128 S129 R136

E140 ARG THR CYS G144 H147 R150 L151 A152 E153 L157 Y158 R159 D160 L161 G164 A165 T166 V171 V175 A176 Y177 A178 V179 G180 E181 E182 D183 L184 I185 P186 V187 Y188 N191 A198 S199 R200 A201 V204 T205 TYR GLU ALA ASP LYS ASP S212 L213 W214 T215

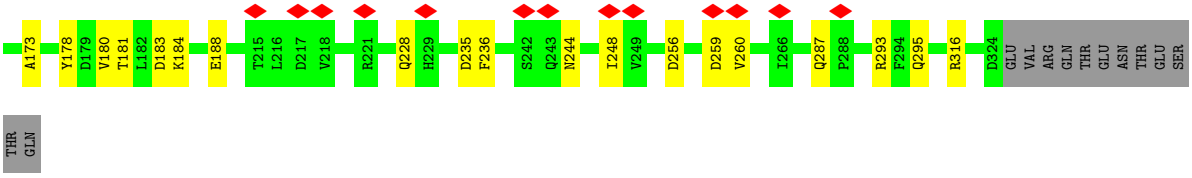
L216 I219 N220 L226 E227 A230 E231 H234 L237 I240 P241 S242 N243 R244 V245 A246 E247 G248 Y254 P257 L271 D276 K277 P278 I279 N280 F281 S282 E283 D284 T285 S288 P289 C290 L293 A294 Q295 R296 R299 D302 F303 Y304 Q308 E309 A310

L316 A317 F318 F319 Q320 D325 L334 R338 E339 F344 V345 R346 P347 P348 P349 Y350 H351 P352 K353 Q354 K355 R356 F357 P358 H359 E360 Q361 P362 L363 R364 Y365 L366 D367 R368 Y369 R370 D371 S372 H373 GLU PRO THR TYR GLY ILE TYR

- Molecule 26: Large ribosomal subunit protein mL39

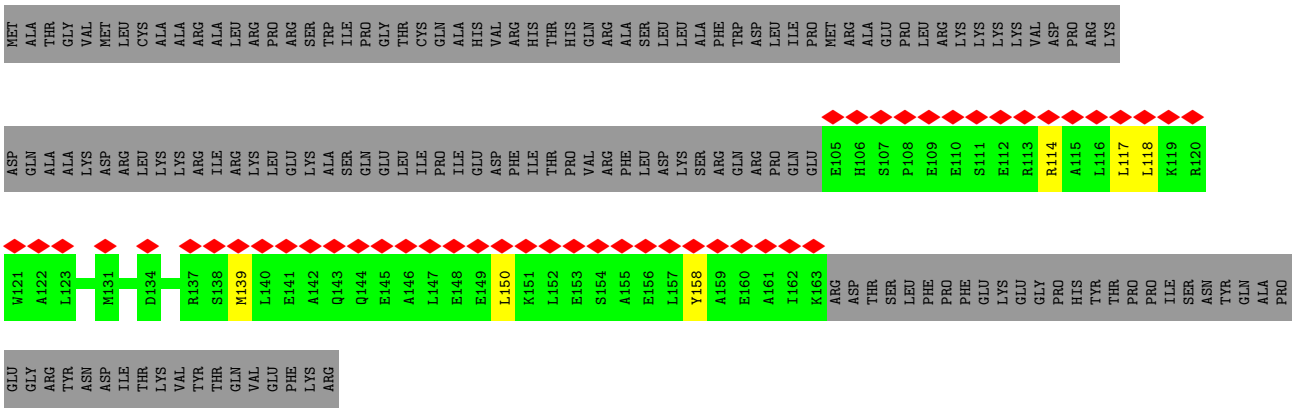
Chain 7:

MET ALA THR ALA VAL GLY ARG LEU VAL LEU ARG ARG PRO GLY ALA GLY GLY GLY ALA ARG TRP ARG PHE ILE ALA THR SER PRO ALA ALA GLU LEU S33 M42 K61 V67 D71 V77 N81 F127 K128 L147 I151 F155 D158 Y159 V160 V161 S162



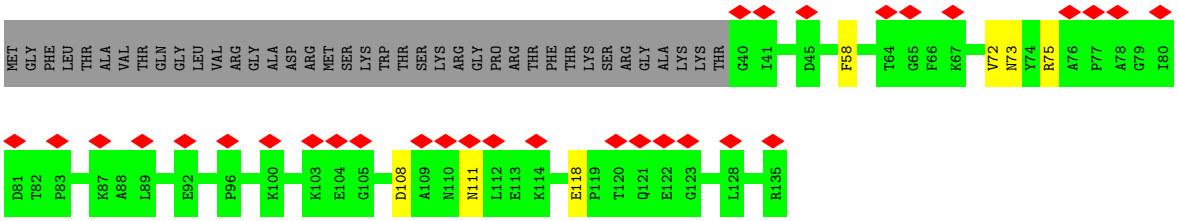
• Molecule 27: Large ribosomal subunit protein mL40

Chain 8:



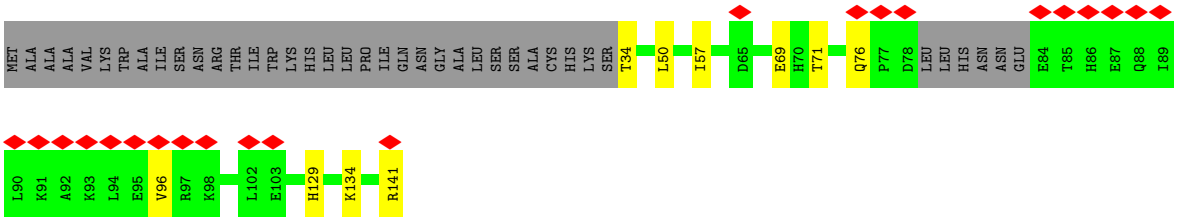
• Molecule 28: Large ribosomal subunit protein mL41

Chain 9:



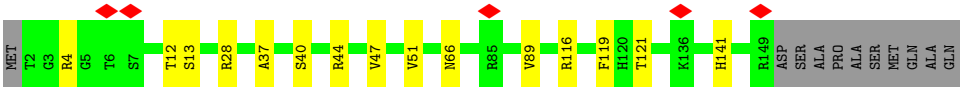
• Molecule 29: Large ribosomal subunit protein mL42

Chain a:



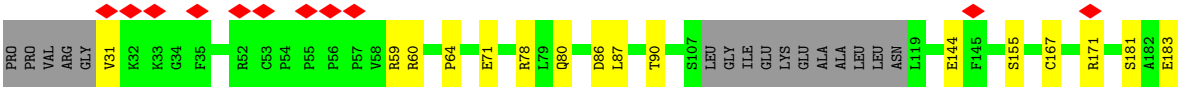
• Molecule 30: Large ribosomal subunit protein mL43

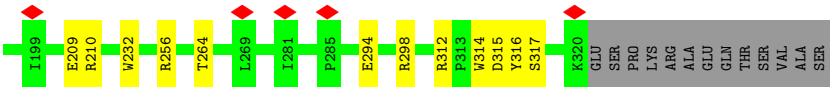
Chain b:



• Molecule 31: Large ribosomal subunit protein mL44

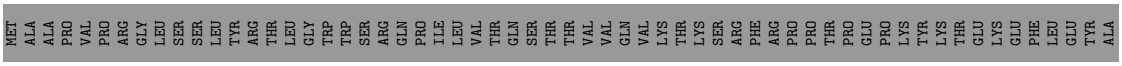
Chain c:

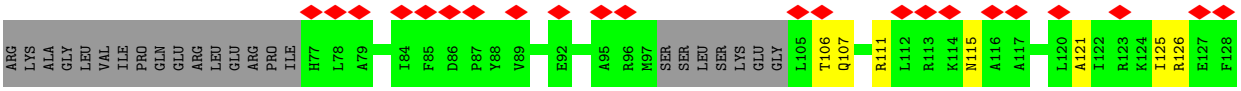


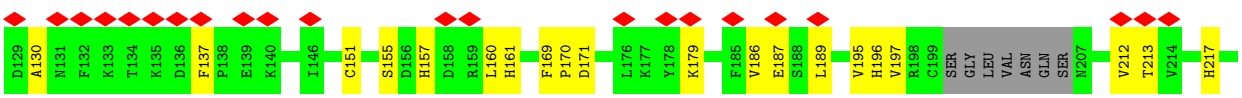


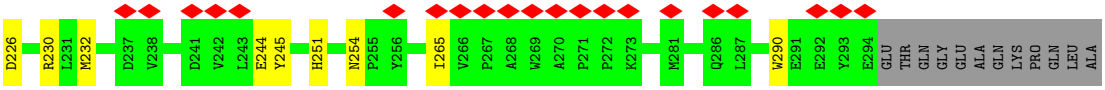
• Molecule 32: Large ribosomal subunit protein mL45

Chain d:



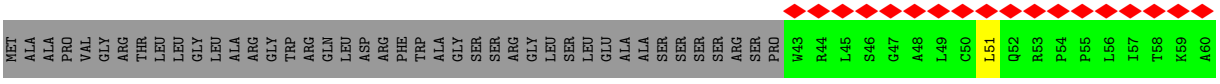


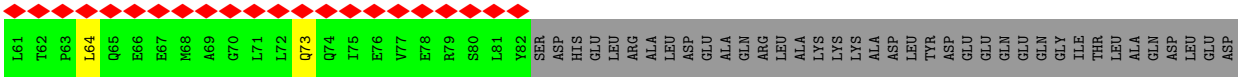


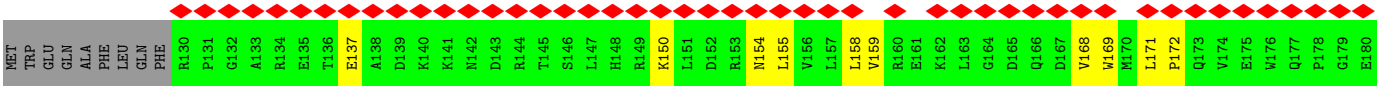


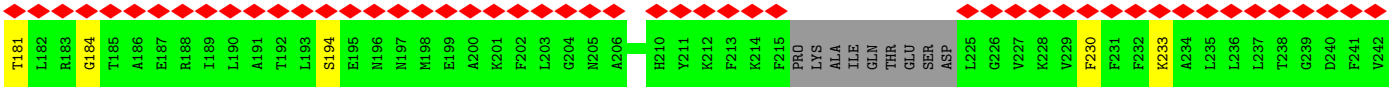
• Molecule 33: Large ribosomal subunit protein mL46

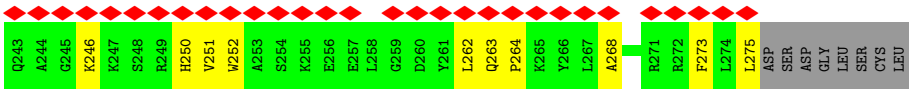
Chain e:





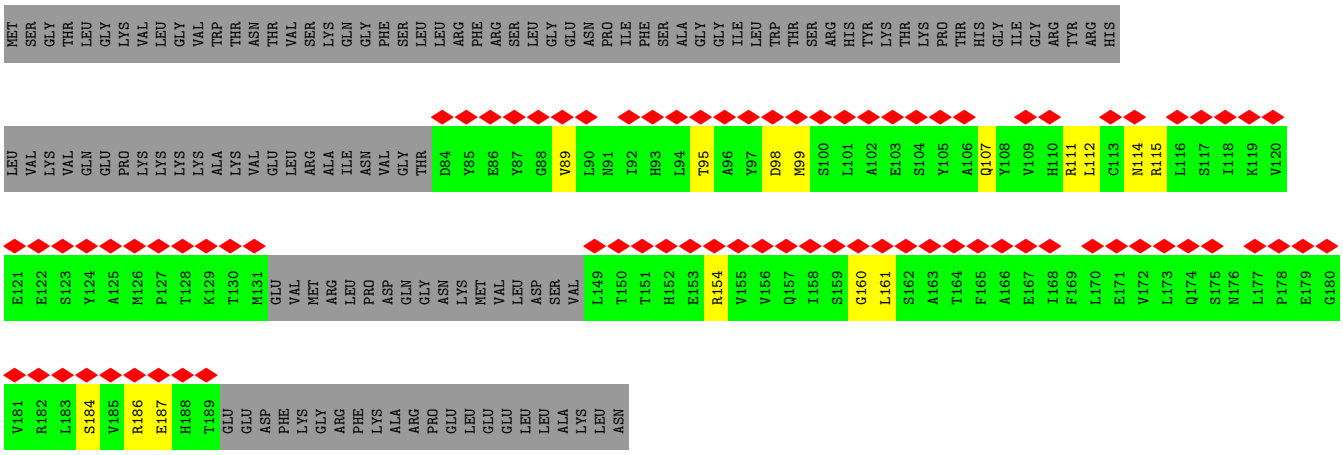






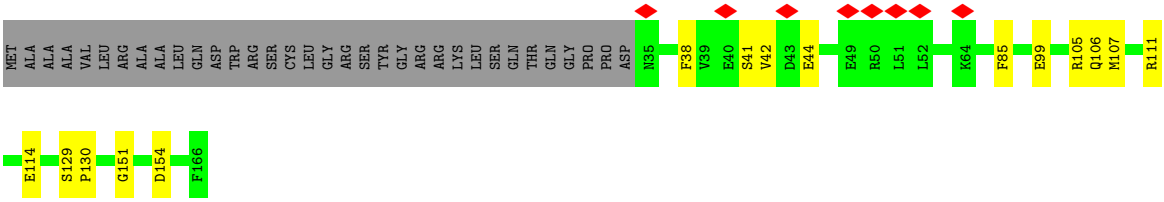
• Molecule 34: Large ribosomal subunit protein mL48

Chain f:



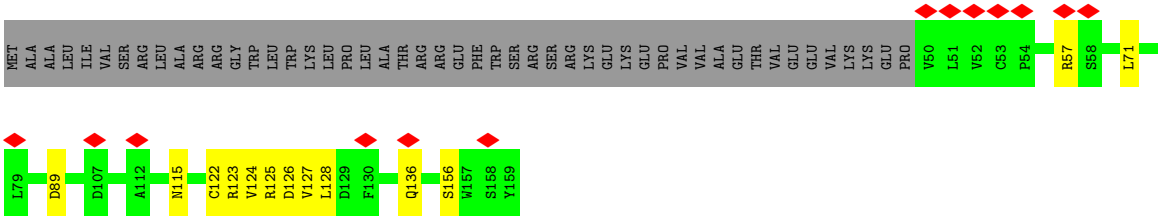
• Molecule 35: Large ribosomal subunit protein mL49

Chain g:



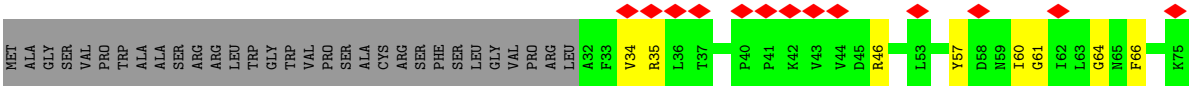
• Molecule 36: Large ribosomal subunit protein mL50

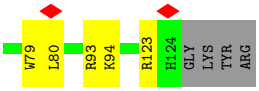
Chain h:



• Molecule 37: Large ribosomal subunit protein mL51

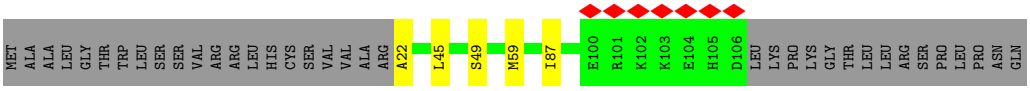
Chain i:





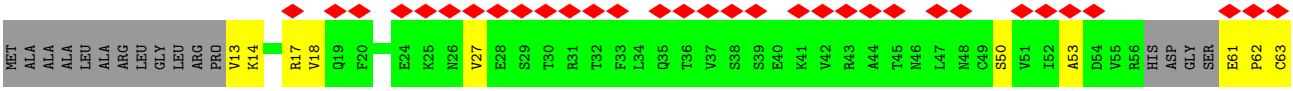
• Molecule 38: Large ribosomal subunit protein mL52

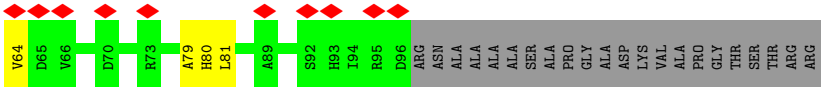
Chain j:



• Molecule 39: Large ribosomal subunit protein mL53

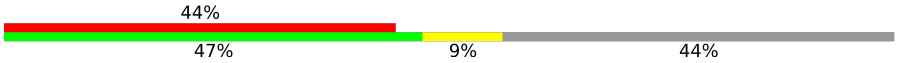
Chain k:

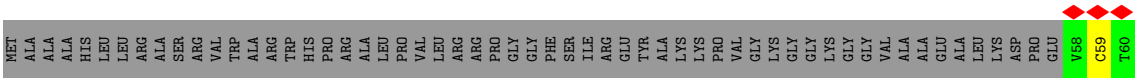


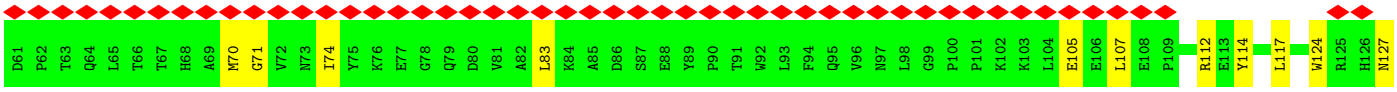


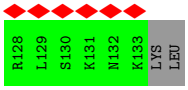
• Molecule 40: Large ribosomal subunit protein mL54

Chain l:



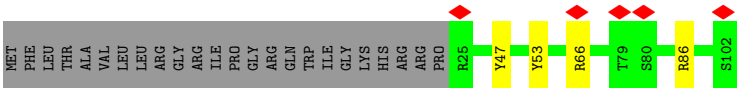






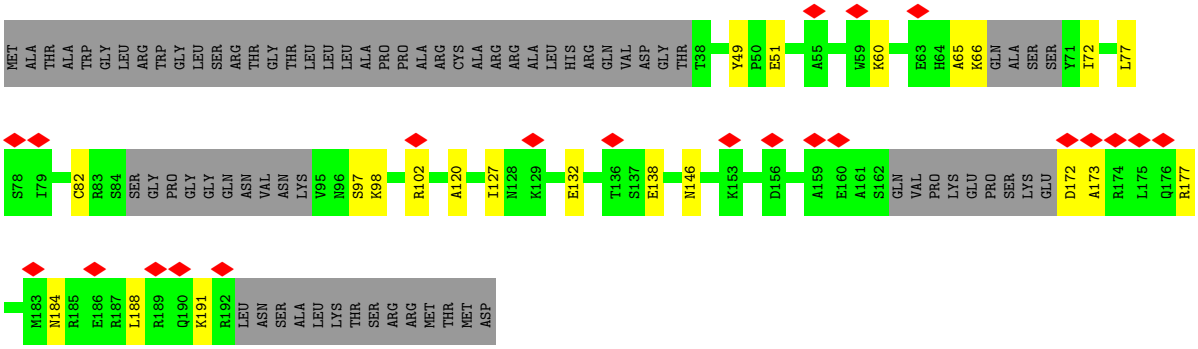
• Molecule 41: Large ribosomal subunit protein mL63

Chain o:



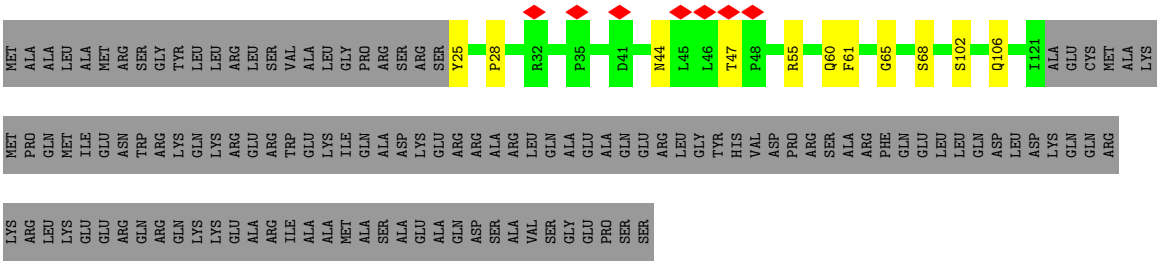
• Molecule 42: Large ribosomal subunit protein mL62

Chain p:



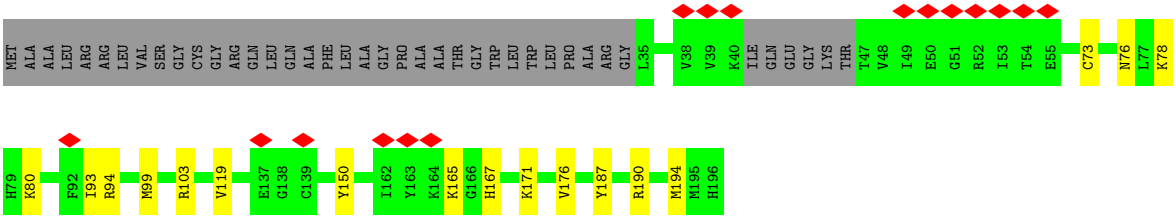
- Molecule 43: Large ribosomal subunit protein mL64

Chain q:



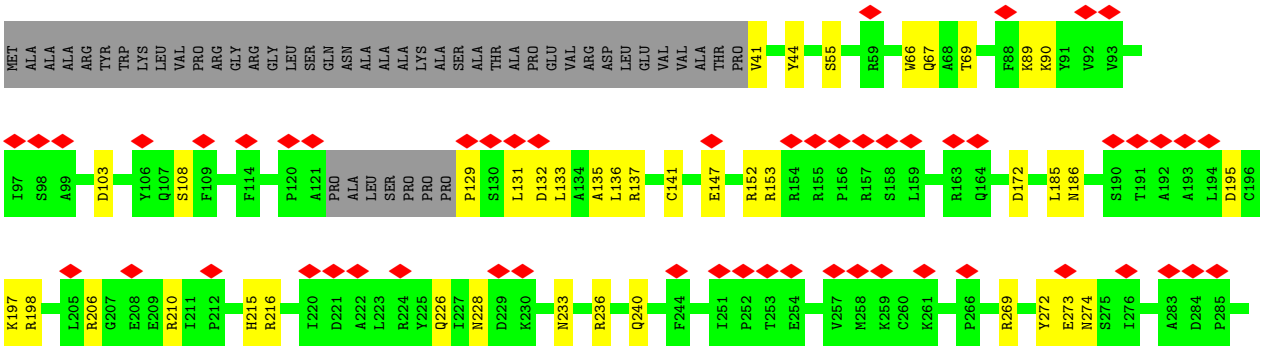
- Molecule 44: Large ribosomal subunit protein mL66

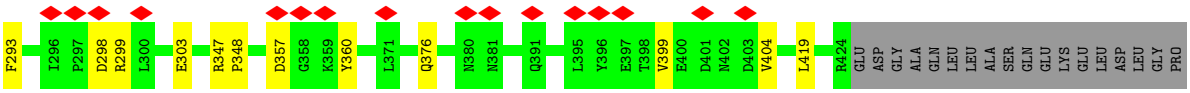
Chain r:



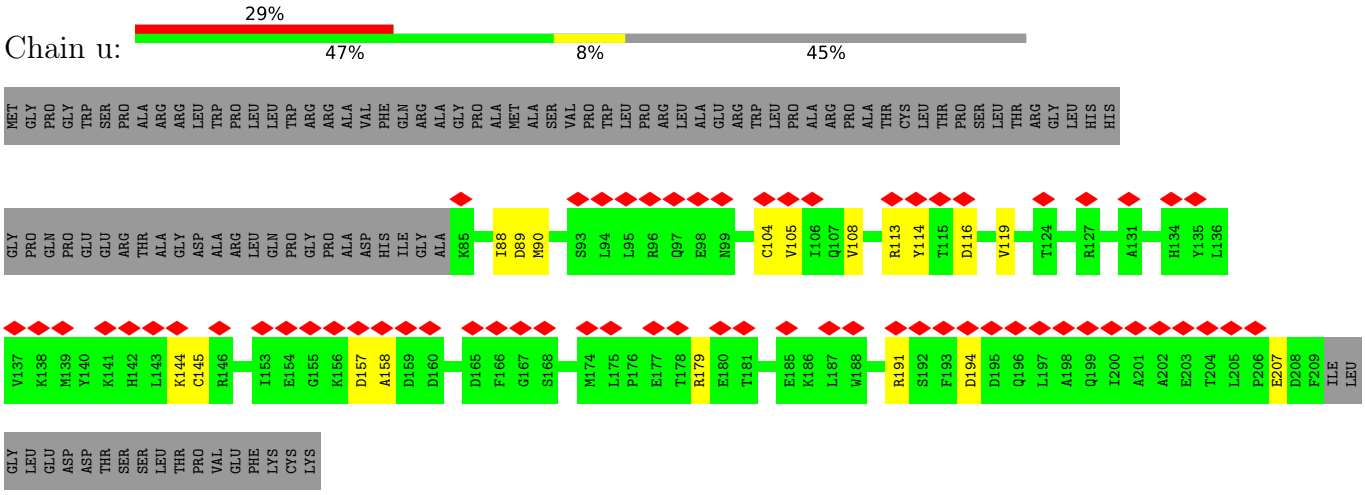
- Molecule 45: Large ribosomal subunit protein mL65

Chain s:

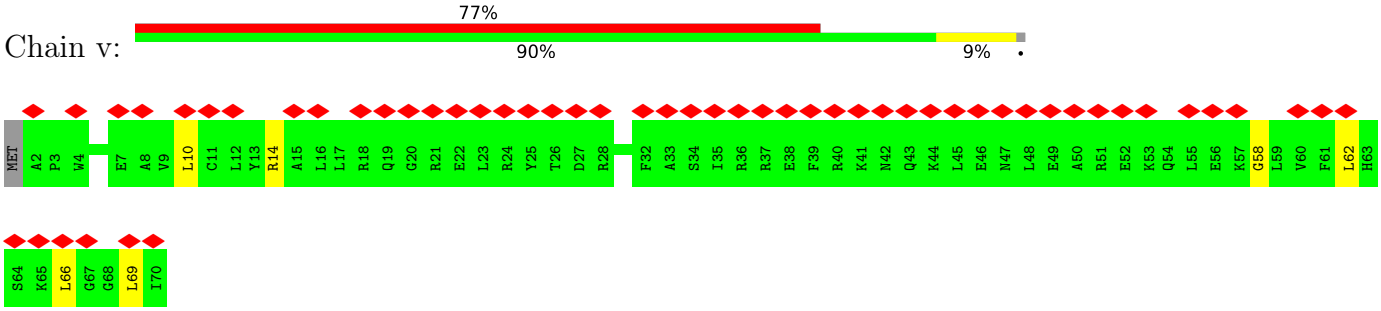




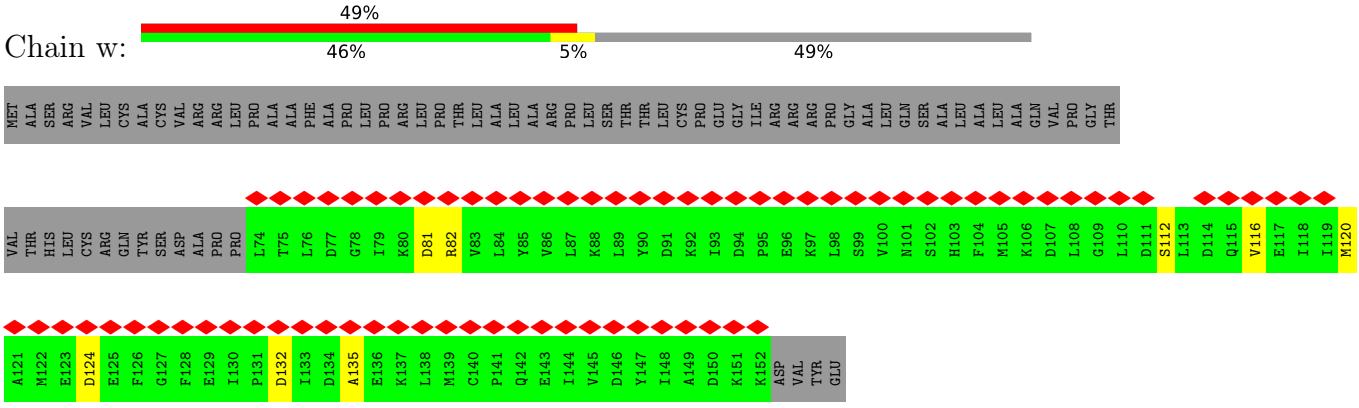
- Molecule 46: Mitochondrial assembly of ribosomal large subunit protein 1



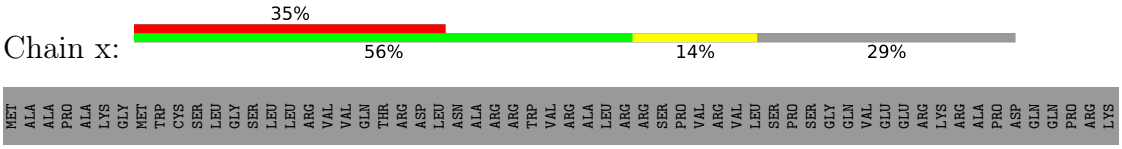
- Molecule 47: Predicted gene, 55359

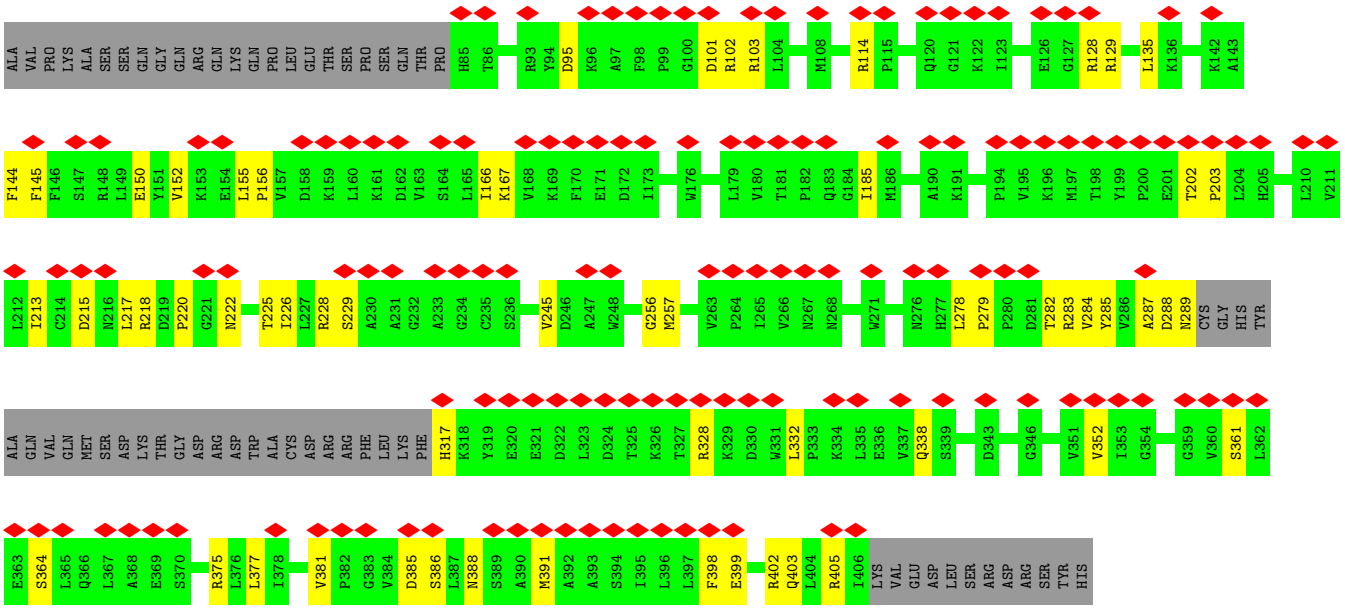


- Molecule 48: Acyl carrier protein, mitochondrial



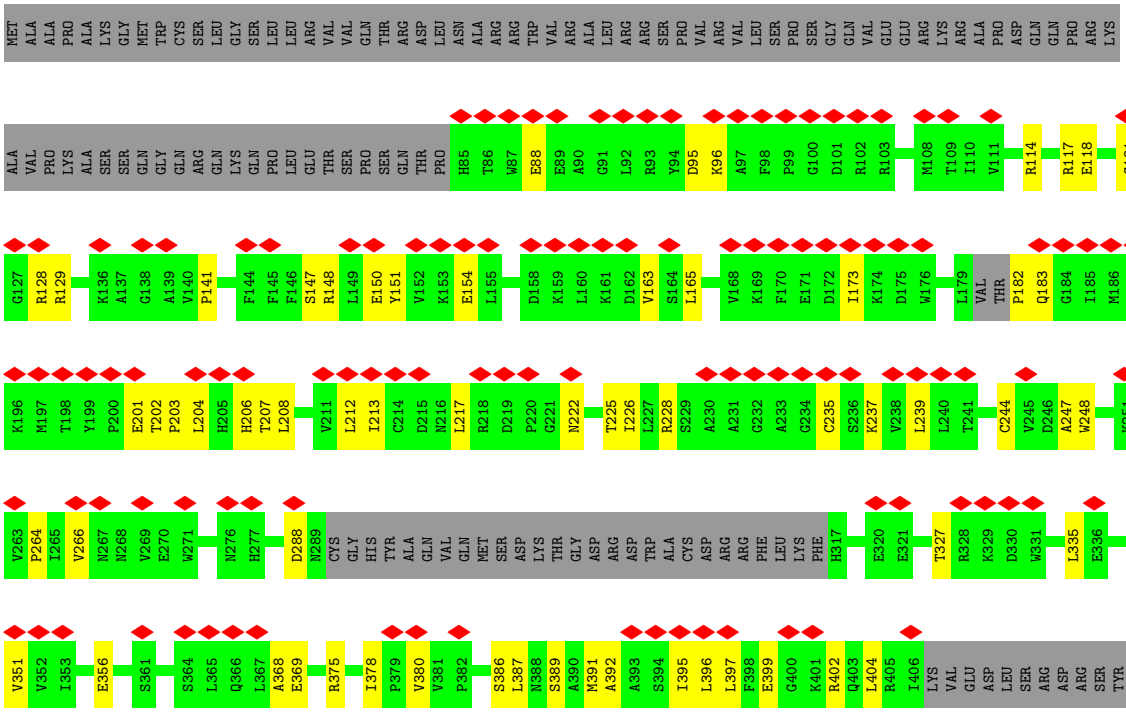
- Molecule 49: rRNA methyltransferase 3, mitochondrial





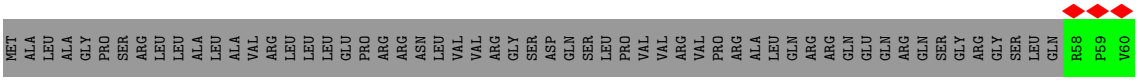
- Molecule 49: rRNA methyltransferase 3, mitochondrial

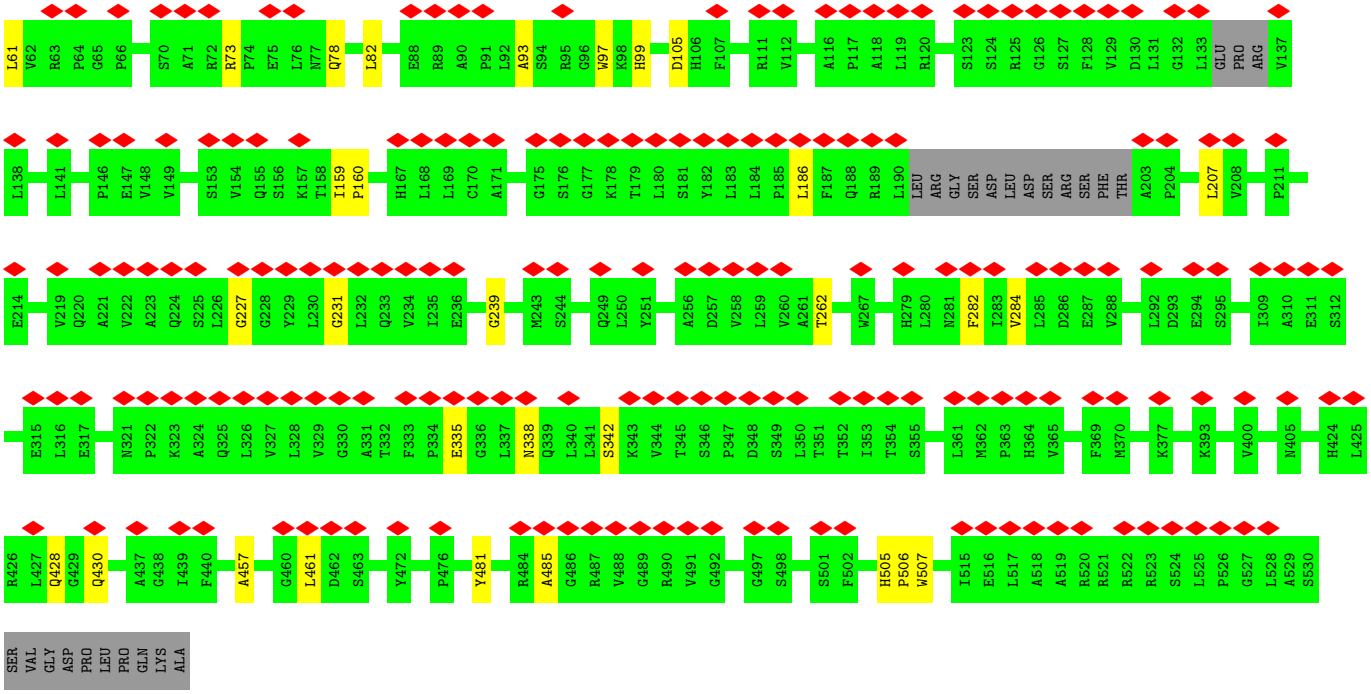
Chain y:



- Molecule 50: Probable ATP-dependent RNA helicase DDX28

Chain z:




L61 V62 R63 P64 G65 P66 S70 A71 R72 R73 P74 E75 L76 N77 Q78 L82 E88 R89 A90 P91 L92 A93 S94 R95 G96 W97 K98 H99 D105 H106 F107 R111 V112 A116 P117 A118 L119 R120 S123 S124 R125 G126 S127 F128 V129 D130 L131 G132 L133 GLU PRO ARG V137
L138 L141 P146 E147 V148 V149 S153 V154 Q155 S156 K157 T158 I159 P160 H167 L168 L169 C170 A171 G175 S176 G177 K178 T179 L180 S181 Y182 L183 L184 P185 L186 F187 Q188 R189 L190 LEU ARG GLY SER ASP LEU ASP SER ARG SER PHE THR A203 P204 L207 V208 P211
E214 V219 Q220 A221 V222 A223 Q224 S225 L226 G227 G228 Y229 L230 G231 L232 Q233 V234 I235 E236 G239 M243 S244 Q249 L250 Y251 A256 D257 V258 L259 V260 A261 T262 W267 H279 L280 N281 F282 I283 V284 L285 D286 E287 V288 L292 D293 E294 S295 I309 A310 E311 S312
E315 L316 E317 N321 P322 K323 A324 Q325 L326 V327 L328 V329 G330 A331 T332 F333 P334 E335 G336 L337 N338 Q339 L340 L341 S342 K343 V344 T345 S346 P347 D348 S349 L350 T351 T352 I353 T354 S355 L361 M362 P363 H364 V365 F369 M370 K377 K393 V400 N405 H424 L425
R426 L427 Q428 G429 Q430 A437 G438 I439 F440 A457 G460 L461 D462 S463 Y472 P476 Y481 R484 A485 G486 R487 V488 G489 R490 V491 G492 G497 S498 S501 F502 H505 P506 W507 I515 E516 L517 A518 A519 R520 R521 R522 R523 S524 L525 P526 G527 L528 A529 S530
SER VAL GLY ASP PRO LEU PRO GLN LYS ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6223	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)	400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.503	Depositor
Minimum map value	-0.186	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	457.2936, 457.2936, 457.2936	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84684, 0.84684, 0.84684	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: ZN, FES

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	0.07	0/26881	0.18	0/41775
2	B	0.07	0/1459	0.17	0/2266
3	D	0.08	0/1357	0.23	0/1831
4	E	0.07	0/2186	0.20	0/2972
5	F	0.07	0/1772	0.20	0/2415
6	H	0.08	0/793	0.23	0/1066
7	I	0.09	0/1273	0.24	0/1722
8	J	0.09	0/1093	0.25	0/1472
9	K	0.06	0/1436	0.19	0/1948
10	L	0.07	0/908	0.21	0/1224
11	M	0.08	0/2054	0.24	0/2776
12	O	0.06	0/1246	0.19	0/1679
13	P	0.07	0/1181	0.21	0/1600
14	Q	0.08	0/1832	0.21	0/2471
15	R	0.06	0/1096	0.17	0/1469
16	S	0.08	0/1328	0.22	0/1798
17	T	0.07	0/1402	0.19	0/1885
18	U	0.07	0/1062	0.21	0/1441
19	V	0.07	0/1669	0.20	0/2259
20	X	0.07	0/2075	0.20	0/2806
21	Y	0.06	0/1561	0.17	0/2093
22	Z	0.07	0/959	0.21	0/1298
23	0	0.07	0/896	0.20	0/1200
24	5	0.07	0/3256	0.21	0/4432
25	6	0.09	0/2622	0.23	0/3560
26	7	0.07	0/2436	0.21	0/3300
27	8	0.06	0/499	0.17	0/666
28	9	0.09	0/800	0.22	0/1082
29	a	0.07	0/884	0.20	0/1197
30	b	0.07	0/1203	0.21	0/1625
31	c	0.07	0/2297	0.20	0/3106
32	d	0.07	0/1736	0.20	0/2353

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	e	0.07	0/1465	0.22	0/1971
34	f	0.09	0/726	0.22	0/983
35	g	0.08	0/1126	0.22	0/1533
36	h	0.09	0/894	0.24	0/1216
37	i	0.07	0/818	0.21	0/1099
38	j	0.06	0/698	0.18	0/937
39	k	0.07	0/636	0.20	0/857
40	l	0.07	0/651	0.19	0/882
41	o	0.06	0/655	0.17	0/880
42	p	0.07	0/1104	0.22	0/1476
43	q	0.07	0/825	0.19	0/1126
44	r	0.08	0/1301	0.21	0/1756
45	s	0.07	0/3118	0.20	0/4232
46	u	0.07	0/1053	0.20	0/1425
47	v	0.08	0/596	0.23	0/795
48	w	0.11	0/646	0.27	0/869
49	x	0.08	0/2357	0.24	0/3198
49	y	0.09	0/2342	0.25	0/3174
50	z	0.07	0/3623	0.20	0/4918
All	All	0.07	0/97886	0.20	0/138114

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	24019	12126	12156	204	0
2	B	1303	657	658	14	0
3	D	1335	1373	1373	14	0
4	E	2122	2097	2097	14	0
5	F	1728	1755	1754	20	0
6	H	779	814	814	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	I	1245	1330	1330	17	0
8	J	1075	1145	1145	15	0
9	K	1396	1398	1398	9	0
10	L	893	944	944	10	0
11	M	2010	2080	2080	29	0
12	O	1222	1254	1254	14	0
13	P	1154	1148	1148	21	0
14	Q	1790	1822	1822	18	0
15	R	1077	1137	1137	6	0
16	S	1301	1372	1372	11	0
17	T	1369	1402	1402	12	0
18	U	1034	1038	1038	9	0
19	V	1628	1622	1622	23	0
20	X	2021	2051	2051	20	0
21	Y	1523	1553	1553	13	0
22	Z	934	979	979	5	0
23	0	881	908	908	13	0
24	5	3168	3187	3187	18	0
25	6	2534	2420	2418	45	0
26	7	2379	2378	2378	15	0
27	8	493	484	484	7	0
28	9	778	772	772	6	0
29	a	860	843	843	9	0
30	b	1181	1195	1195	13	0
31	c	2246	2256	2256	20	0
32	d	1688	1670	1670	24	0
33	e	1437	1474	1474	21	0
34	f	714	704	704	11	0
35	g	1090	1094	1094	12	0
36	h	872	868	867	10	0
37	i	795	816	816	11	0
38	j	684	692	692	5	0
39	k	629	639	639	8	0
40	l	635	631	631	10	0
41	o	640	623	623	4	0
42	p	1089	1112	1112	16	0
43	q	799	785	785	9	0
44	r	1267	1319	1319	15	0
45	s	3045	3057	3057	34	0
46	u	1029	1012	1012	12	0
47	v	586	603	603	5	0
48	w	637	640	640	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	x	2305	2356	2356	50	0
49	y	2291	2340	2340	59	0
50	z	3555	3681	3681	22	0
51	0	1	0	0	0	0
52	r	4	0	0	2	0
All	All	93270	81656	81683	823	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 823 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2168:U:O2'	50:z:99:HIS:O	1.83	0.95
1:A:1093:A:O2'	1:A:1094:A:OP1	1.92	0.87
34:f:99:MET:SD	34:f:154:ARG:NH2	2.48	0.86
5:F:209:TYR:O	36:h:57:ARG:NH1	2.08	0.86
1:A:1477:A:OP1	35:g:105:ARG:NH2	2.09	0.86

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	168/246 (68%)	164 (98%)	4 (2%)	0	100	100
4	E	260/348 (75%)	253 (97%)	7 (3%)	0	100	100
5	F	210/294 (71%)	205 (98%)	5 (2%)	0	100	100
6	H	93/268 (35%)	89 (96%)	4 (4%)	0	100	100
7	I	150/262 (57%)	142 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	J	140/192 (73%)	136 (97%)	4 (3%)	0	100	100
9	K	169/178 (95%)	168 (99%)	1 (1%)	0	100	100
10	L	113/145 (78%)	106 (94%)	7 (6%)	0	100	100
11	M	245/295 (83%)	239 (98%)	6 (2%)	0	100	100
12	O	147/176 (84%)	144 (98%)	3 (2%)	0	100	100
13	P	139/180 (77%)	138 (99%)	1 (1%)	0	100	100
14	Q	215/292 (74%)	211 (98%)	4 (2%)	0	100	100
15	R	129/149 (87%)	129 (100%)	0	0	100	100
16	S	157/209 (75%)	152 (97%)	5 (3%)	0	100	100
17	T	164/206 (80%)	164 (100%)	0	0	100	100
18	U	121/146 (83%)	121 (100%)	0	0	100	100
19	V	196/216 (91%)	196 (100%)	0	0	100	100
20	X	240/294 (82%)	238 (99%)	2 (1%)	0	100	100
21	Y	174/252 (69%)	174 (100%)	0	0	100	100
22	Z	113/160 (71%)	112 (99%)	1 (1%)	0	100	100
23	0	106/187 (57%)	106 (100%)	0	0	100	100
24	5	383/423 (90%)	379 (99%)	4 (1%)	0	100	100
25	6	289/380 (76%)	278 (96%)	11 (4%)	0	100	100
26	7	290/336 (86%)	286 (99%)	4 (1%)	0	100	100
27	8	57/206 (28%)	56 (98%)	1 (2%)	0	100	100
28	9	94/135 (70%)	93 (99%)	1 (1%)	0	100	100
29	a	99/142 (70%)	96 (97%)	3 (3%)	0	100	100
30	b	146/159 (92%)	141 (97%)	5 (3%)	0	100	100
31	c	275/308 (89%)	275 (100%)	0	0	100	100
32	d	198/306 (65%)	195 (98%)	3 (2%)	0	100	100
33	e	171/283 (60%)	160 (94%)	11 (6%)	0	100	100
34	f	85/211 (40%)	81 (95%)	4 (5%)	0	100	100
35	g	130/166 (78%)	129 (99%)	1 (1%)	0	100	100
36	h	108/159 (68%)	106 (98%)	2 (2%)	0	100	100
37	i	91/128 (71%)	91 (100%)	0	0	100	100
38	j	83/121 (69%)	82 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	k	76/118 (64%)	74 (97%)	2 (3%)	0	100	100
40	l	74/135 (55%)	72 (97%)	2 (3%)	0	100	100
41	o	76/102 (74%)	76 (100%)	0	0	100	100
42	p	124/206 (60%)	122 (98%)	2 (2%)	0	100	100
43	q	95/222 (43%)	95 (100%)	0	0	100	100
44	r	152/196 (78%)	146 (96%)	6 (4%)	0	100	100
45	s	373/442 (84%)	365 (98%)	8 (2%)	0	100	100
46	u	123/228 (54%)	121 (98%)	2 (2%)	0	100	100
47	v	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
48	w	77/156 (49%)	75 (97%)	2 (3%)	0	100	100
49	x	291/418 (70%)	285 (98%)	6 (2%)	0	100	100
49	y	287/418 (69%)	282 (98%)	5 (2%)	0	100	100
50	z	452/540 (84%)	441 (98%)	11 (2%)	0	100	100
All	All	8215/11409 (72%)	8055 (98%)	160 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	D	143/197 (73%)	143 (100%)	0	100	100
4	E	237/298 (80%)	237 (100%)	0	100	100
5	F	190/250 (76%)	190 (100%)	0	100	100
6	H	86/231 (37%)	86 (100%)	0	100	100
7	I	143/230 (62%)	143 (100%)	0	100	100
8	J	116/152 (76%)	116 (100%)	0	100	100
9	K	151/158 (96%)	151 (100%)	0	100	100
10	L	99/122 (81%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	M	219/252 (87%)	219 (100%)	0	100	100
12	O	129/152 (85%)	129 (100%)	0	100	100
13	P	123/157 (78%)	123 (100%)	0	100	100
14	Q	197/258 (76%)	197 (100%)	0	100	100
15	R	110/128 (86%)	110 (100%)	0	100	100
16	S	145/180 (81%)	145 (100%)	0	100	100
17	T	147/180 (82%)	147 (100%)	0	100	100
18	U	112/133 (84%)	112 (100%)	0	100	100
19	V	176/190 (93%)	176 (100%)	0	100	100
20	X	219/265 (83%)	219 (100%)	0	100	100
21	Y	162/228 (71%)	162 (100%)	0	100	100
22	Z	108/146 (74%)	108 (100%)	0	100	100
23	0	97/170 (57%)	97 (100%)	0	100	100
24	5	349/372 (94%)	349 (100%)	0	100	100
25	6	264/335 (79%)	264 (100%)	0	100	100
26	7	269/301 (89%)	269 (100%)	0	100	100
27	8	51/182 (28%)	51 (100%)	0	100	100
28	9	83/114 (73%)	83 (100%)	0	100	100
29	a	97/129 (75%)	97 (100%)	0	100	100
30	b	130/138 (94%)	130 (100%)	0	100	100
31	c	243/266 (91%)	243 (100%)	0	100	100
32	d	182/272 (67%)	182 (100%)	0	100	100
33	e	152/238 (64%)	152 (100%)	0	100	100
34	f	80/185 (43%)	80 (100%)	0	100	100
35	g	122/148 (82%)	122 (100%)	0	100	100
36	h	100/143 (70%)	100 (100%)	0	100	100
37	i	84/111 (76%)	84 (100%)	0	100	100
38	j	68/99 (69%)	68 (100%)	0	100	100
39	k	72/95 (76%)	72 (100%)	0	100	100
40	l	70/112 (62%)	70 (100%)	0	100	100
41	o	65/85 (76%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	p	118/177 (67%)	118 (100%)	0	100	100
43	q	84/187 (45%)	84 (100%)	0	100	100
44	r	141/168 (84%)	141 (100%)	0	100	100
45	s	329/378 (87%)	329 (100%)	0	100	100
46	u	115/197 (58%)	115 (100%)	0	100	100
47	v	60/61 (98%)	60 (100%)	0	100	100
48	w	73/135 (54%)	73 (100%)	0	100	100
49	x	251/358 (70%)	251 (100%)	0	100	100
49	y	249/358 (70%)	249 (100%)	0	100	100
50	z	394/464 (85%)	394 (100%)	0	100	100
All	All	7404/9885 (75%)	7404 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
42	p	123	HIS
49	y	317	HIS
42	p	146	ASN
49	x	403	GLN
50	z	388	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1100/1584 (69%)	357 (32%)	27 (2%)
2	B	59/68 (86%)	24 (40%)	1 (1%)
All	All	1159/1652 (70%)	381 (32%)	28 (2%)

5 of 381 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1094	A
1	A	1100	C
1	A	1101	C
1	A	1102	U

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Mol	Chain	Res	Type
1	A	1103	A

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1894	C
2	B	20	A
1	A	2275	A
1	A	2564	G
1	A	2182	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is 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	$\#\|Z\| > 2$
52	FES	r	301	44,7	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
52	FES	r	301	44,7	-	-	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	r	301	FES	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

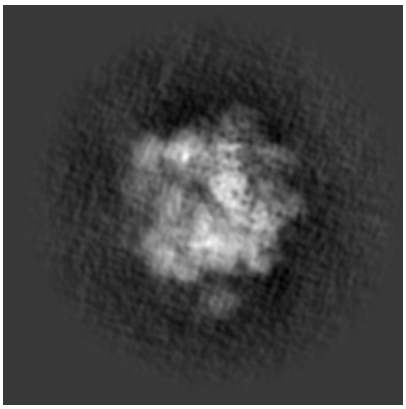
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-52044. These allow visual inspection of the internal detail of the map and identification of artifacts.

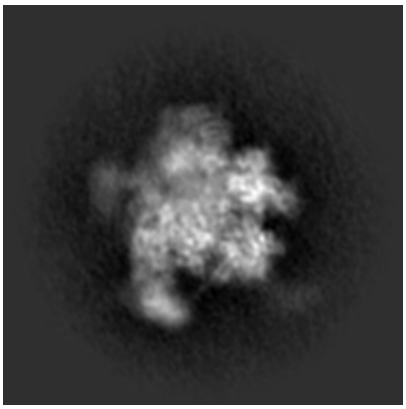
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

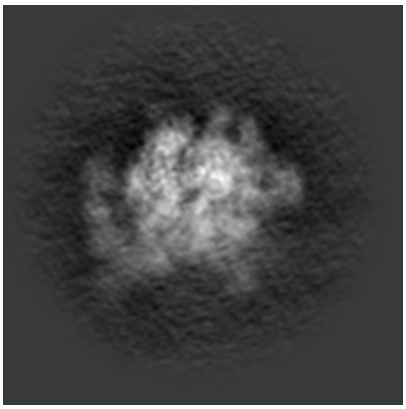
6.1.1 Primary map



X

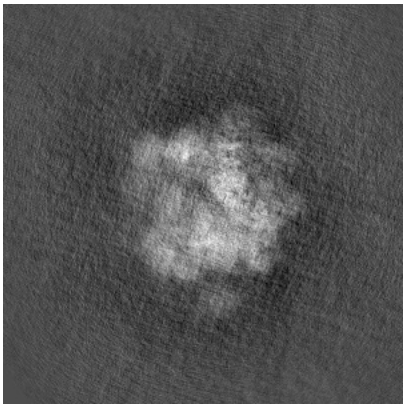


Y

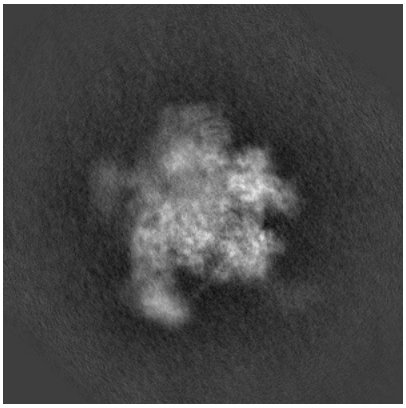


Z

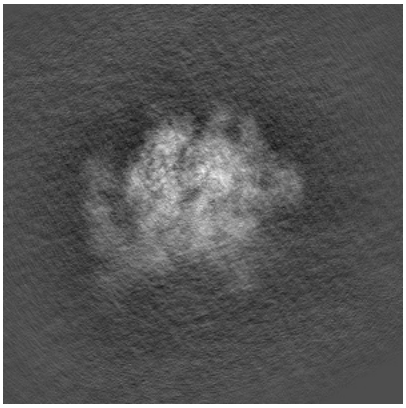
6.1.2 Raw map



X



Y

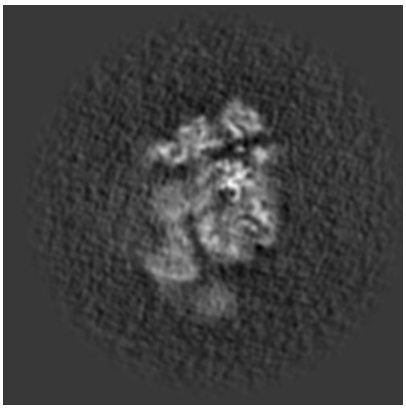


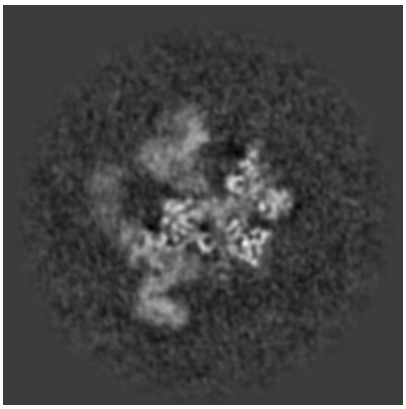
Z

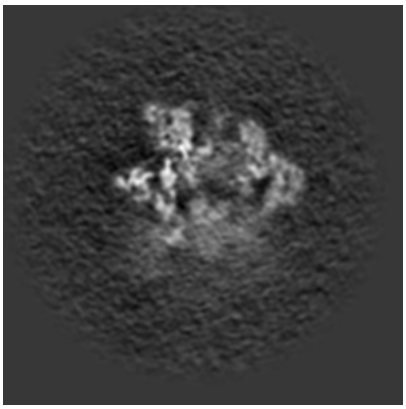
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

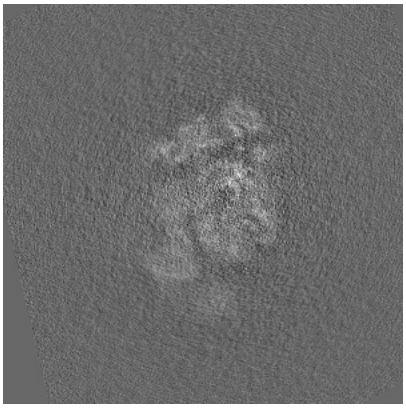
6.2.1 Primary map

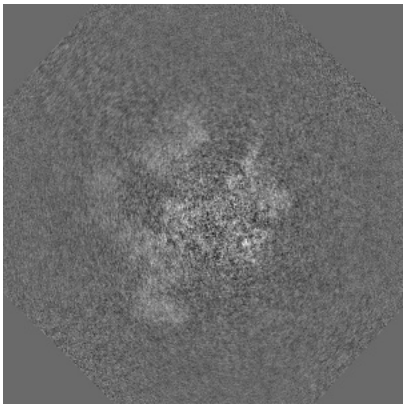

X Index: 270

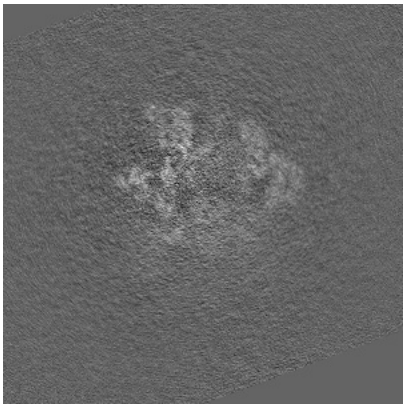

Y Index: 270


Z Index: 270

6.2.2 Raw map


X Index: 270

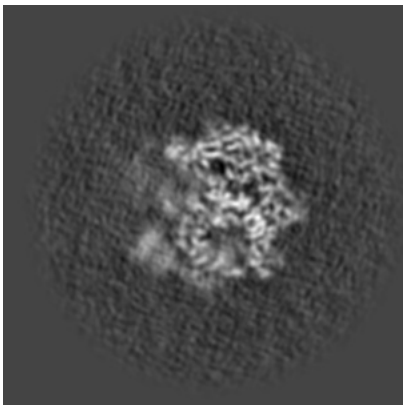

Y Index: 270


Z Index: 270

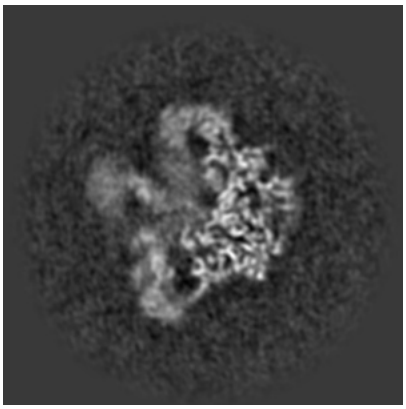
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

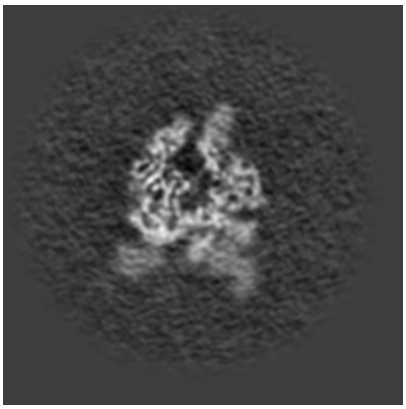
6.3.1 Primary map



X Index: 222

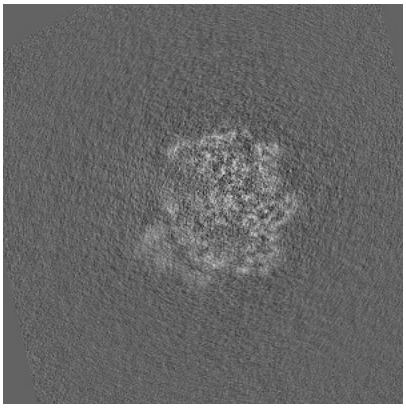


Y Index: 298

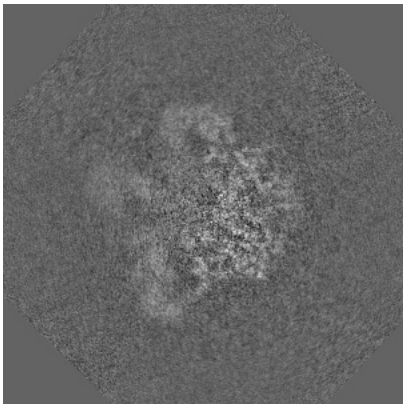


Z Index: 340

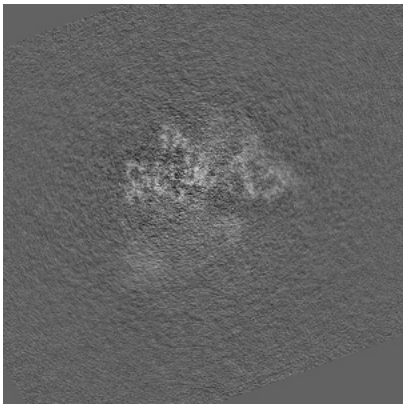
6.3.2 Raw map



X Index: 229



Y Index: 299

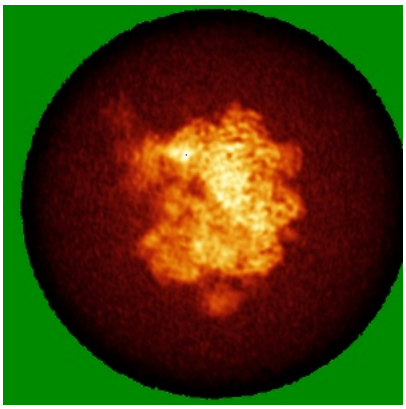


Z Index: 296

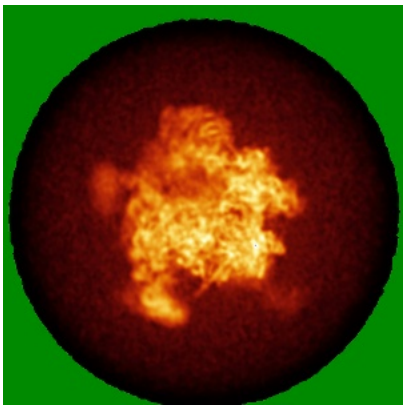
The images above show the largest variance slices of the map in three orthogonal directions.

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

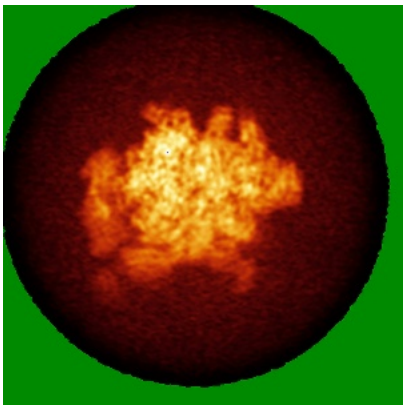
6.4.1 Primary map



X

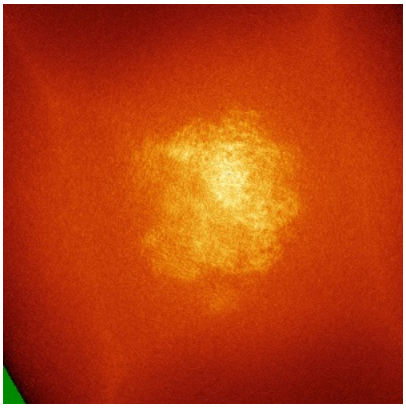


Y

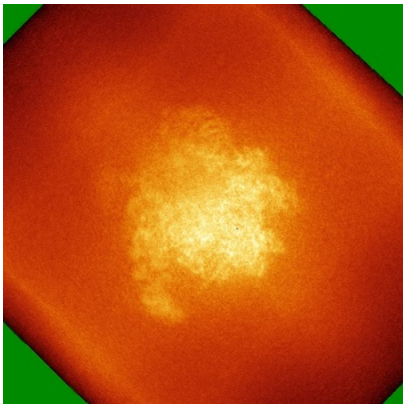


Z

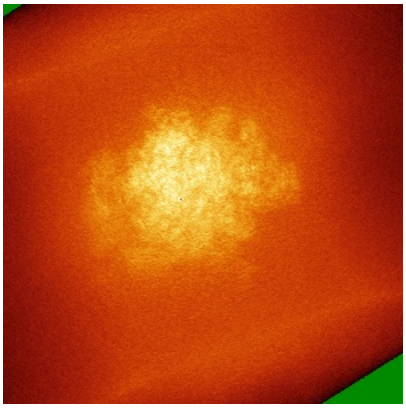
6.4.2 Raw map



X



Y



Z

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

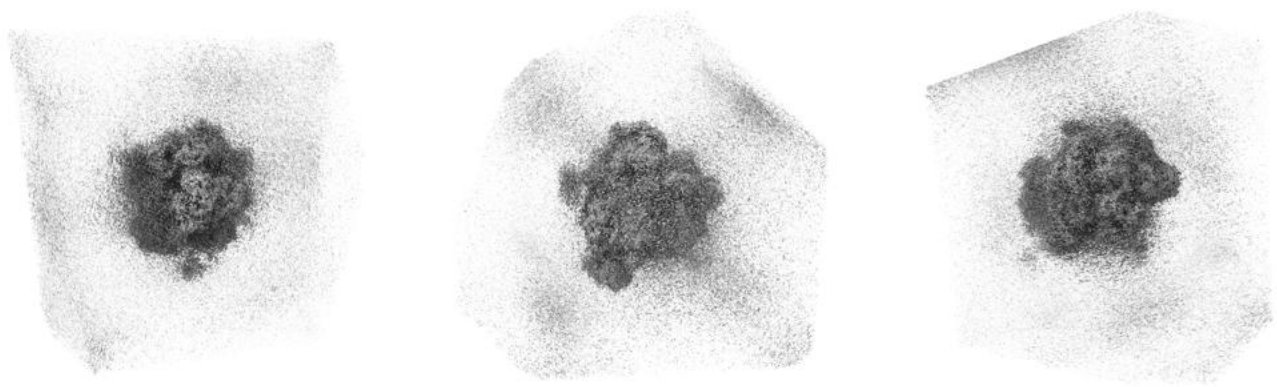
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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.

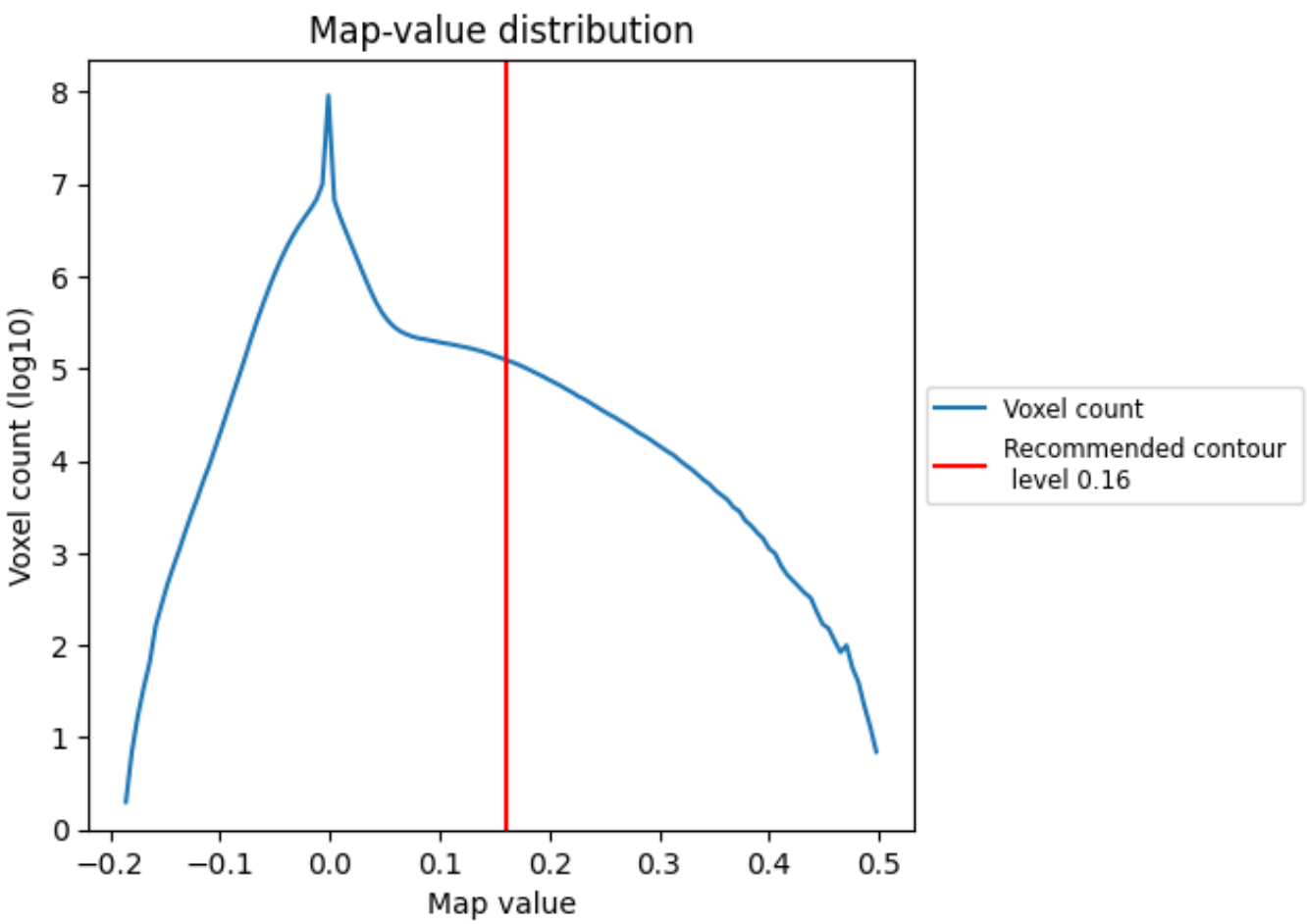
6.6 Mask visualisation (i)

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

7 Map analysis (i)

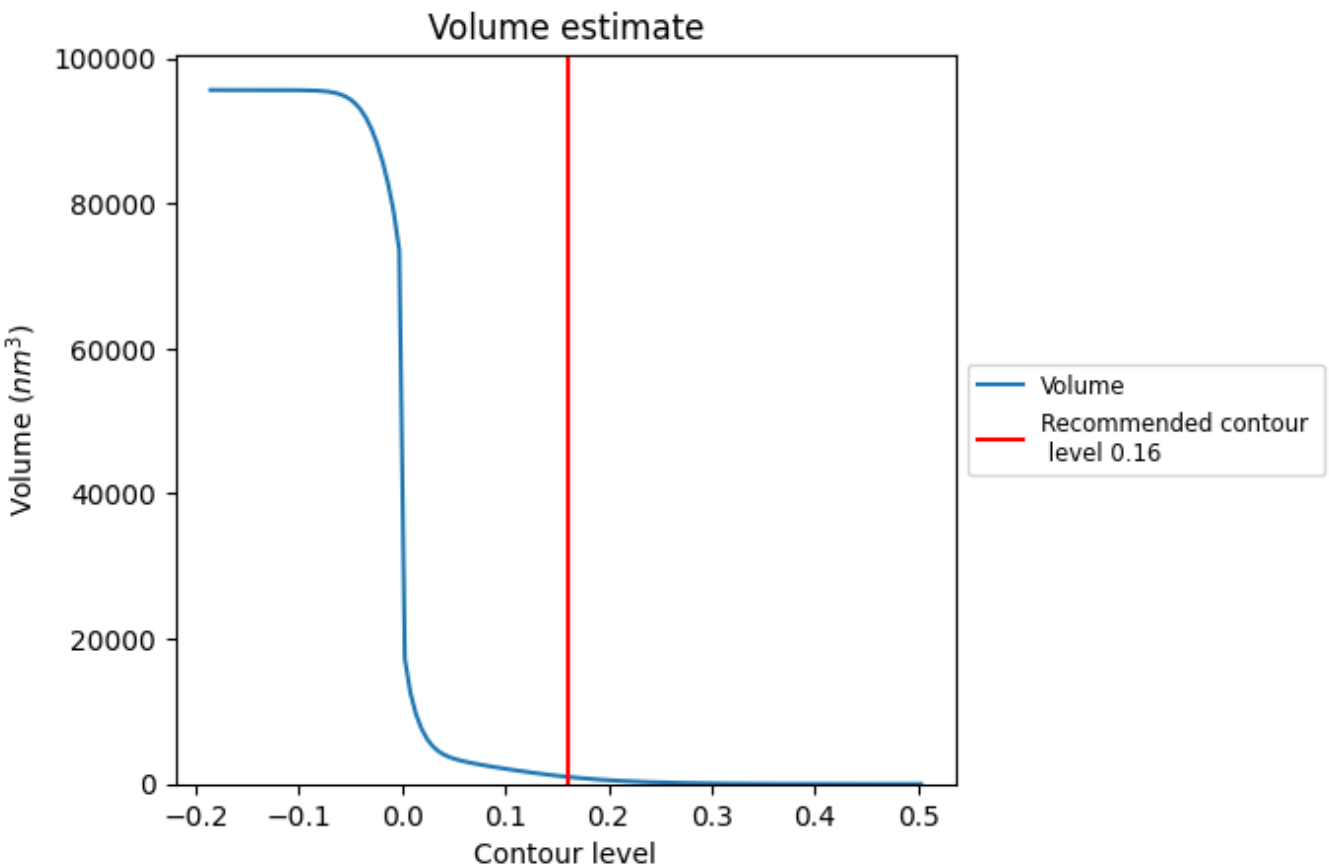
This section contains the results of statistical analysis of the map.

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.

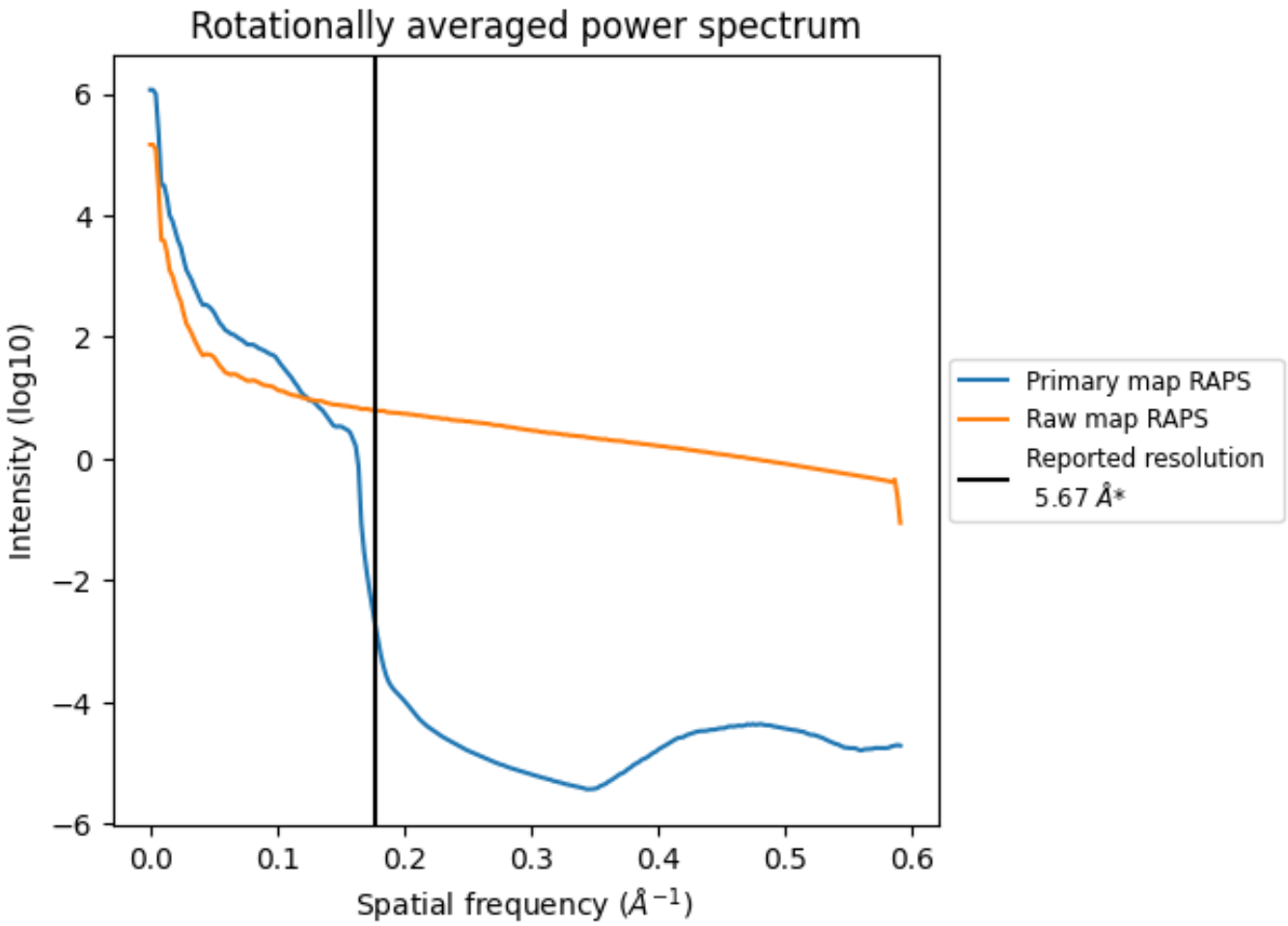
7.2 Volume estimate (i)



The volume at the recommended contour level is 982 nm^3; this corresponds to an approximate mass of 887 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)

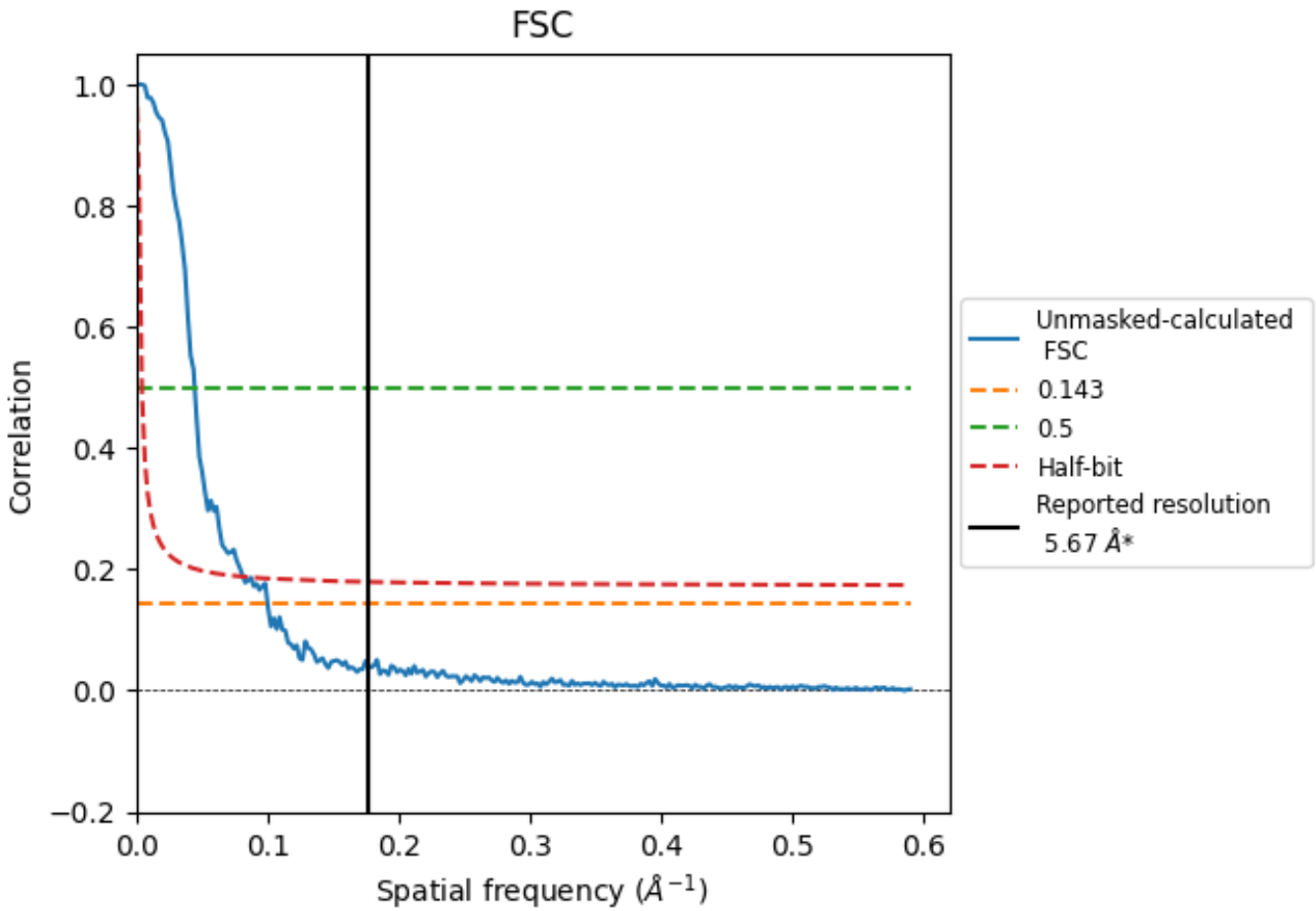


*Reported resolution corresponds to spatial frequency of 0.176 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.176 Å^{-1}

8.2 Resolution estimates (i)

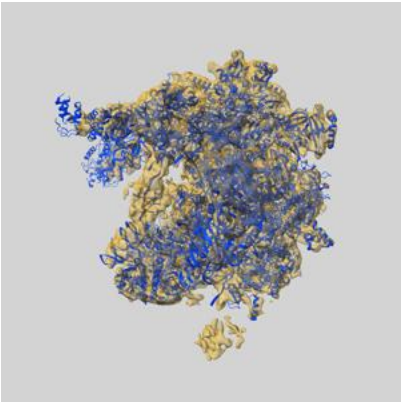
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.67	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.98	22.42	12.29

*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 9.98 differs from the reported value 5.67 by more than 10 %

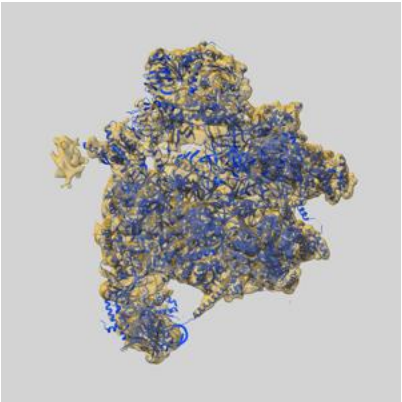
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-52044 and PDB model 9HCC. Per-residue inclusion information can be found in section 3 on page 14.

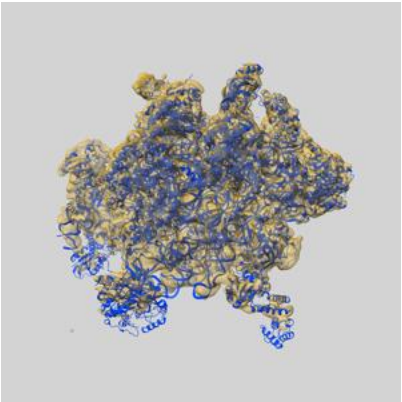
9.1 Map-model overlay (i)



X



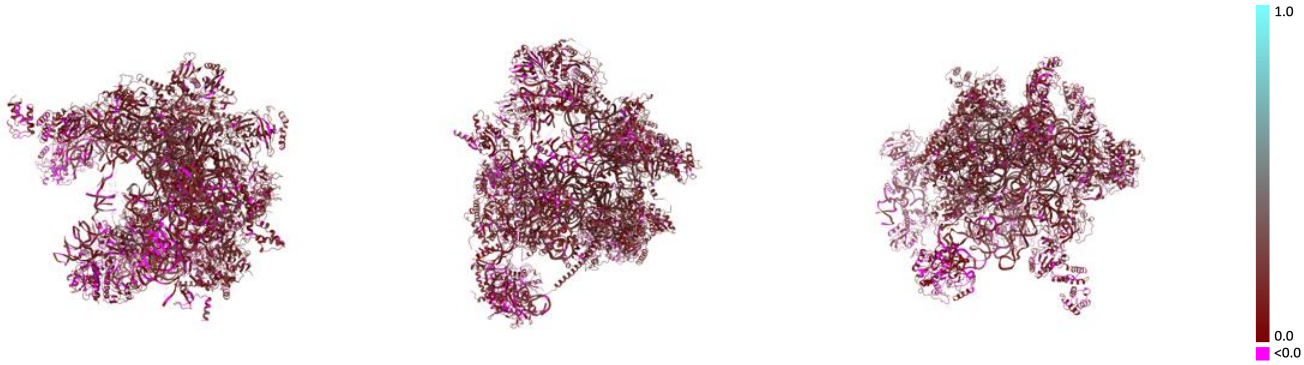
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.16 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.

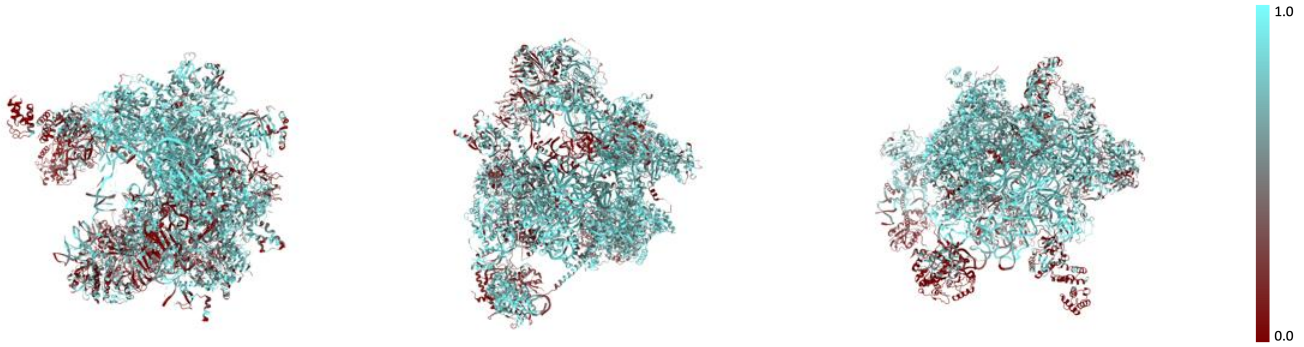
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

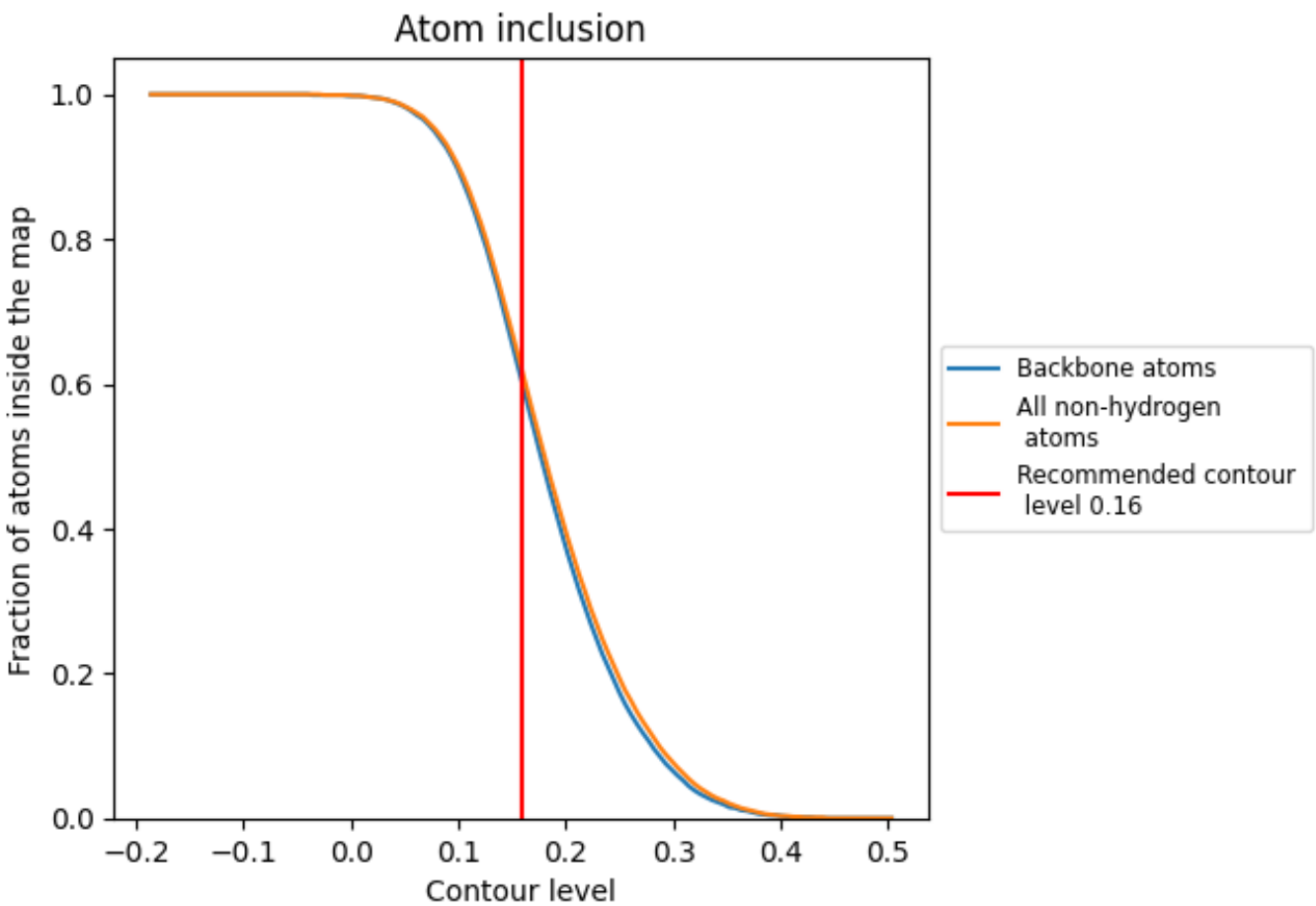
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.16).

9.4 Atom inclusion (i)



At the recommended contour level, 60% of all backbone atoms, 62% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6160	0.1460
0	0.7730	0.1800
5	0.3780	0.1160
6	0.5750	0.0880
7	0.7260	0.1710
8	0.1770	0.1090
9	0.5780	0.1330
A	0.7570	0.1640
B	0.6740	0.1230
D	0.2500	0.0740
E	0.7660	0.1590
F	0.7240	0.1510
H	0.5590	0.1060
I	0.2300	0.1160
J	0.0470	0.0410
K	0.7450	0.1800
L	0.3200	0.1180
M	0.7090	0.1750
O	0.7510	0.1570
P	0.7430	0.1090
Q	0.7490	0.1720
R	0.6850	0.1680
S	0.7250	0.1900
T	0.7200	0.1690
U	0.5850	0.1190
V	0.3010	0.1330
X	0.5350	0.1460
Y	0.5990	0.1130
Z	0.6840	0.1920
a	0.6210	0.1840
b	0.7340	0.1830
c	0.7270	0.1700
d	0.5810	0.1580
e	0.0440	0.0740
f	0.1020	0.0360

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Chain	Atom inclusion	Q-score
g	0.8250	0.1900
h	0.6960	0.1930
i	0.6380	0.1510
j	0.7050	0.2010
k	0.3500	0.1210
l	0.1970	0.0570
o	0.7430	0.1700
p	0.6460	0.1490
q	0.7420	0.2080
r	0.7340	0.1730
s	0.6670	0.1570
u	0.4210	0.1190
v	0.2220	0.1080
w	0.0440	0.0920
x	0.4320	0.0830
y	0.5060	0.1080
z	0.4680	0.1380