



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 10:56 am GMT

PDB ID : 6XYW
EMDB ID : EMD-10654
Title : Structure of the plant mitochondrial ribosome
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Deposited on : 2020-01-31
Resolution : 3.86 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

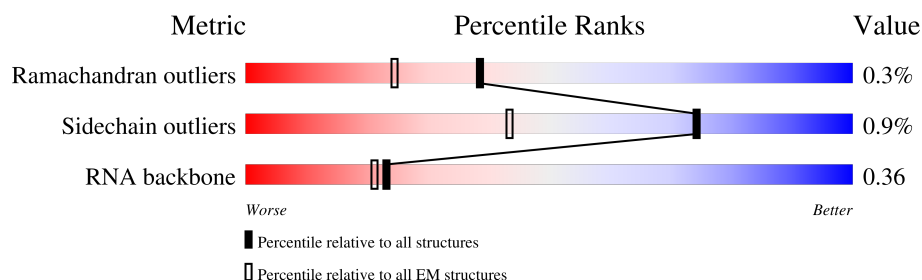
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.86 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Aa	349	
2	Ab	214	
3	Ac	324	
4	AD	173	
5	Ad	300	
6	Ae	185	
7	Af	102	
8	Ag	221	

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Mol	Chain	Length	Quality of chain
9	Ai	155	
10	Aj	205	
11	Ak	173	
12	Al	281	
13	Am	179	
14	An	160	
15	Ao	114	
16	Ap	222	
17	Aq	126	
18	Ar	270	
19	As	269	
20	At	178	
21	Au	159	
22	Av	249	
23	Aw	154	
24	Ax	212	
25	Ay	144	
26	AA	76	
27	AB	134	
28	AC	58	
29	AE	103	
30	AF	250	
31	AG	94	
32	AH	146	
33	AI	233	

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Mol	Chain	Length	Quality of chain
34	AJ	127	
35	AK	130	
36	AL	81	
37	AM	151	
38	AN	188	
39	AO	491	
40	AP	669	
41	AQ	521	
42	AR	29	
43	1	2842	
44	3	118	
45	Bb	556	
46	Bf	148	
47	Bh	430	
48	Bi	241	
49	Bl	154	
50	Bm	164	
51	Br	212	
52	Bw	480	
53	Bx	102	
54	Bz	419	
55	BA	91	
56	Bt	98	
57	BG	576	
58	BP	91	

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Mol	Chain	Length	Quality of chain
59	BF	123	
60	Ba	219	
61	Bc	362	
62	Bd	515	
63	Be	139	
64	Bg	129	
65	Bj	314	
66	Bn	419	
67	Bo	135	
68	Bp	116	
69	Bq	261	
70	Bs	101	
71	Bu	195	
72	Bv	195	
73	By	142	
74	BB	137	
75	BC	112	
76	BD	420	
77	BE	409	
78	BI	266	
79	BJ	349	
80	BH	390	
81	BN	69	
82	BM	79	
83	BO	30	

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Mol	Chain	Length	Quality of chain
84	BL	64	
85	2	1743	
86	Az	109	
87	Ah	171	
88	BK	316	
89	Bk	125	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 189336 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 60S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	96	Total	C	N	O	S	0	0
			753	465	152	133	3		

- Molecule 2 is a protein called Expressed protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	155	Total	C	N	O	S	0	0
			1144	709	224	200	11		

- Molecule 3 is a protein called 50S ribosomal protein L3-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ac	218	Total	C	N	O	S	0	0
			1674	1058	318	288	10		

- Molecule 4 is a protein called Ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	60	Total	C	N	O	S	0	0
			506	327	102	76	1		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ad	209	Total	C	N	O	S	0	0
			1649	1043	311	288	7		

- Molecule 6 is a protein called 60S ribosomal protein L5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ae	144	Total	C	N	O	S	0	0
			1171	760	191	212	8		

- Molecule 7 is a protein called Putative ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Af	100	Total	C	N	O	S	0	0
			797	517	141	134	5		

- Molecule 8 is a protein called Ribosomal protein L9/RNase H1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Ag	51	Total	C	N	O	S	0	0
			406	265	70	70	1		

- Molecule 9 is a protein called At4g35490.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ai	138	Total	C	N	O	S	0	0
			1056	677	182	190	7		

- Molecule 10 is a protein called At1g01640.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Aj	155	Total	C	N	O	S	0	0
			1267	800	244	217	6		

- Molecule 11 is a protein called 50S ribosomal protein HLP, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ak	127	Total	C	N	O	S	0	0
			962	605	183	169	5		

- Molecule 12 is a protein called Ribosomal protein L18e/L15 superfamily protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Al	180	Total	C	N	O	S	0	0
			1407	897	274	234	2		

- Molecule 13 is a protein called 60S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Am	142	Total	C	N	O	S	0	0
			1111	702	219	182	8		

- Molecule 14 is a protein called At5g09770.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	An	141	Total	C	N	O	S	0	0
			1139	708	228	198	5		

- Molecule 15 is a protein called At5g27820.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ao	106	Total	C	N	O	S	0	0
			835	532	152	146	5		

- Molecule 16 is a protein called At1g24240/F3I6_17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ap	114	Total	C	N	O	S	0	0
			935	600	178	155	2		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aq	106	Total	C	N	O	S	0	0
			888	557	178	148	5		

- Molecule 18 is a protein called 50S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ar	137	Total	C	N	O	S	0	0
			1106	707	196	201	2		

- Molecule 19 is a protein called AT1G52370 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	As	121	Total	C	N	O	S	0	0
			937	587	184	163	3		

- Molecule 20 is a protein called At4g39880.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	At	105	Total	C	N	O	S	0	0
			840	545	148	145	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Au	142	Total	C	N	O	S	0	0
			1112	702	210	196	4		

- Molecule 22 is a protein called Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Av	198	Total	C	N	O	S	0	0
			1523	968	270	281	4		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Aw	76	Total	C	N	O	S	0	0
			606	387	117	102			

- Molecule 24 is a protein called AT4g31460/F3L17_30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ax	99	Total	C	N	O	S	0	0
			809	511	151	143	4		

- Molecule 25 is a protein called At1g07830/F24B9_7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Ay	111	Total	C	N	O	S	0	0
			943	592	175	168	8		

- Molecule 26 is a protein called Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AA	37	Total	C	N	O	S	0	0
			299	187	57	54	1		

- Molecule 27 is a protein called At1g26740/T24P13_11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AB	41	Total	C	N	O	S	0	0
			319	203	67	45	4		

- Molecule 28 is a protein called At3g06320.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AC	51	Total	C	N	O	S	0	0
			432	283	77	70	2		

- Molecule 29 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AE	36	Total	C	N	O	S	0	0
			297	183	63	47	4		

- Molecule 30 is a protein called At4g05400.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	84	Total	C	N	O	S	0	0
			663	419	115	127	2		

- Molecule 31 is a protein called At5g40080.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	61	Total	C	N	O	S	0	0
			485	316	84	83	2		

- Molecule 32 is a protein called Mitochondrial ribosomal protein L51/S25/CI-B8 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AH	110	Total	C	N	O	S	0	0
			879	553	168	154	4		

- Molecule 33 is a protein called At1g14620/T5E21_15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AI	207	Total	C	N	O	S	0	0
			1714	1118	282	306	8		

- Molecule 34 is a protein called 39S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AJ	81	Total	C	N	O	S	0	0
			632	392	115	121	4		

- Molecule 35 is a protein called At4g22000.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AK	87	Total	C	N	O	S	0	0
			732	456	143	125	8		

- Molecule 36 is a protein called Uncharacterized protein At1g27435/F17L21.30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AL	52	Total	C	N	O	S	0	0
			400	246	82	71	1		

- Molecule 37 is a protein called At1g73940/F2P9_19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AM	82	Total	C	N	O	S	0	0
			651	425	114	108	4		

- Molecule 38 is a protein called At3g51010.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AN	80	Total	C	N	O	S	0	0
			664	406	141	115	2		

- Molecule 39 is a protein called Pentatricopeptide repeat-containing protein At1g60770.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AO	452	Total	C	N	O	S	0	0
			3595	2276	615	682	22		

- Molecule 40 is a protein called rPPR*.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	AP	669	Total	C	N	O	0	0
			3345	2007	669	669		

- Molecule 41 is a protein called Pentatricopeptide repeat-containing protein PNM1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AQ	366	Total	C	N	O	S	0	0
			2900	1835	501	537	27		

- Molecule 42 is a protein called UNK-6.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	AR	29	Total	C	N	O	0	0
			145	87	29	29		

- Molecule 43 is a RNA chain called RNA (2842-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1	2842	Total	C	N	O	P	6	0
			60842	27171	11068	19760	2843		

- Molecule 44 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	3	118	Total	C	N	O	P	0	0
			2513	1124	453	819	117		

- Molecule 45 is a protein called Ribosomal protein S3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bb	281	Total	C	N	O	S	0	0
			2293	1489	413	383	8		

- Molecule 46 is a protein called Ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Bf	136	Total	C	N	O	S	0	0
			1106	699	216	187	4		

- Molecule 47 is a protein called 30S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Bh	123	Total	C	N	O	S	0	0
			975	616	187	168	4		

- Molecule 48 is a protein called 40S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bi	101	Total	C	N	O	S	0	0
			857	556	161	135	5		

- Molecule 49 is a protein called Small ribosomal subunit protein S13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Bl	91	Total	C	N	O	S	0	0
			729	442	153	132	2		

- Molecule 50 is a protein called At2g34520.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Bm	96	Total	C	N	O	S	0	0
			794	495	165	130	4		

- Molecule 51 is a protein called 40S ribosomal protein S19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Br	83	Total	C	N	O	S	0	0
			685	439	130	112	4		

- Molecule 52 is a protein called Mitochondrial 28S ribosomal protein S29-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bw	337	Total	C	N	O	S	0	0
			2722	1752	469	488	13		

- Molecule 53 is a protein called 37S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Bx	79	Total	C	N	O	S	0	0
			641	402	125	112	2		

- Molecule 54 is a protein called AT3G18240 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bz	123	Total	C	N	O	S	0	0
			1010	634	198	175	3		

- Molecule 55 is a protein called CX9C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BA	38	Total	C	N	O	S	0	0
			293	181	50	54	8		

- Molecule 56 is a protein called 30S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bt	29	Total	C	N	O	S	0	0
			239	149	50	39	1		

- Molecule 57 is a protein called Pentatricopeptide repeat-containing protein At3g02650, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BG	364	Total	C	N	O		0	0
			1795	1067	364	364			

- Molecule 58 is a protein called UNK-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BP	91	Total	C	N	O		0	0
			455	273	91	91			

- Molecule 59 is a protein called mS31/mS46.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BF	123	Total	C	N	O		0	0
			615	369	123	123			

- Molecule 60 is a protein called Ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Ba	195	Total	C	N	O	S	0	0
			1563	1003	276	273	11		

- Molecule 61 is a protein called Ribosomal protein S4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bc	327	Total	C	N	O	S	0	0
			2772	1781	526	454	11		

- Molecule 62 is a protein called At1g64880.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bd	216	Total	C	N	O	S	0	0
			1730	1097	310	317	6		

- Molecule 63 is a protein called Translation elongation factor EF1B/ribosomal protein S6 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Be	99	Total	C	N	O	S	0	0
			819	529	147	137	6		

- Molecule 64 is a protein called 40S ribosomal protein S15a-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bg	128	Total	C	N	O	S	0	0
			1042	657	194	188	3		

- Molecule 65 is a protein called Probable ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bj	123	Total	C	N	O	S	0	0
			955	590	188	172	5		

- Molecule 66 is a protein called At1g15810/F7H2_23.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bn	100	Total	C	N	O	S	0	0
			814	509	150	149	6		

- Molecule 67 is a protein called 30S ribosomal protein S16-2, chloroplastic/mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bo	99	Total	C	N	O	S	0	0
			780	496	152	127	5		

- Molecule 68 is a protein called Nucleic acid-binding, OB-fold-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bp	78	Total	C	N	O	S	0	0
			636	405	120	108	3		

- Molecule 69 is a protein called F10K1.8 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bq	62	Total	C	N	O	S	0	0
			492	313	91	87	1		

- Molecule 70 is a protein called Ribosomal protein S21 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bs	66	Total	C	N	O	S	0	0
			539	337	106	94	2		

- Molecule 71 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bu	100	Total	C	N	O	S	0	0
			800	508	147	140	5		

- Molecule 72 is a protein called AT5g49210/K21P3_8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bv	149	Total	C	N	O	S	0	0
			1278	800	237	237	4		

- Molecule 73 is a protein called 28S ribosomal S34 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	By	76	Total	C	N	O	S	0	0
			619	404	115	98	2		

- Molecule 74 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BB	23	Total	C	N	O	S	0	0
			203	129	46	27	1		

- Molecule 75 is a protein called At5g26800.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BC	68	Total	C	N	O	S	0	0
			544	356	99	88	1		

- Molecule 76 is a protein called Gb|AAC32909.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BD	210	Total	C	N	O	S	0	0
			1768	1113	317	328	10		

- Molecule 77 is a protein called 3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BE	348	Total	C	N	O	S	0	0
			2697	1716	446	517	18		

- Molecule 78 is a protein called rPPR*.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	BI	266	Total	C	N	O	0	0
			1330	798	266	266		

- Molecule 79 is a protein called rPPR*.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	BJ	349	Total	C	N	O	0	0
			1745	1047	349	349		

- Molecule 80 is a protein called Adenylyl cyclase.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	BH	206	Total	C	N	O	0	0
			1023	611	206	206		

- Molecule 81 is a protein called UNK-3.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	BN	69	Total	C	N	O	0	0
			345	207	69	69		

- Molecule 82 is a protein called UNK-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	BM	79	Total	C	N	O	0	0
			395	237	79	79		

- Molecule 83 is a protein called UNK-4.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	BO	30	Total	C	N	O	0	0
			150	90	30	30		

- Molecule 84 is a protein called UNK-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	BL	64	Total	C	N	O	0	0
			320	192	64	64		

- Molecule 85 is a RNA chain called RNA (1743-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
85	2	1743	Total	C	N	O	P	0	0
			37379	16678	6858	12100	1743		

- Molecule 86 is a protein called At5g55140.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Az	82	Total	C	N	O	S	0	0
			660	406	135	114	5		

- Molecule 87 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Ah	137	Total	C	N	O	S	0	0
			1098	706	187	200	5		

- Molecule 88 is a protein called rPPR*.

Mol	Chain	Residues	Atoms				AltConf	Trace
88	BK	316	Total	C	N	O	0	0
			1580	948	316	316		

- Molecule 89 is a protein called Ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Bk	121	Total	C	N	O	S	0	0
			968	598	204	162	4		

PHE
MET
LEU
ALA
GLU

• Molecule 4: Ribosomal protein L35

Chain AD:  35% 65%

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

VAL PHE PRO PRO ASN VAL SER MET THR THR PHE VAL HIS HIS PHE VAL GLN VAL ARG ASN ILE SER SER LYS LEU MET ALA LYS TRP LYS LYS TRP ARG PRO THR THR ILE THR SER LYS VAL MET LYS V110 D127 I169 ASN PHE CYS ASN

• Molecule 5: 50S ribosomal protein L4

Chain Ad:  69% 30%

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

THR PRO ASP ASP SER PHE PRO SER ASP LEU THR LYS LYS THR VAL THR PRO ASP THR ARG L89 V105 Q154 K155 G156 R159 G196 E234 E243 D248 Y260 P297 ILE ASN ARG

• Molecule 6: 60S ribosomal protein L5, mitochondrial

Chain Ae:  11% 77% 22%

MET PHE F3 F6 E9 D10 L18 K19 L20 M43 F44 F61 I62 GLN THR GLN ARG GLY THR SER LYS SER PHE ARG ASN PRO PHE LEU GLY SER ASN LYS ASP GLY TYR VAL ASP ALA ARG Q94 G99 H100 F105 F119 M125

E134 F135 F138 E141 L142 E143 I152 T165 Q166 D167 F176 L177 GLN LYS ASP GLY GLY THR GLN

• Molecule 7: Putative ribosomal protein L6

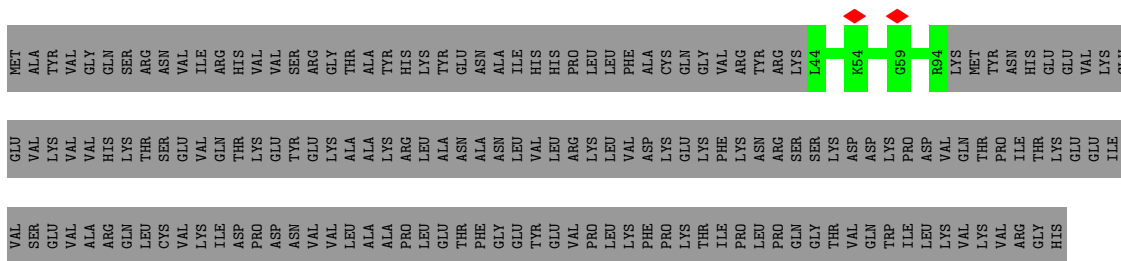
Chain Af:  55% 98%

MET E2 A3 K4 F5 F6 R7 F8 L9 K10 I11 V12 G15 Y16 K17 A18 R19 A20 E21 E22 A23 G24 R25 F26 L27 Y28 L29 E38 L39 A40 V41 A44 V45 R46 V47 F48 C49 F50 K51 N52 N53 V54 C57 T58 Q59 I60 D61 K62 Q63 R64 V72 R73 S74 C75 K76

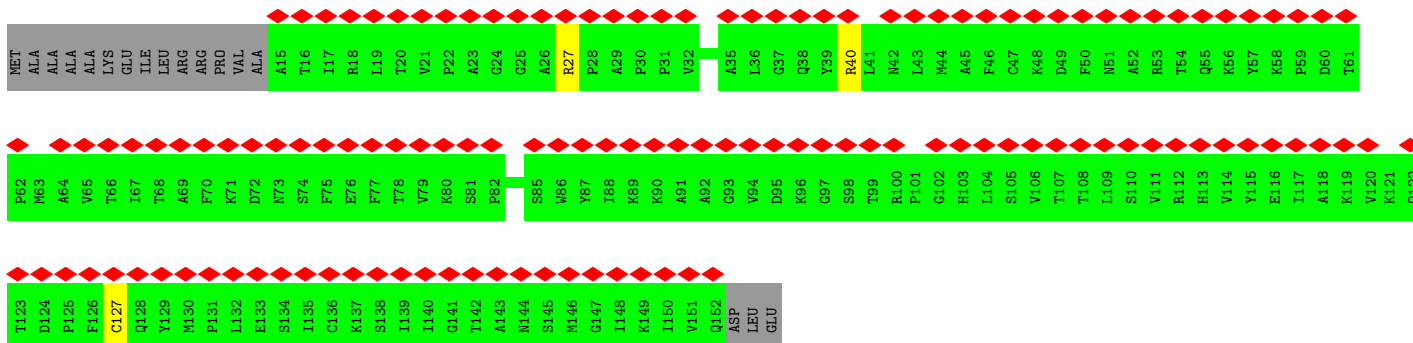
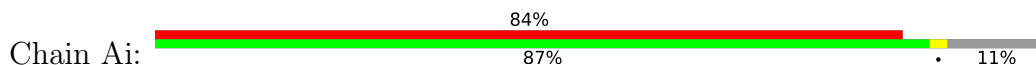
E79 M87 Y88 T89 D90 E91 V92 V93 X94 K99 K100 S101 LYS

• Molecule 8: Ribosomal protein L9/RNase H1

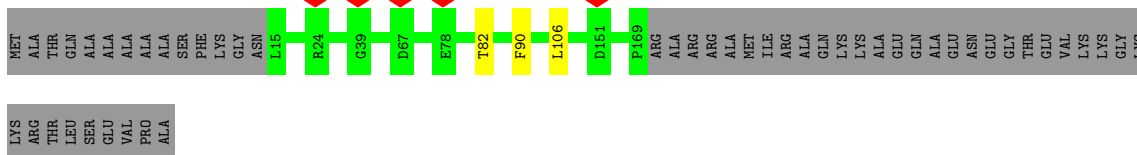
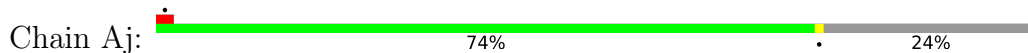
Chain Ag:  23% 77%



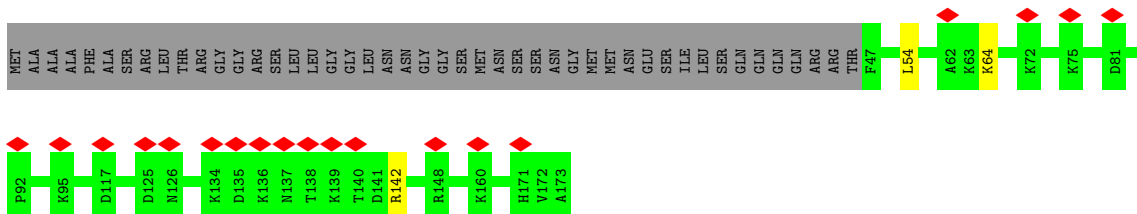
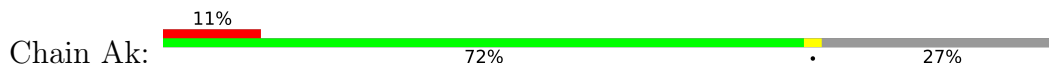
- Molecule 9: At4g35490



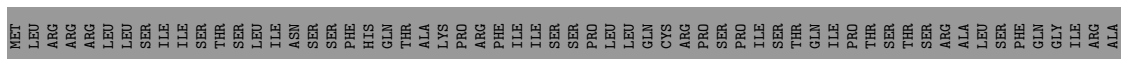
- Molecule 10: At1g01640

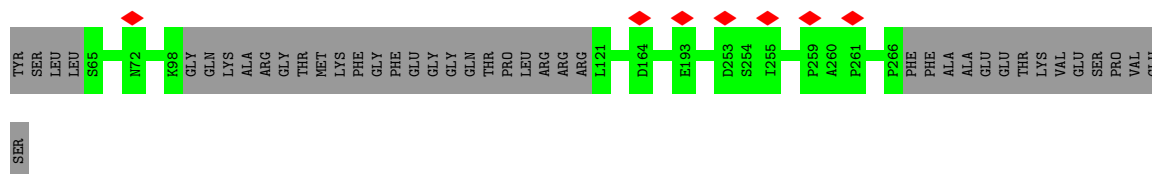


- Molecule 11: 50S ribosomal protein HLP, mitochondrial

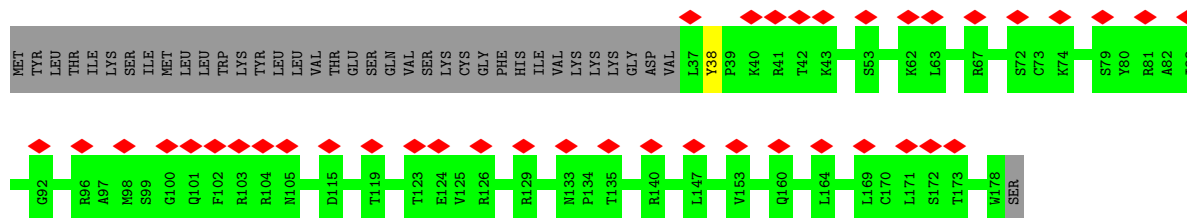
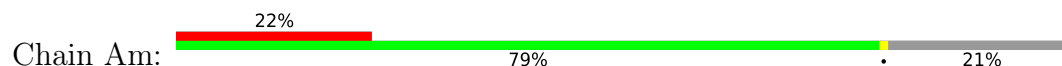


- Molecule 12: Ribosomal protein L18e/L15 superfamily protein

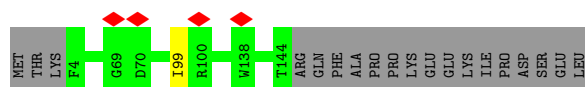
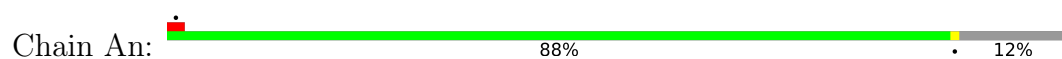




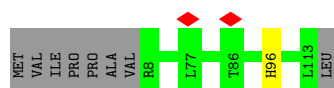
- Molecule 13: 60S ribosomal protein L16, mitochondrial



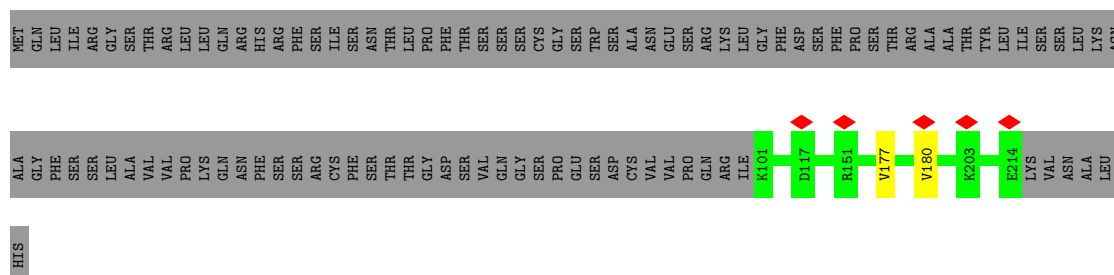
- Molecule 14: At5g09770



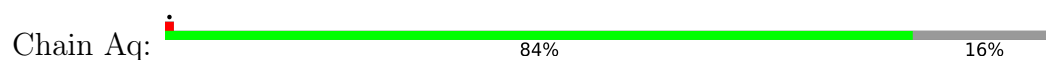
- Molecule 15: At5g27820

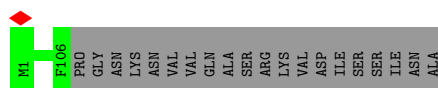


- Molecule 16: At1g24240/F3I6 17



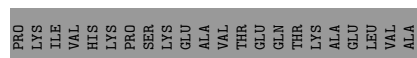
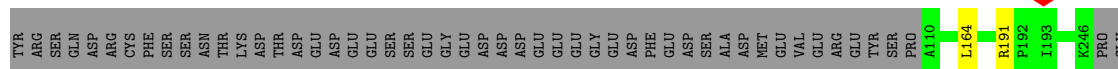
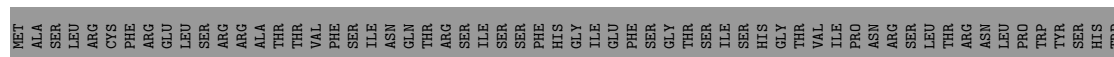
- Molecule 17: 50S ribosomal protein L20





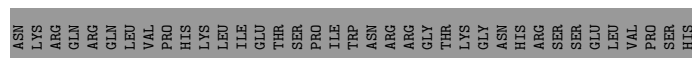
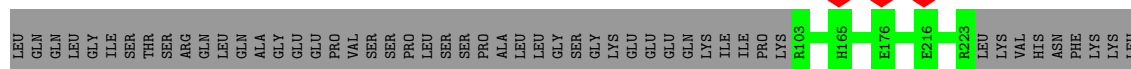
- Molecule 18: 50S ribosomal protein L21, mitochondrial

Chain Ar: 50% 49%



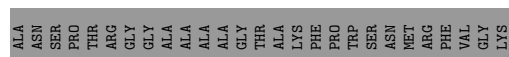
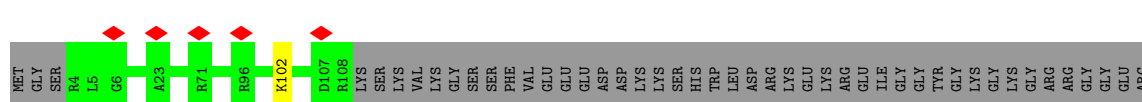
- Molecule 19: AT1G52370 protein

Chain As: 45% 55%



- Molecule 20: At4g39880

Chain At: 58% 41%



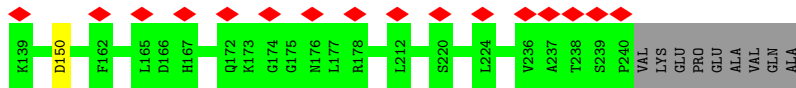
- Molecule 21: 50S ribosomal protein L24

Chain Au: 6% 86% 11%

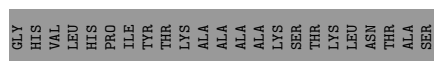


- Molecule 22: Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein

Chain Av: 10% 79% 20%




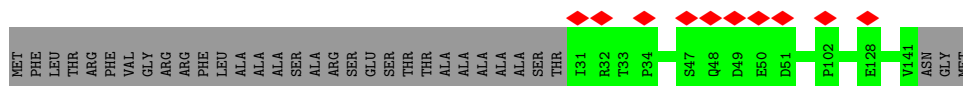
- Chain Aw: 



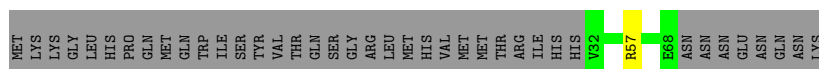
- Chain Ax: 46% 53%



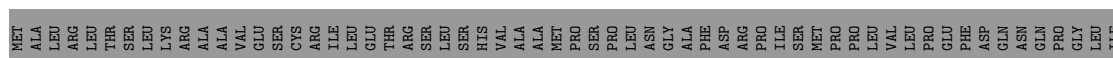
- Chain A_y: 

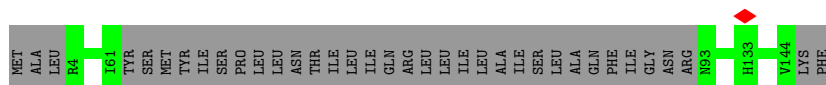


- Chain AA: 47% . 51%



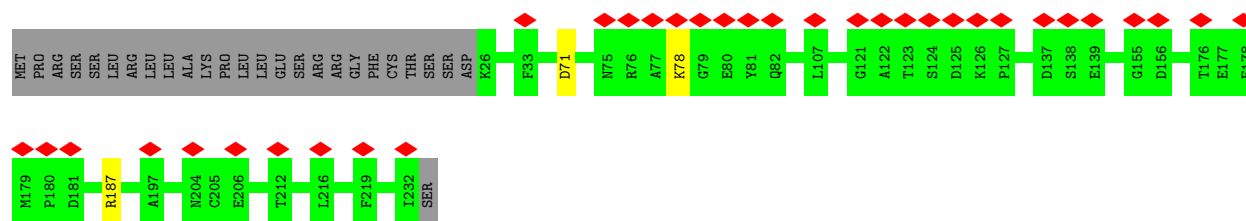
- Chain AB:  29% 69%





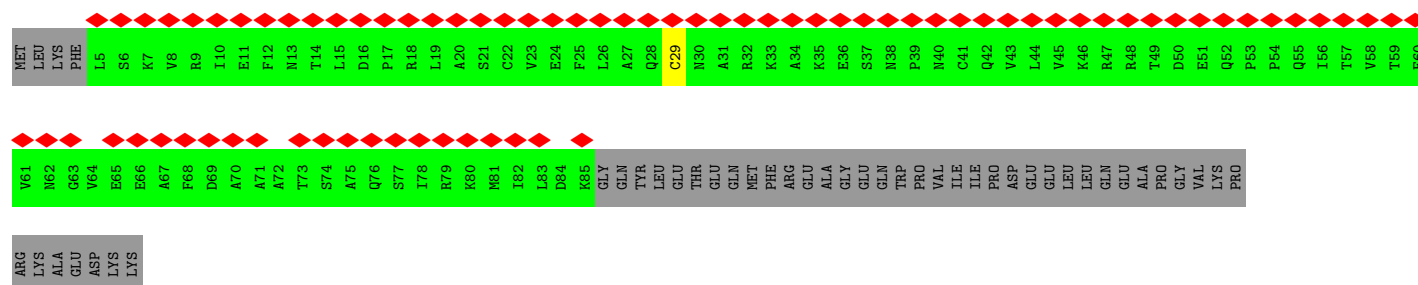
- Molecule 33: At1g14620/T5E21_15

Chain AI: 15% 88% 11%



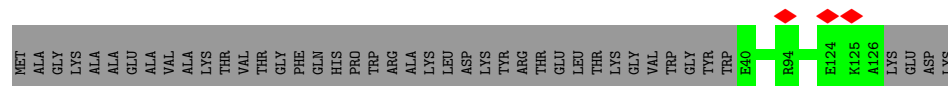
- Molecule 34: 39S ribosomal protein

Chain AJ: 61% 63% 36%



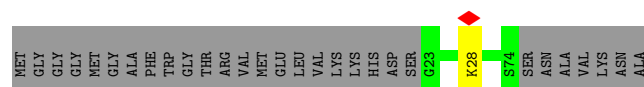
- Molecule 35: At4g22000

Chain AK: 67% 33%



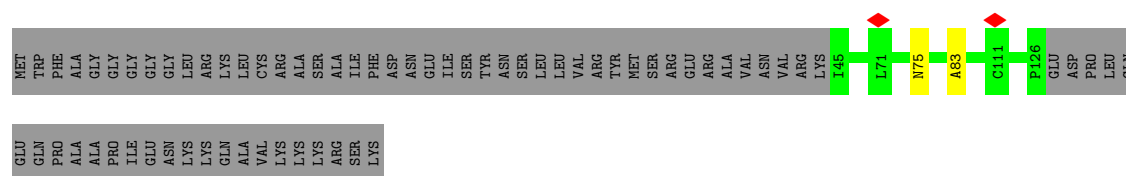
- Molecule 36: Uncharacterized protein At1g27435/F17L21.30

Chain AL: 63% 36%



- Molecule 37: At1g73940/F2P9_19

Chain AM: 53% 46%



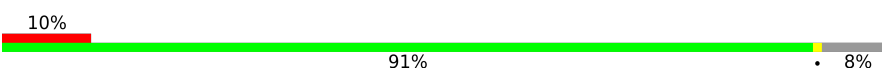
- Molecule 38: At3g51010

Chain AN:  43% 57%

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

ASN HIS PHE HIS SER LEU SER THR ASP THR ARG LEU PRO LYS ARG PRO LYS MET THR HIS GLU PRO LYS ARG ASN LYS ARG SER SER LEU LYS PHE ALA LYS THR TYR ALA TYR VAL GLN THR PRO GLY GLN PRO PRO ILE S107 E181 K182 K183 K184 S185 M186 SER SER

- Molecule 39: Pentatricopeptide repeat-containing protein At1g60770

Chain AO:  10% 91% 8%

MET ALA HIS ARG ARG LEU SER ARG SER ASP VAL THR LYS ARG THR LYS TYR ILE GLU PRO LEU TYR ASN ARG LYS PHE LEU LYS ASP GLY THR GLU V37 R104 E118 E136 L137 E140 E187 N188 A204 N207 E217 D222 K247

K258 N259 T272 R276 L277 I284 A327 N328 C329 Y332 G348 G364 F375 L389 S393 S397 I398 G399 G403 G404 K405 W406 L407 P408 S409 P410 K424 D425 V426 N427 I443 G444 A445 E446 I447 F448 P463 A464 M465 R466 E475 V476 K482

E486 V487 S488 GLN ASP VAL

- Molecule 40: rPPR*

Chain AP:  23% 99%

A91 A92 A93 A94 A95 A96 A99 A100 A101 A102 A103 A104 A110 A111 A112 A113 A114 A115 A116 A117 A120 A121 A122 A123 A124 A127 A130 A134 A140 A141 A142 A143 A144 A145 A146 A149 A153 A154 A155 A156 A157 A161 A162 A166 A174 A175 A176 A177


A178 A179 A188 A191 A192 A193 A194 A195 A202 A224 A228 A229 A232 A233 A241 A246 A267 A270 A284 A300 A301 A302 A303 A322 A330 A336 A352 A353 A354 A366 A371 A372 A376 A377 A378 A379 A388 A395

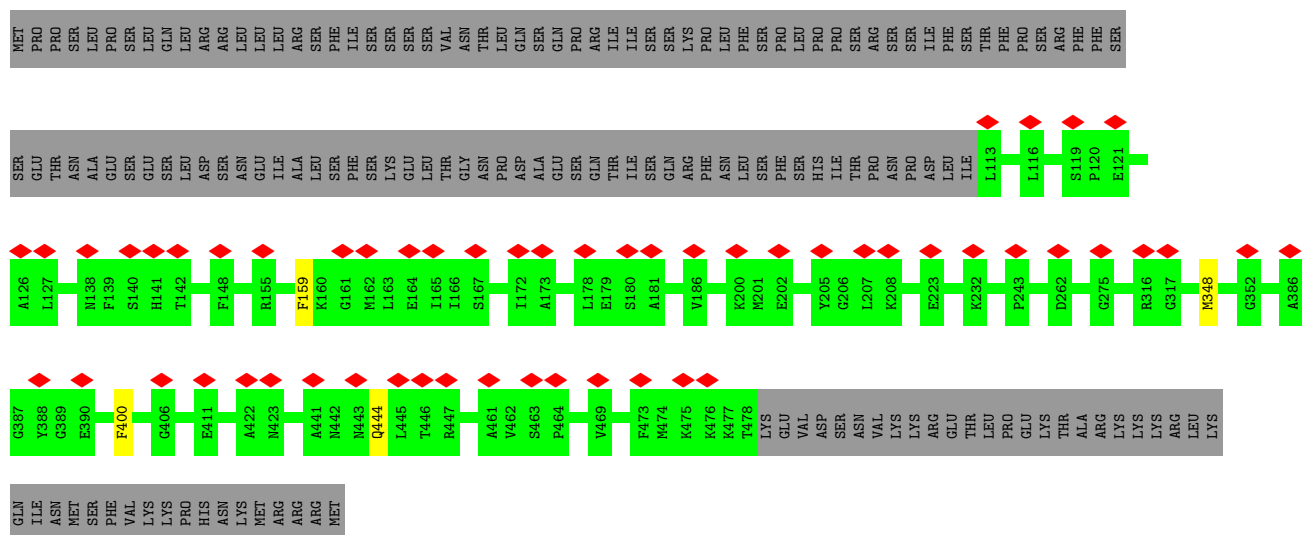
A399 A400 A405 A406 A407 A408 A409 A410 A411 A416 A420 A421 A424 A428 A429 A430 A434 A435 A436 A437 A438 A441 A442 A443 A444 A445 A446 A447 A448 A451 A452 A459 A460 A461 A462 A477 A478 A479 A480 A483 A493 A494 A510 A511 A512 A513 A514

A515 A516 A517 A524 A527 A528 A529 A530 A536 A547 A548 A549 A550 A556 A581 A584 A585 A586 A590 A593 A604 A605 A620 A621 A622 A623 A624 A625 A626 A635 A652 A656 A657 A663 A669 A670 A671 A672 A673 A674 A675 A676 A690

A712 A713 A714 A723 A724 A725 A726 A729 A730 A731 A734 A756 A759

- Molecule 41: Pentatricopeptide repeat-containing protein PNM1, mitochondrial

Chain AQ:  11% 69% 30%



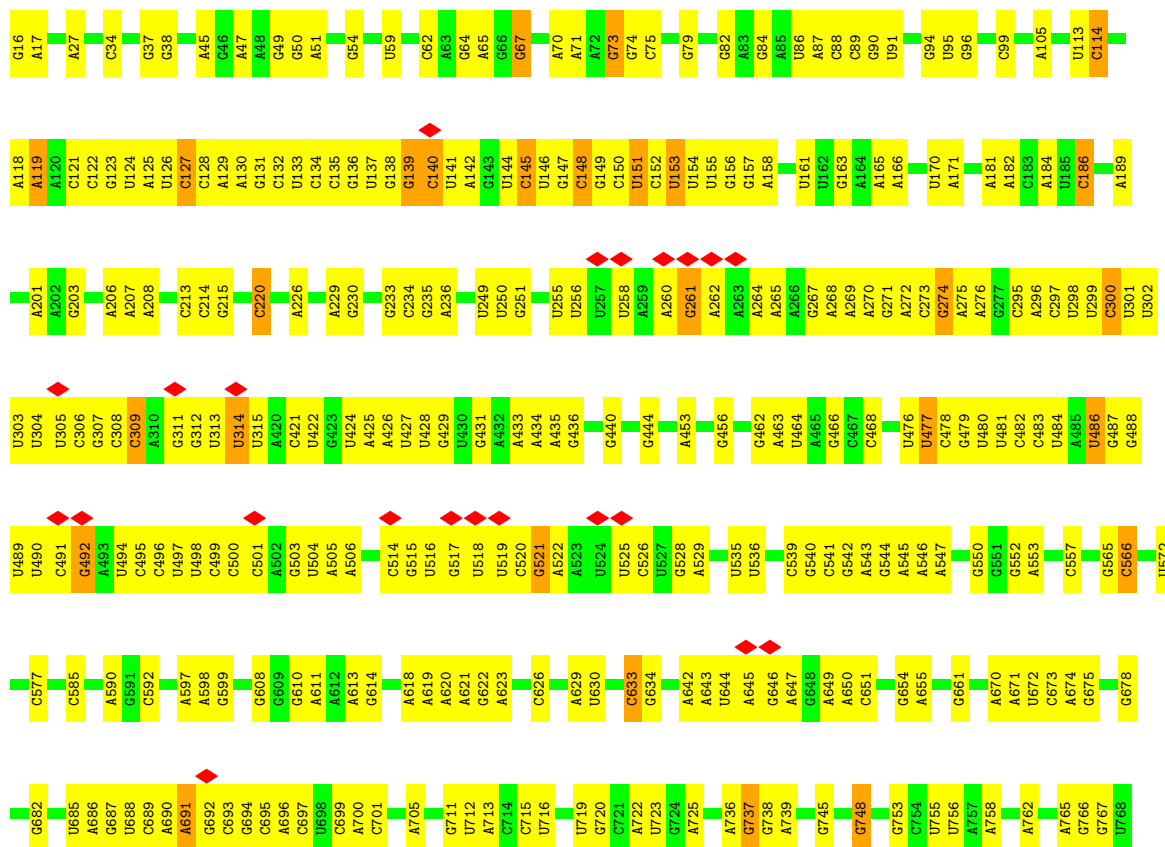
- Molecule 42: UNK-6

Chain AR:  100%

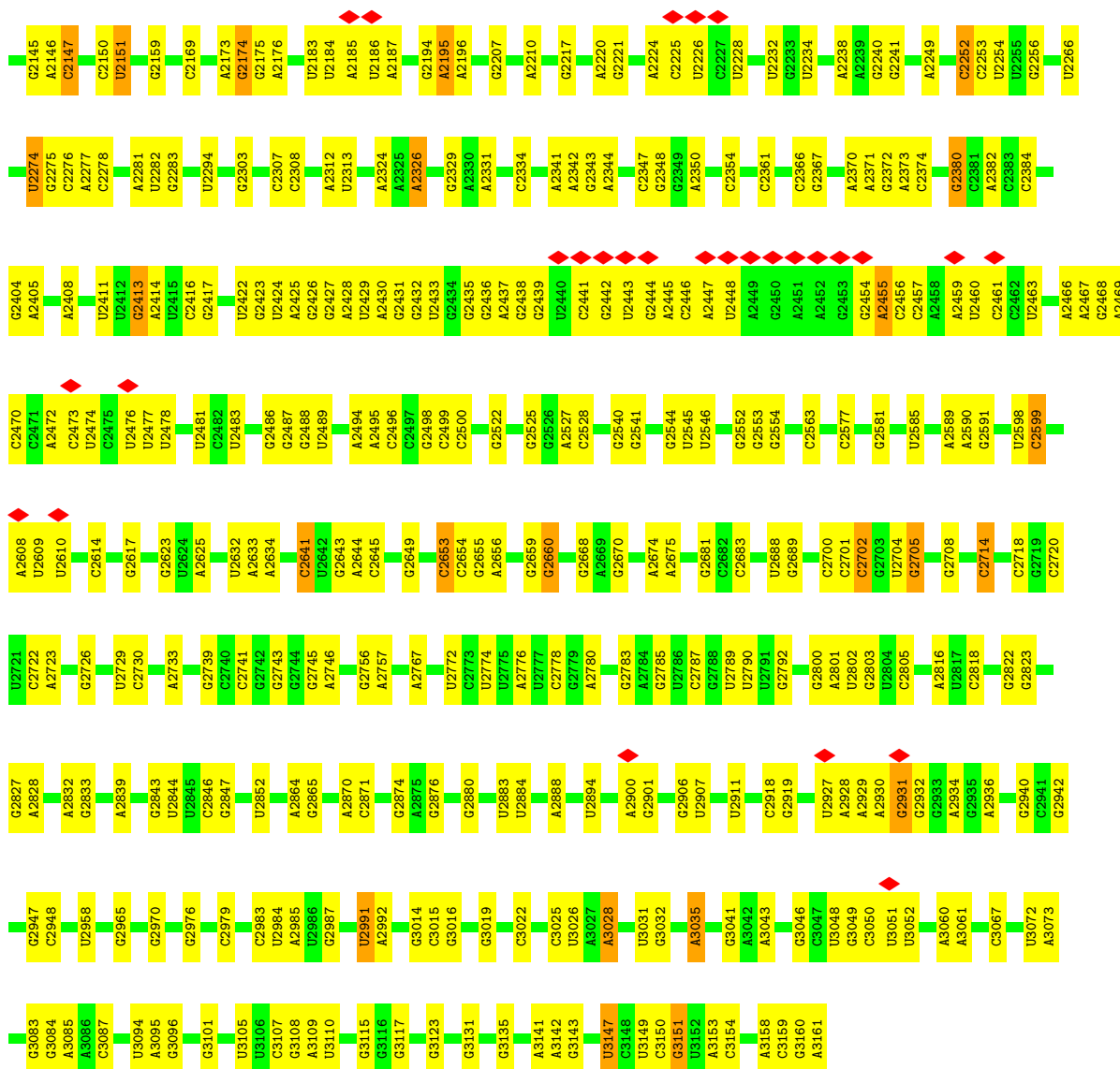
There are no outlier residues recorded for this chain.

- Molecule 43: RNA (2842-MER)

Chain 1:  57%

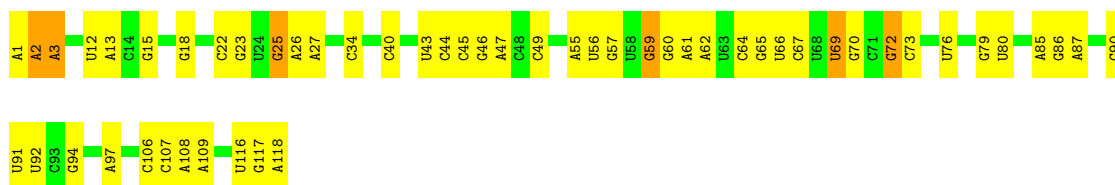


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U2046	G1908	G1843	U1669	U1481	G1255	G1189	G1101	G1003	U770
C2047	U1844	U1845	C1570	U1482	U1259	G1194	G1105	A1010	A771
C2048	U1846	C1631	U1483	C1483	G1260	A1195	C1106	A1011	U777
U2049	U1847	C1632	U1484	A1484	G1261	U1196	U1107	U1012	U778
U2050	U1848	U1633	C1573	A1485	C1262	G1197	A1108	C1013	U779
A2051	G1913	C1634	U1486	U1486	C1265	C1198	A1109	U1013	C780
C2052	G1914	U1635	U1487	C1487	U1268	A1111	U1112	C1020	A784
C2053	G1915	U1636	U1476	U1476	G1268	C1201	U1112	U1021	
U2054	U1851	C1637	U1498	A1498	A1275	C1202	C1113	A1022	G788
U2055	C1852	C1638	U1577	A1500	A1276	A1203	A1116	G1023	G789
U2056	G1853	C1639	U1578	U1501	A1277	G1205	G1123	G1024	A790
C2057	G1854	U1640	C1579	U1502	A1278	U1206	G1124	G1025	U791
A2058	G1855	U1641	U1580	G1503	U1281	G1207	G1125	U1026	A792
U2059	C1857	C1642	U1581	G1504	U1282	U1208	G1126	G1027	C793
U2060	U1858	U1643	C1582	G1505	A1283	U1209	G1130	A1043	U794
A2061	C1859	C1644	U1583	U1506	A1284	U1210	G1131	C1044	U795
G2062	U1860	U1645	C1584	U1507	U1285	G1212	G1132	A1046	C796
G2063	U1861	U1646	U1585	C1508	U1286	C1213	G1133	A1047	U797
A2064	G1862	U1647	U1586	U1509	U1287	U1215	G1134	A1048	A798
A2065	U1863	C1648	U1587	A1514	U1288	G1216	G1135	A1049	C799
A2066	C1864	C1649	U1588	G1521	U1289	G1217	G1136	A1050	
G2067	U1865	U1650	U1589	U1522	U1290	U1218	G1137	A1051	
C2068	A1865	U1651	C1590	A1523	U1291	G1219	G1138	A1052	C802
	U1866	U1652	U1591	U1524	A1292	G1220	G1139	A1053	C806
	U1867	C1653	G1594	U1525	U1300	G1221	U1140	A1054	U807
	G1868	U1654	U1595	U1526	A1301	C1222	A1144	A1055	A808
	U1869	C1655	C1596	U1527	C1302	U1223	G1145	A1056	
	A1870	U1656	C1597	U1528	U1303	C1224	G1146	A1057	G812
	U1871	A1657	U1598	U1529	U1304	C1225	C1147	A1058	G817
	A1872	U1658	C1599	U1530	U1305	U1226	C1154	A1059	A818
	G1873	U1659	U1600	U1531	A1306	A1227	C1155	U1060	U825
	A1874	U1660	U1601	C1532	U1307	C1228	C1156	U1061	C826
	U1875	U1661	G1602	U1533	U1308	U1231	U1157	U1062	G827
	G1876	U1662	G1603	U1534	U1309	U1232	U1158	G1070	A828
	G1877	A1663	G1604	U1535	U1310	C1233	U1159	G1071	U829
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	U1879	C1665	U1606	U1537	U1312	U1235	A1162	G1073	
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	A1881	U1667	U1608	U1539	U1314	U1237	A1170	C973	A853
	A1882	U1668	U1609	U1540	U1315	A1238	G1171	A974	G854
	A1883	G1669	U1610	U1541	U1316	U1239	G1172	G975	C855
	C1887	U1670	C1610	U1542	U1317	U1240	U1173	U988	U856
	C1888	U1671	G1611	U1543	U1318	C1241	G1174	G989	A859
	A1889	U1672	U1612	U1544	U1319	U1242	A1175	C991	A860
	A1892	A1673	C1613	U1545	U1320	G1243	A1176	G992	C861
	U1896	U1674	C1614	U1546	U1321	U1244	A1177	A1094	G862
	A1897	U1675	C1615	U1547	U1322	U1245	A1178	A1095	G863
	C1898	C1676	U1616	U1548	U1323	U1246	A1182	U1096	G870
	U1899	U1677	U1617	U1549	U1324	C1249	G1184	U1097	G873
	U1900	U1678	C1618	U1550	U1325	A1252		C999	
	G1901	A1679	G1619	U1551	U1326	C1253			
	G1902	G1835	C1620	U1552	U1327				
	U1903	C1836	U1621	U1553	U1328				
	A1904	U1837	C1622	U1554	U1329				
	U1905	A1838	C1623	U1555	U1330				
		U1839	C1624	U1556	U1331				
		U1840	C1625	U1557	U1332				
		U1906	C1626	U1558	U1333				
			U1627	U1559	U1334				
				U1560	U1335				
				U1561	U1336				
				U1562	U1337				
				U1563	U1338				
				U1564	U1339				
				U1565	U1340				
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				U1610	U1385				
				U1611	U1386				
				U1612	U1387				
				U1613	U1388				
				U1614	U1389				
				U1615	U1390				
				U1616	U1391				
				U1617	U1392				
				U1618	U1393				
				U1619	U1394				
				U1620	U1395				
				U1621	U1396				
				U1622	U1397				
				U1623	U1398				
				U1624	U1399				
				U1625	U1400				
				U1626	U1401				
				U1627	U1402				
				U1628	U1403				
				U1629	U1404				
				U1630	U1405				
				U1631	U1406				
				U1632	U1407				
				U1633	U1408				
				U1634	U1409				
				U1635	U1410				
				U1636	U1411				
				U1637	U1412				
				U1638	U1413				
				U1639	U1414				
				U1640	U1415				
				U1641	U1416				
				U1642	U1417				
				U1643	U1418				
				U1644	U1419				
				U1645	U1420				
				U1646	U1421				
				U1647	U1422				
				U1648	U1423				
				U1649	U1424				
				U1650	U1425				
				U1651	U1426				
				U1652	U1427				
				U1653	U1428				
				U1654	U1429				
				U1655	U1430				
				U1656	U1431				
				U1657	U1432				
				U1658	U1433				
				U1659	U1434				
				U1660	U1435				
				U1661	U1436				
				U1662	U1437				
				U1663	U1438				
				U1664	U1439				
				U1665	U1440				
				U1666	U1441				
				U1667	U1442				
				U1668	U1443				
				U1669	U1444				
				U1670	U1445				
				U1671	U1446				
				U1672	U1447				
				U1673	U1448				
				U1674	U1449				
				U1675	U1450				
				U1676	U1451				
				U1677	U1452				
				U1678	U1453				



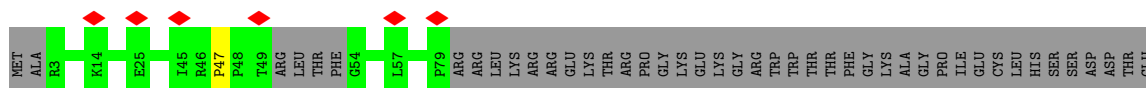
• Molecule 44: RNA (118-MER)

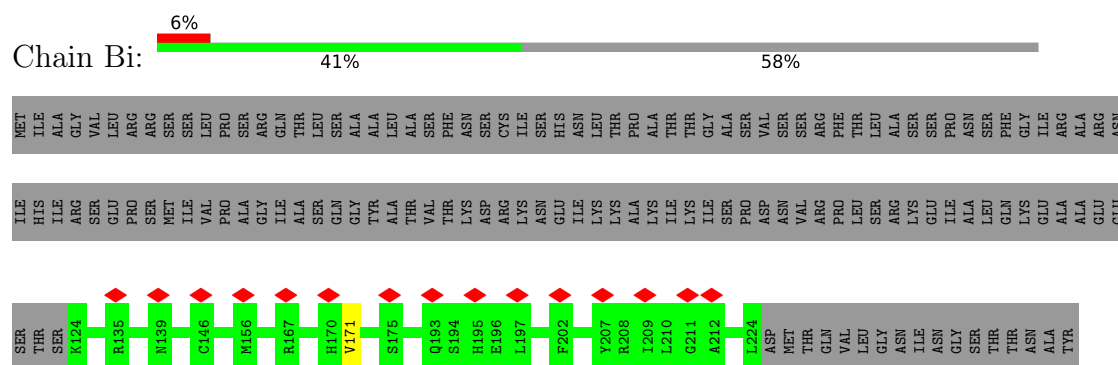
Chain 3: 55% 40% 5%



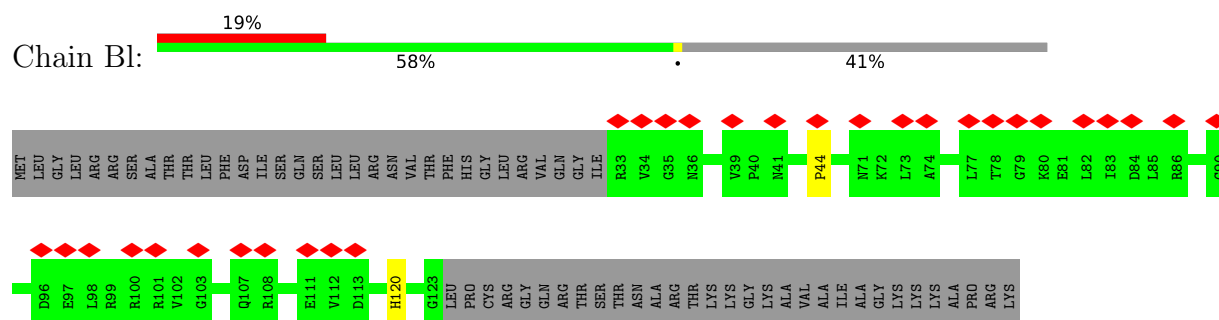
• Molecule 45: Ribosomal protein S3, mitochondrial

Chain Bb: 11% 50% 49%

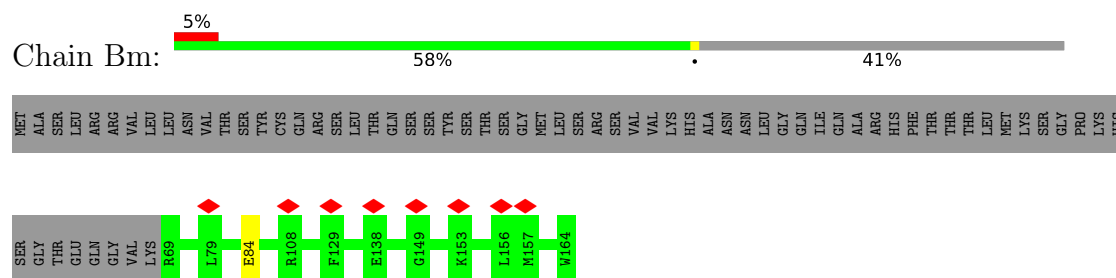




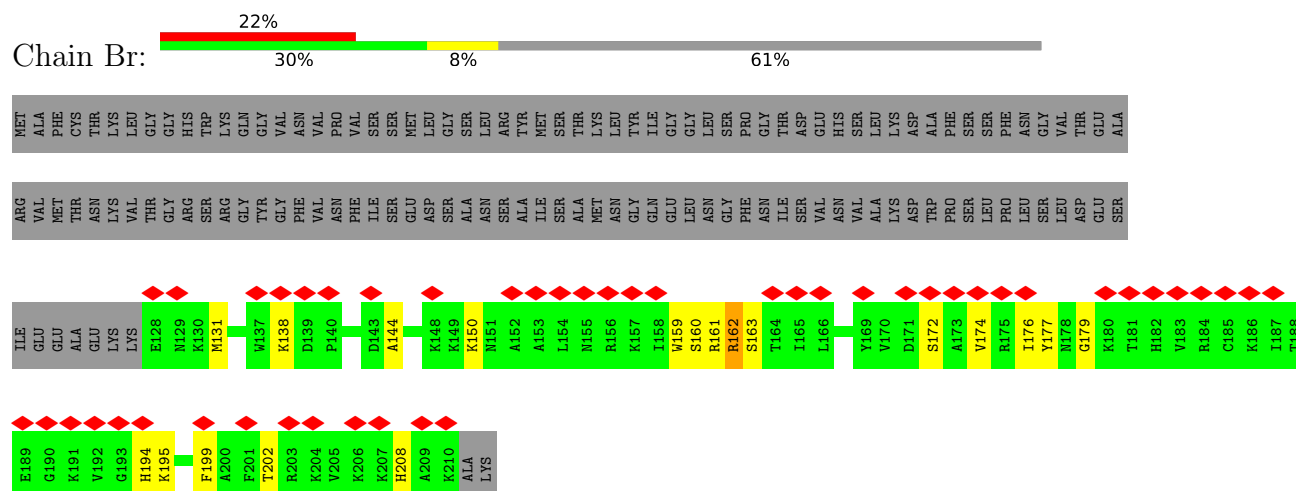
- Molecule 49: Small ribosomal subunit protein S13, mitochondrial



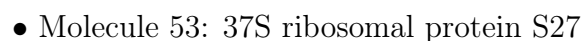
- Molecule 50: At2g34520

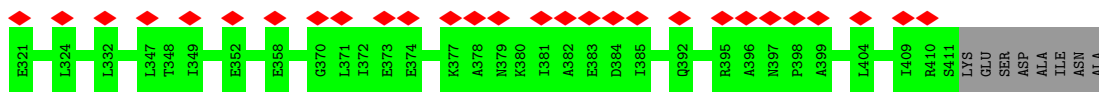


- Molecule 51: 40S ribosomal protein S19, mitochondrial

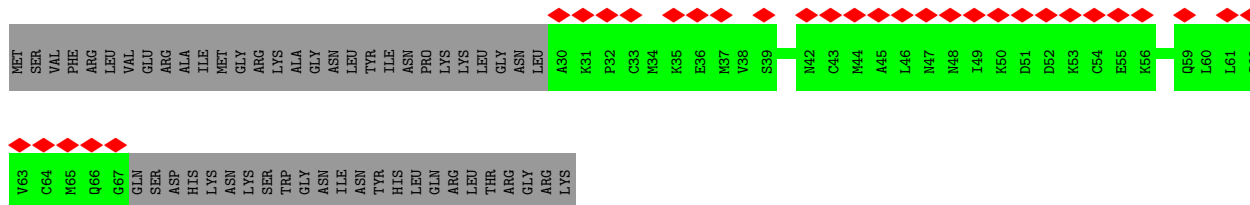
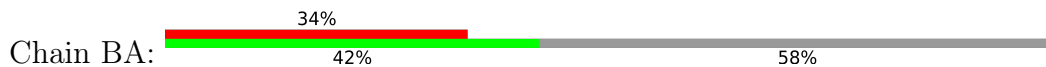


- Molecule 52: Mitochondrial 28S ribosomal protein S29-like protein

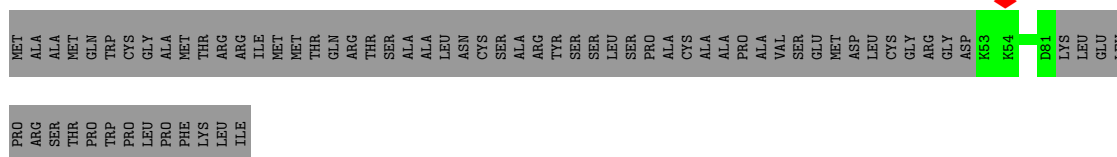




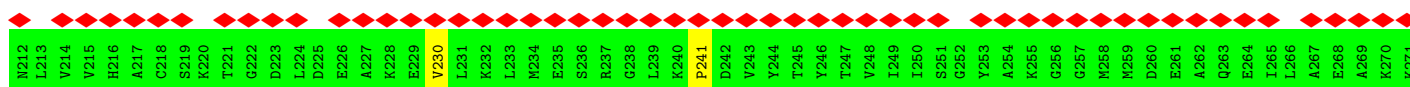
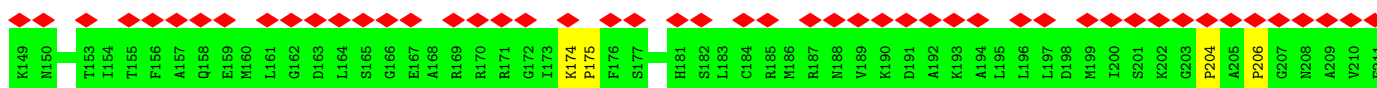
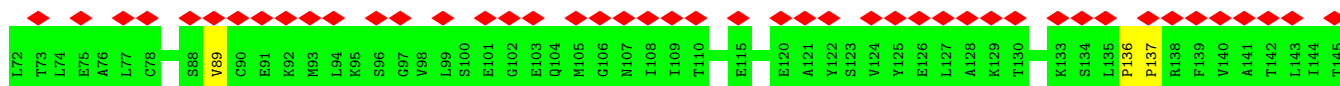
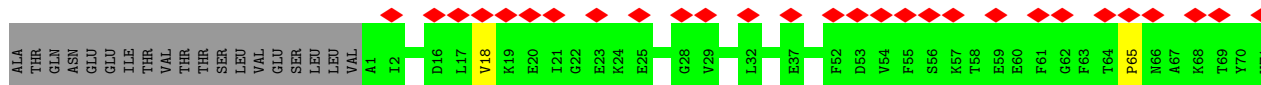
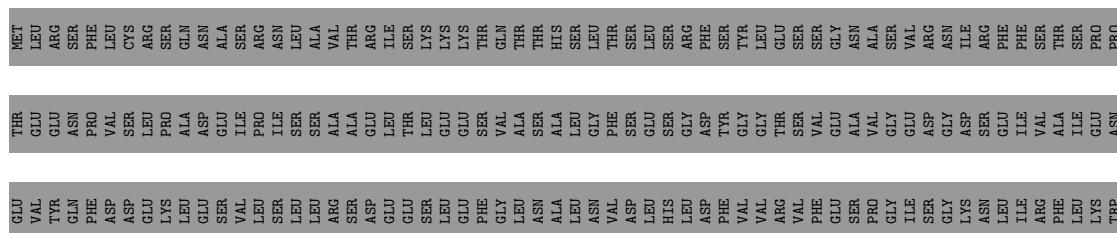
- Molecule 55: CX9C domain-containing protein

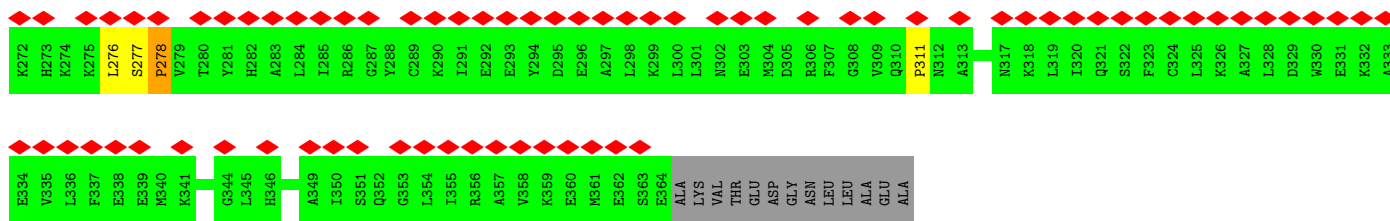


- Molecule 56: 30S ribosomal protein S31, mitochondrial



- Molecule 57: Pentatricopeptide repeat-containing protein At3g02650, mitochondrial

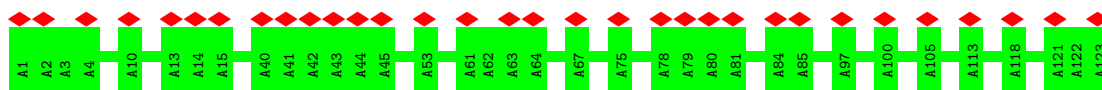




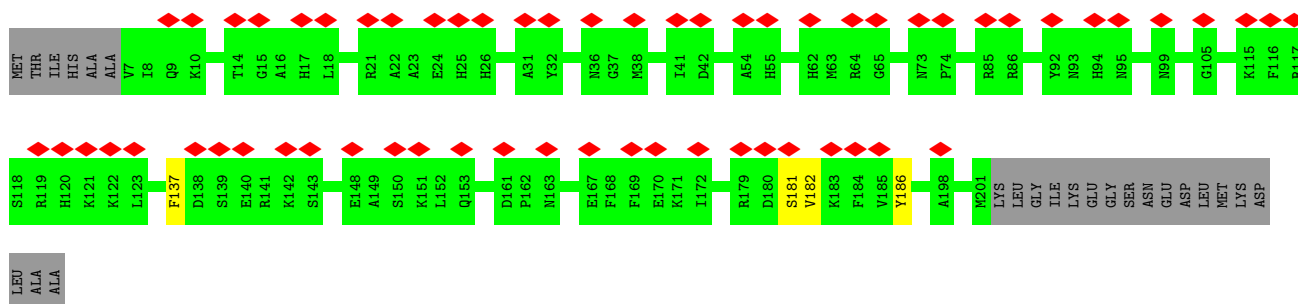
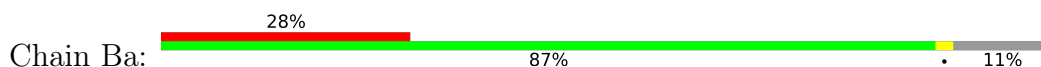
• Molecule 58: UNK-5



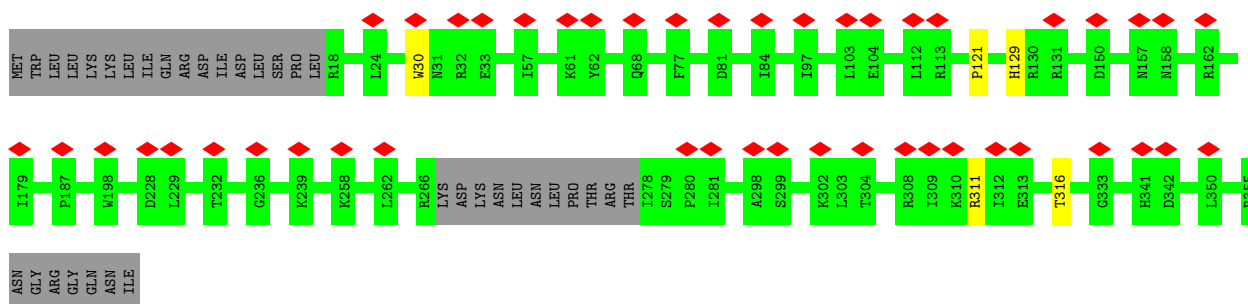
• Molecule 59: mS31/mS46



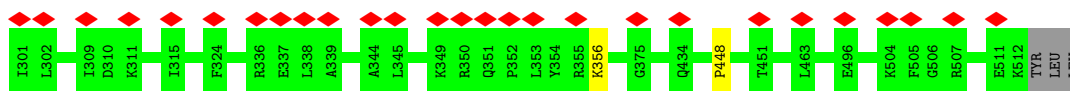
• Molecule 60: Ribosomal protein S2, mitochondrial

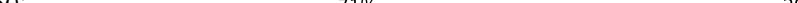


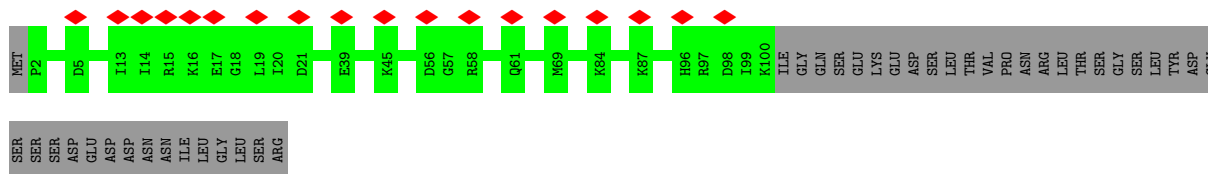
• Molecule 61: Ribosomal protein S4, mitochondrial



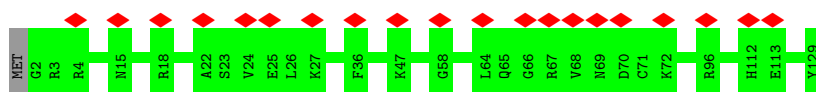
• Molecule 62: At1g64880



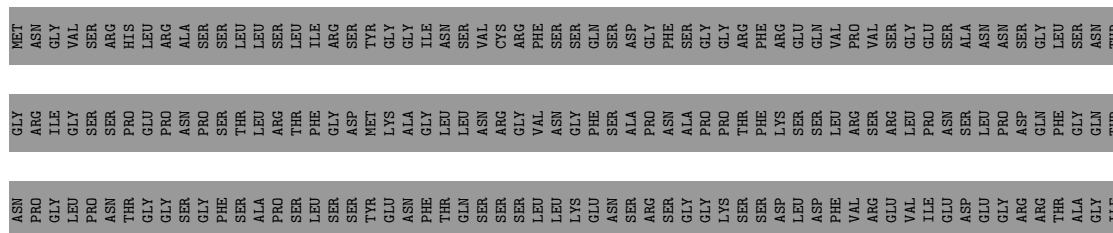
- Chain Be: 

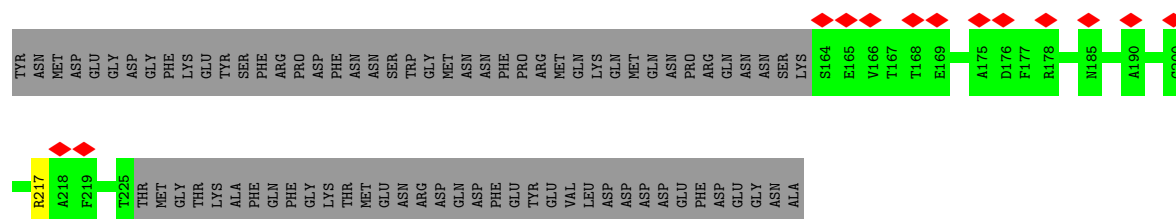


- Chain Bg:  16% 99%

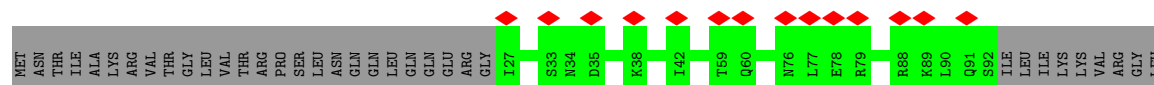


- Chain Bi:

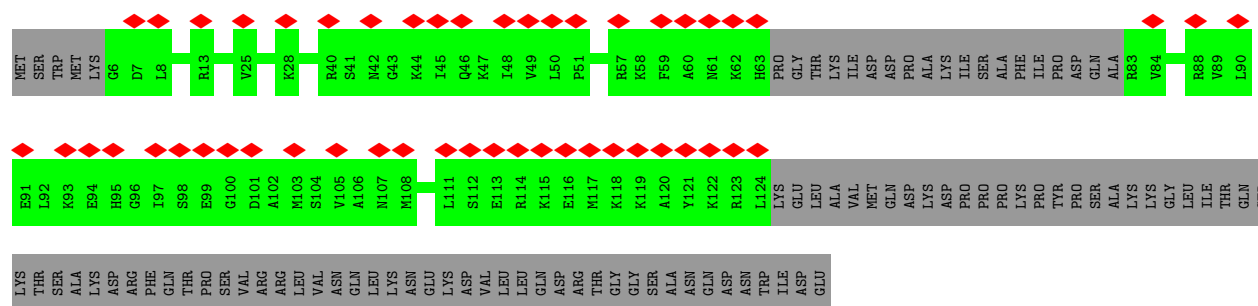




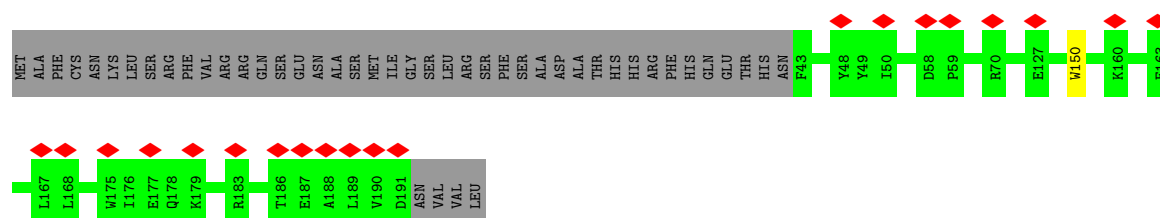
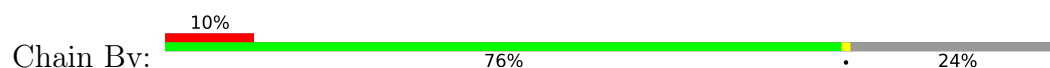
- Molecule 70: Ribosomal protein S21 family protein



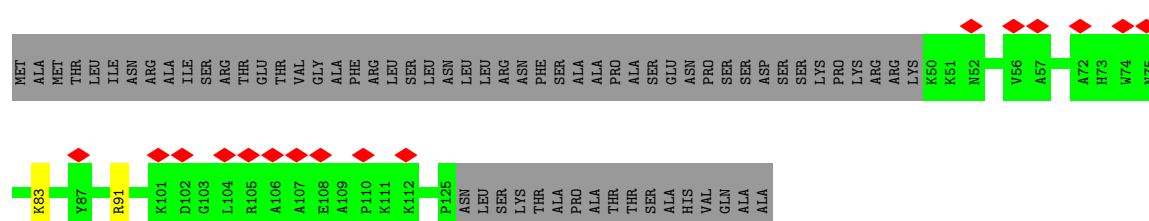
- Molecule 71: Uncharacterized protein



- Molecule 72: AT5g49210/K21P3_8




- Molecule 73: 28S ribosomal S34 protein

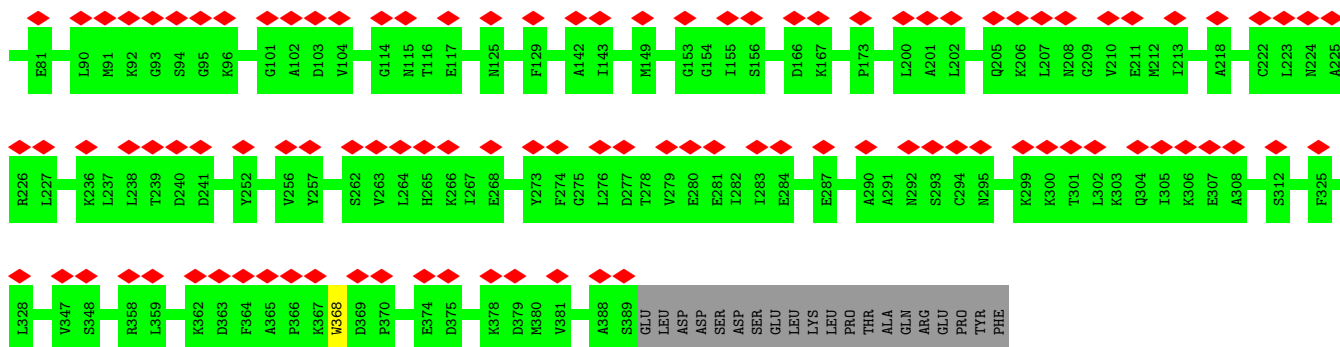


Chain BB: 

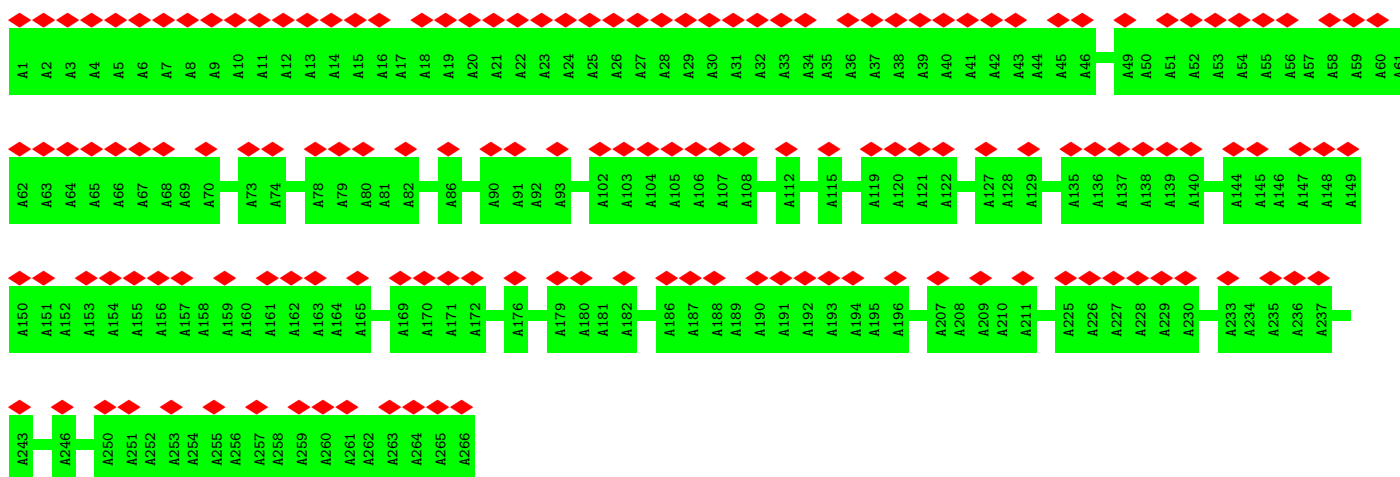
Chain BC: 

Chain BD: 

Chain BE: 

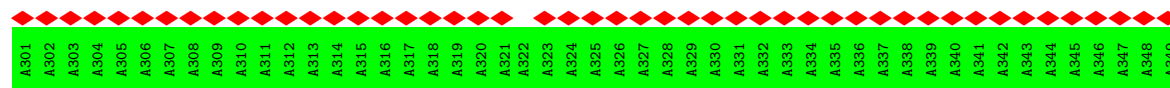


• Molecule 78: rPPR*

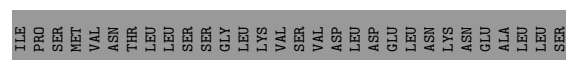
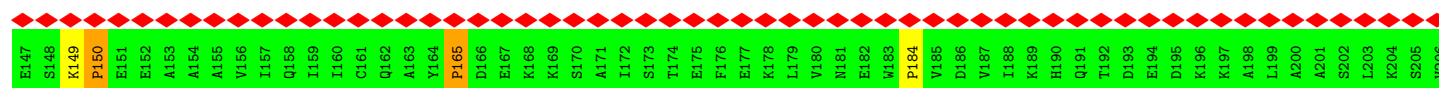
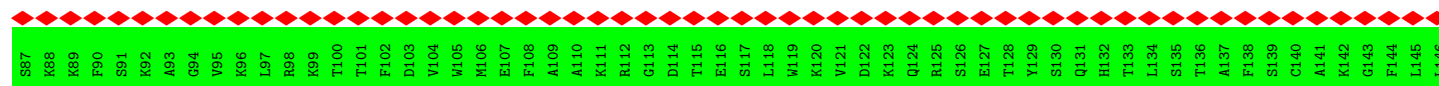
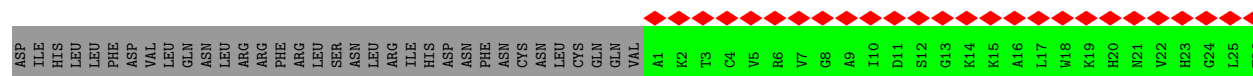
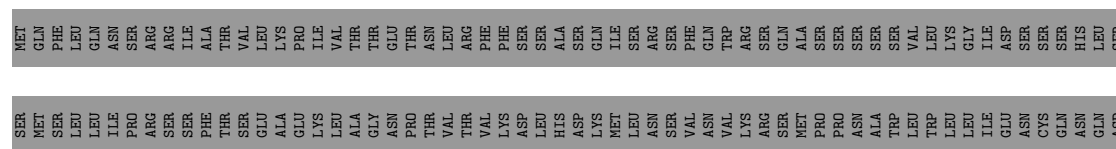


• Molecule 79: rPPR*

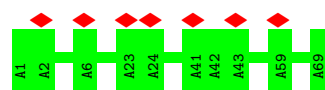




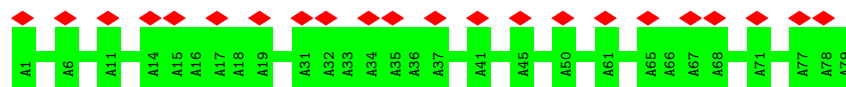
• Molecule 80: Adenylyl cyclase



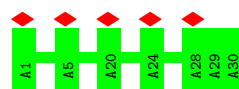
• Molecule 81: UNK-3



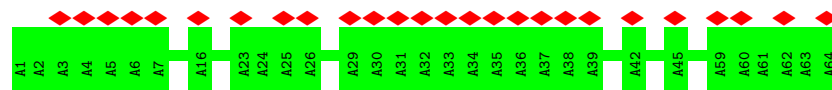
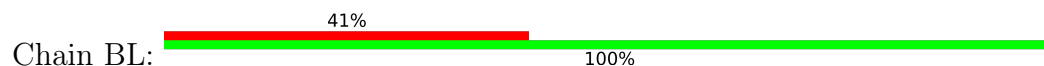
• Molecule 82: UNK-2



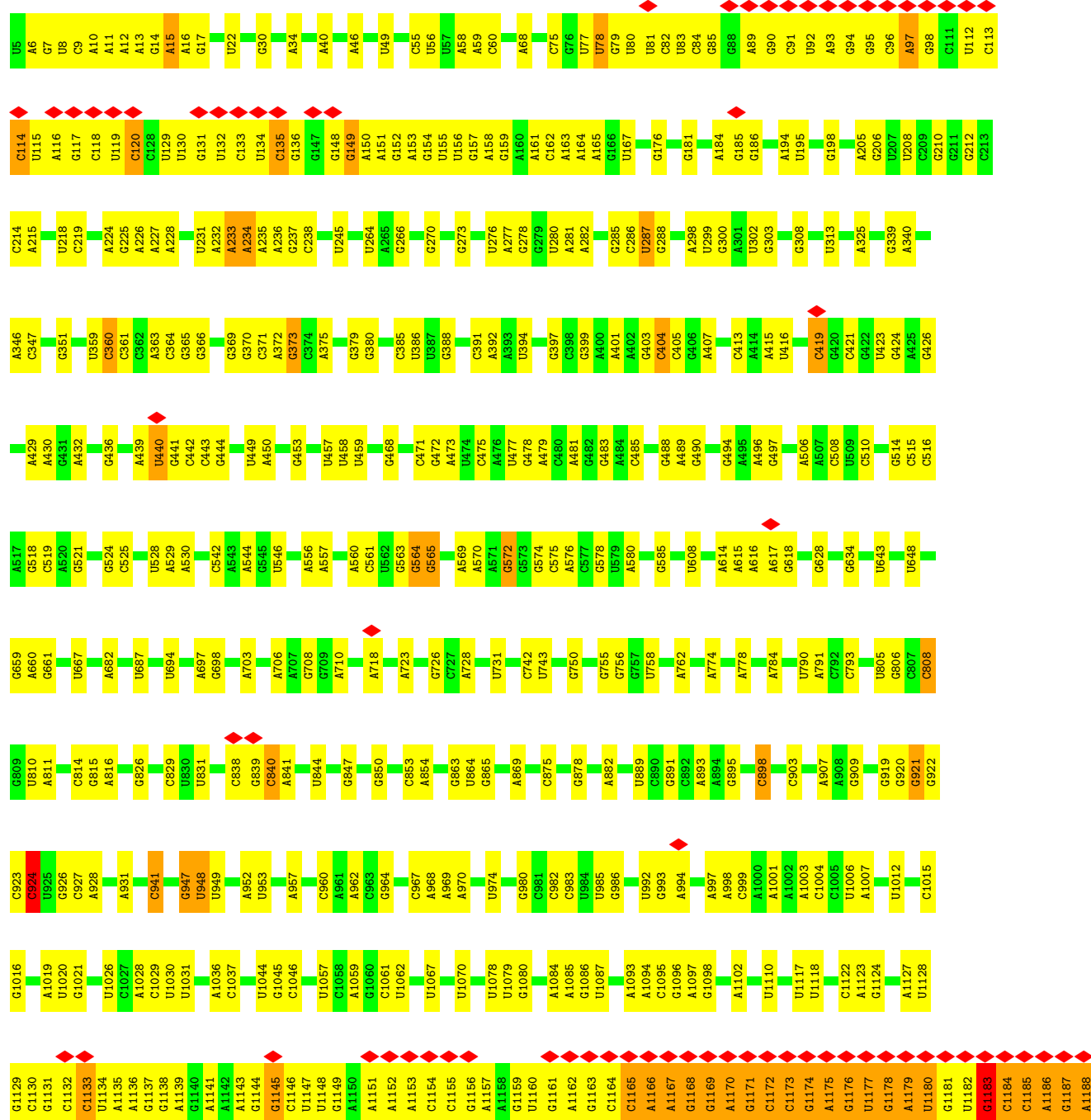
• Molecule 83: UNK-4

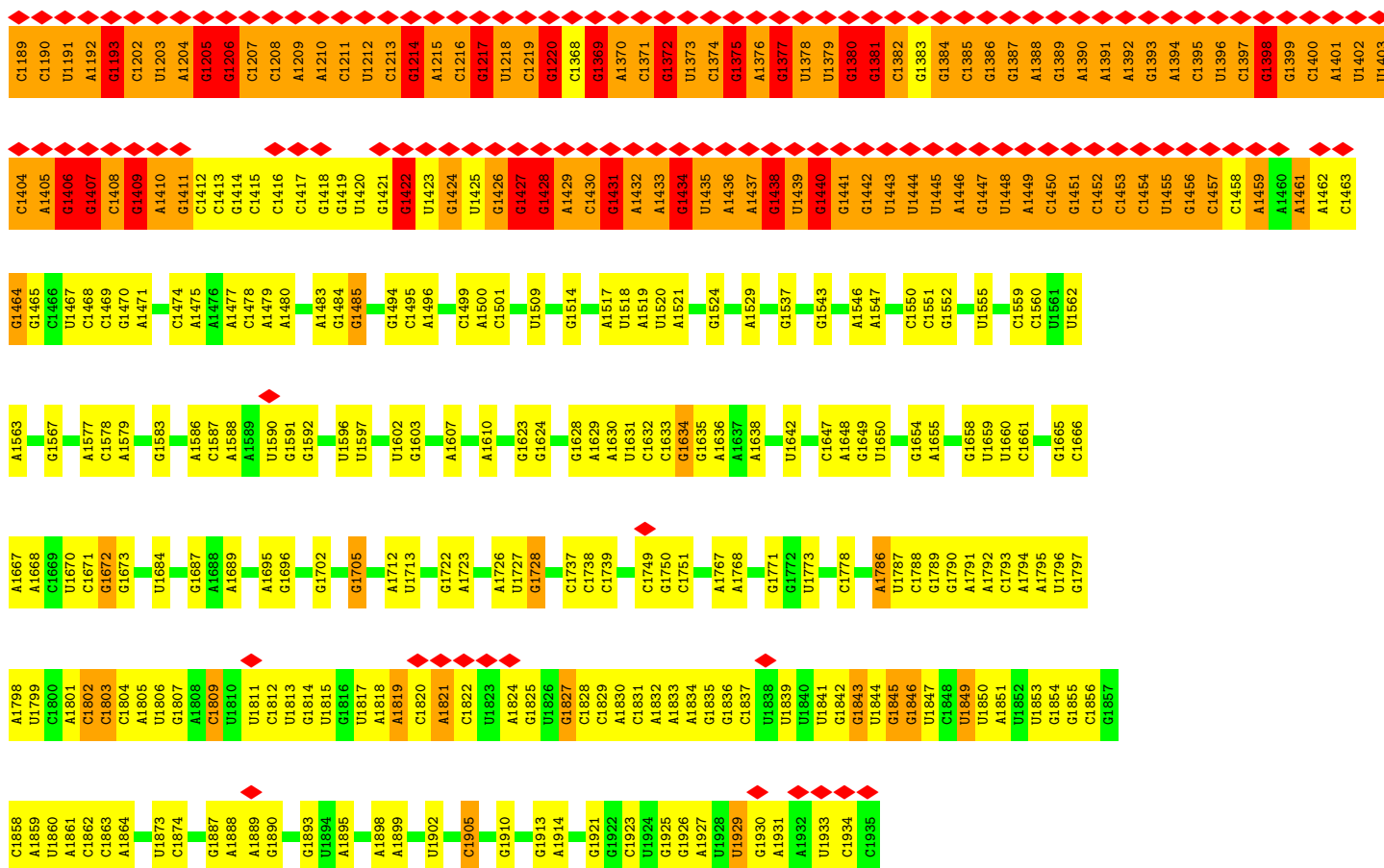


- Molecule 84: UNK-1

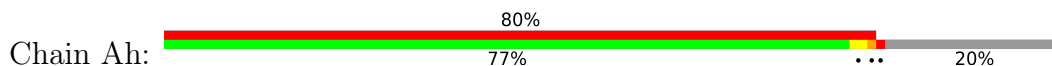


- Molecule 85: RNA (1743-MER)

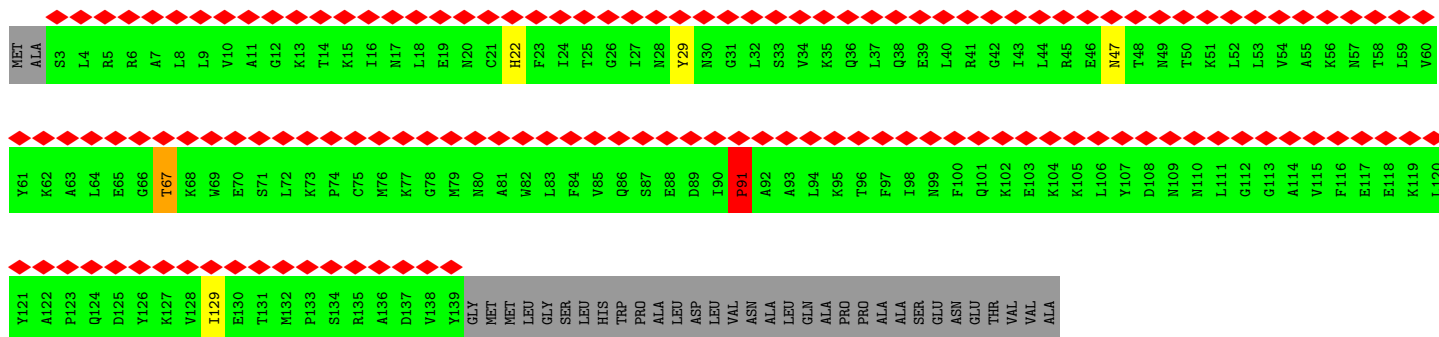


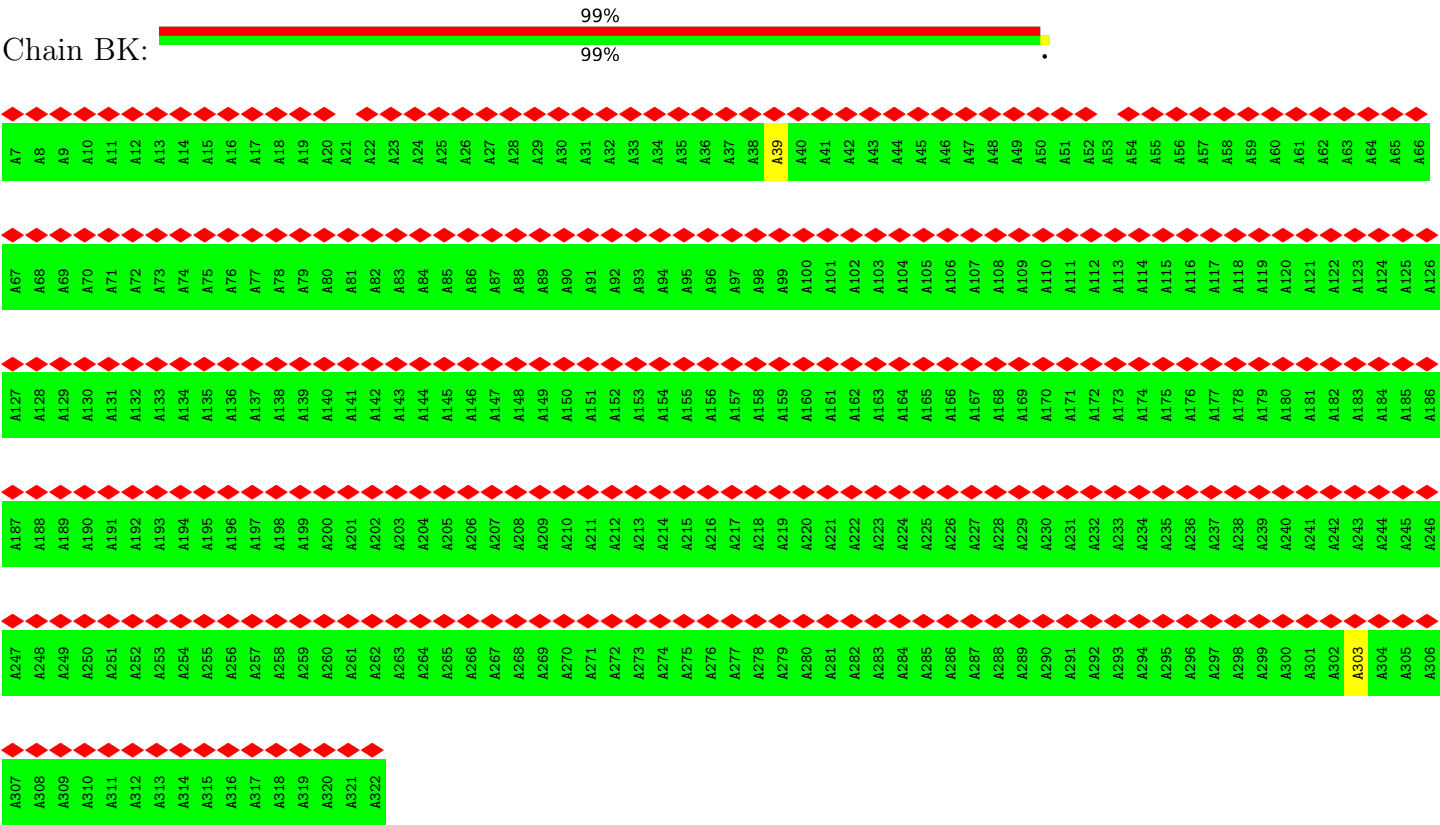


• Molecule 87: 50S ribosomal protein L10

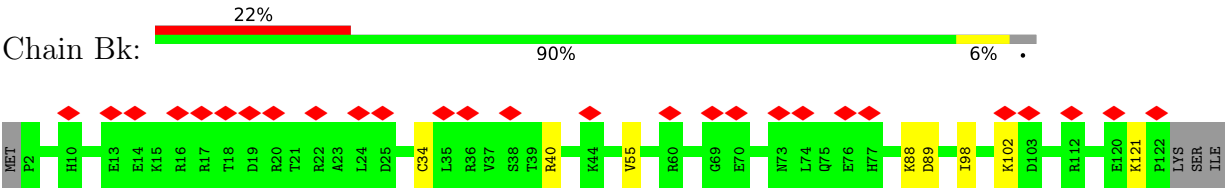


• Molecule 88: rPPR*





● Molecule 89: Ribosomal protein S12, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65280	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 ($e^-/\text{\AA}^2$)	3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.196	Depositor
Minimum map value	-0.082	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	484.0, 484.0, 484.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.21, 1.21, 1.21	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	Aa	0.49	0/764	0.66	1/1020 (0.1%)
2	Ab	0.46	0/1165	0.57	0/1554
3	Ac	0.48	0/1710	0.63	1/2294 (0.0%)
4	AD	0.47	0/518	0.57	0/686
5	Ad	0.47	0/1680	0.59	0/2267
6	Ae	0.39	0/1198	0.62	1/1620 (0.1%)
7	Af	0.36	0/815	0.54	0/1091
8	Ag	0.39	0/413	0.59	0/557
9	Ai	0.33	0/1081	0.53	0/1467
10	Aj	0.45	0/1294	0.55	0/1738
11	Ak	0.46	0/972	0.56	0/1300
12	Al	0.44	0/1433	0.59	0/1914
13	Am	0.40	0/1135	0.60	0/1518
14	An	0.50	0/1159	0.63	0/1556
15	Ao	0.41	0/849	0.55	0/1141
16	Ap	0.48	0/947	0.61	0/1268
17	Aq	0.48	0/902	0.57	0/1195
18	Ar	0.45	0/1124	0.61	0/1508
19	As	0.51	0/947	0.62	0/1273
20	At	0.49	0/854	0.60	0/1145
21	Au	0.47	0/1133	0.68	0/1527
22	Av	0.40	0/1546	0.60	0/2091
23	Aw	0.49	0/620	0.55	0/829
24	Ax	0.50	0/826	0.54	0/1105
25	Ay	0.49	0/962	0.65	0/1290
26	AA	0.44	0/303	0.70	0/400
27	AB	0.53	0/326	0.68	1/433 (0.2%)
28	AC	0.51	0/441	0.56	0/584
29	AE	0.39	0/300	0.49	0/394
30	AF	0.40	0/674	0.59	0/908
31	AG	0.55	0/500	0.65	0/677
32	AH	0.42	0/894	0.59	0/1205
33	AI	0.39	0/1765	0.54	0/2388
34	AJ	0.34	0/639	0.58	0/862

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AK	0.40	0/744	0.56	0/984
36	AL	0.40	0/407	0.57	0/549
37	AM	0.39	0/667	0.56	0/899
38	AN	0.37	0/667	0.48	0/877
39	AO	0.38	0/3654	0.56	0/4927
40	AP	0.30	0/3344	0.50	1/4680 (0.0%)
41	AQ	0.36	0/2947	0.56	0/3942
42	AR	0.26	0/144	0.44	0/200
43	1	1.01	19/68131 (0.0%)	1.17	290/106225 (0.3%)
44	3	0.79	0/2810	1.13	8/4378 (0.2%)
45	Bb	0.40	0/2346	0.54	0/3146
46	Bf	0.32	0/1121	0.53	0/1501
47	Bh	0.34	0/995	0.54	0/1336
48	Bi	0.37	0/878	0.61	0/1175
49	Bl	0.34	0/738	0.63	0/987
50	Bm	0.36	0/807	0.54	0/1072
51	Br	0.65	1/700 (0.1%)	1.16	7/932 (0.8%)
52	Bw	0.33	0/2793	0.58	0/3785
53	Bx	0.36	0/653	0.54	0/873
54	Bz	0.35	0/1027	0.50	0/1371
55	BA	0.33	0/294	0.52	0/388
56	Bt	0.35	0/240	0.52	0/307
57	BG	0.27	0/1794	0.58	9/2495 (0.4%)
58	BP	0.25	0/451	0.33	0/625
59	BF	0.28	0/614	0.47	0/858
60	Ba	0.42	0/1600	0.65	4/2162 (0.2%)
61	Bc	0.36	0/2831	0.56	0/3795
62	Bd	0.46	0/1755	0.59	0/2351
63	Be	0.37	0/834	0.59	0/1115
64	Bg	0.43	0/1059	0.58	0/1424
65	Bj	0.35	0/967	0.54	0/1293
66	Bn	0.38	0/826	0.53	0/1099
67	Bo	0.40	0/800	0.62	0/1074
68	Bp	0.40	0/647	0.57	0/868
69	Bq	0.39	0/497	0.54	0/664
70	Bs	0.32	0/542	0.49	0/716
71	Bu	0.33	0/815	0.53	0/1091
72	Bv	0.35	0/1294	0.51	0/1721
73	By	0.36	0/639	0.55	0/860
74	BB	0.39	0/204	0.41	0/260
75	BC	0.32	0/556	0.53	0/745
76	BD	0.38	0/1805	0.55	0/2409
77	BE	0.36	0/2751	0.55	0/3723

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BI	0.28	0/1329	0.44	0/1859
79	BJ	0.28	0/1744	0.43	0/2440
80	BH	0.26	0/1022	0.57	6/1425 (0.4%)
81	BN	0.27	0/344	0.43	0/480
82	BM	0.27	0/394	0.39	0/550
83	BO	0.24	0/149	0.33	0/207
84	BL	0.27	0/319	0.43	0/445
85	2	1.38	186/41845 (0.4%)	1.37	337/65247 (0.5%)
86	Az	0.72	0/669	0.95	1/898 (0.1%)
87	Ah	0.71	0/1117	0.97	2/1505 (0.1%)
88	BK	0.70	0/1579	0.81	0/2209
89	Bk	0.59	0/985	0.78	0/1315
All	All	0.91	206/202773 (0.1%)	1.03	669/297267 (0.2%)

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
18	Ar	0	2
20	At	0	1
21	Au	0	1
24	Ax	0	1
26	AA	0	1
27	AB	0	1
33	AI	0	1
37	AM	0	2
39	AO	0	2
40	AP	0	3
41	AQ	0	1
48	Bi	0	1
49	Bl	0	1
51	Br	0	2
52	Bw	0	1
61	Bc	0	1
62	Bd	0	2
65	Bj	0	1
79	BJ	0	1
85	2	5	30
87	Ah	0	2
All	All	5	58

The worst 5 of 206 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	2	1391	A	O3'-P	-54.84	0.95	1.61
85	2	1402	U	O3'-P	-47.11	1.04	1.61
85	2	1450	C	O3'-P	46.76	2.17	1.61
85	2	1385	C	O3'-P	-44.51	1.07	1.61
85	2	1379	U	O3'-P	-44.30	1.07	1.61

The worst 5 of 669 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	2	1428	G	P-O3'-C3'	39.63	167.26	119.70
85	2	1404	C	P-O3'-C3'	35.06	161.77	119.70
85	2	1454	C	P-O3'-C3'	34.74	161.39	119.70
85	2	1457	C	P-O3'-C3'	32.50	158.70	119.70
85	2	1391	A	P-O3'-C3'	32.21	158.35	119.70

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	2	1165	C	C4'
85	2	1206	G	C3'
85	2	1404	C	C3'
85	2	1409	G	C4'
85	2	1410	A	C2'

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	Ar	164	LEU	Peptide
18	Ar	191	ARG	Peptide
20	At	102	LYS	Peptide
21	Au	132	THR	Peptide
24	Ax	57	ASN	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 ⓘ

5.3.1 Protein backbone ⓘ

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	Aa	94/349 (27%)	78 (83%)	14 (15%)	2 (2%)	5	33
2	Ab	153/214 (72%)	129 (84%)	24 (16%)	0	100	100
3	Ac	216/324 (67%)	167 (77%)	49 (23%)	0	100	100
4	AD	58/173 (34%)	49 (84%)	9 (16%)	0	100	100
5	Ad	207/300 (69%)	186 (90%)	21 (10%)	0	100	100
6	Ae	142/185 (77%)	114 (80%)	28 (20%)	0	100	100
7	Af	98/102 (96%)	80 (82%)	18 (18%)	0	100	100
8	Ag	49/221 (22%)	43 (88%)	6 (12%)	0	100	100
9	Ai	136/155 (88%)	120 (88%)	16 (12%)	0	100	100
10	Aj	153/205 (75%)	119 (78%)	34 (22%)	0	100	100
11	Ak	125/173 (72%)	102 (82%)	23 (18%)	0	100	100
12	Al	176/281 (63%)	145 (82%)	31 (18%)	0	100	100
13	Am	140/179 (78%)	122 (87%)	18 (13%)	0	100	100
14	An	139/160 (87%)	114 (82%)	24 (17%)	1 (1%)	19	54
15	Ao	104/114 (91%)	83 (80%)	21 (20%)	0	100	100
16	Ap	112/222 (50%)	91 (81%)	21 (19%)	0	100	100
17	Aq	104/126 (82%)	92 (88%)	12 (12%)	0	100	100
18	Ar	135/270 (50%)	101 (75%)	34 (25%)	0	100	100
19	As	119/269 (44%)	106 (89%)	13 (11%)	0	100	100
20	At	103/178 (58%)	80 (78%)	23 (22%)	0	100	100
21	Au	138/159 (87%)	97 (70%)	39 (28%)	2 (1%)	9	39
22	Av	194/249 (78%)	166 (86%)	28 (14%)	0	100	100
23	Aw	74/154 (48%)	63 (85%)	11 (15%)	0	100	100
24	Ax	97/212 (46%)	85 (88%)	12 (12%)	0	100	100
25	Ay	109/144 (76%)	87 (80%)	22 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AA	35/76 (46%)	27 (77%)	8 (23%)	0	100	100
27	AB	39/134 (29%)	27 (69%)	12 (31%)	0	100	100
28	AC	49/58 (84%)	43 (88%)	6 (12%)	0	100	100
29	AE	34/103 (33%)	29 (85%)	5 (15%)	0	100	100
30	AF	82/250 (33%)	74 (90%)	8 (10%)	0	100	100
31	AG	59/94 (63%)	40 (68%)	18 (30%)	1 (2%)	7	36
32	AH	106/146 (73%)	90 (85%)	16 (15%)	0	100	100
33	AI	205/233 (88%)	161 (78%)	44 (22%)	0	100	100
34	AJ	79/127 (62%)	59 (75%)	20 (25%)	0	100	100
35	AK	85/130 (65%)	74 (87%)	11 (13%)	0	100	100
36	AL	50/81 (62%)	39 (78%)	11 (22%)	0	100	100
37	AM	80/151 (53%)	71 (89%)	9 (11%)	0	100	100
38	AN	78/188 (42%)	70 (90%)	8 (10%)	0	100	100
39	AO	450/491 (92%)	387 (86%)	63 (14%)	0	100	100
40	AP	667/669 (100%)	531 (80%)	133 (20%)	3 (0%)	30	65
41	AQ	364/521 (70%)	312 (86%)	51 (14%)	1 (0%)	37	70
42	AR	27/29 (93%)	21 (78%)	6 (22%)	0	100	100
45	Bb	271/556 (49%)	218 (80%)	52 (19%)	1 (0%)	30	65
46	Bf	134/148 (90%)	122 (91%)	12 (9%)	0	100	100
47	Bh	121/430 (28%)	100 (83%)	21 (17%)	0	100	100
48	Bi	99/241 (41%)	76 (77%)	23 (23%)	0	100	100
49	Bl	89/154 (58%)	53 (60%)	35 (39%)	1 (1%)	12	45
50	Bm	94/164 (57%)	63 (67%)	30 (32%)	1 (1%)	12	45
51	Br	81/212 (38%)	64 (79%)	12 (15%)	5 (6%)	1	16
52	Bw	331/480 (69%)	234 (71%)	94 (28%)	3 (1%)	14	48
53	Bx	77/102 (76%)	61 (79%)	16 (21%)	0	100	100
54	Bz	121/419 (29%)	110 (91%)	11 (9%)	0	100	100
55	BA	36/91 (40%)	28 (78%)	8 (22%)	0	100	100
56	Bt	27/98 (28%)	22 (82%)	5 (18%)	0	100	100
57	BG	362/576 (63%)	309 (85%)	46 (13%)	7 (2%)	6	35
58	BP	83/91 (91%)	81 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	BF	121/123 (98%)	98 (81%)	23 (19%)	0	100	100
60	Ba	193/219 (88%)	146 (76%)	47 (24%)	0	100	100
61	Bc	323/362 (89%)	255 (79%)	66 (20%)	2 (1%)	22	57
62	Bd	214/515 (42%)	170 (79%)	44 (21%)	0	100	100
63	Be	97/139 (70%)	72 (74%)	25 (26%)	0	100	100
64	Bg	126/129 (98%)	101 (80%)	25 (20%)	0	100	100
65	Bj	121/314 (38%)	97 (80%)	24 (20%)	0	100	100
66	Bn	98/419 (23%)	86 (88%)	12 (12%)	0	100	100
67	Bo	97/135 (72%)	75 (77%)	22 (23%)	0	100	100
68	Bp	76/116 (66%)	59 (78%)	17 (22%)	0	100	100
69	Bq	60/261 (23%)	51 (85%)	9 (15%)	0	100	100
70	Bs	64/101 (63%)	53 (83%)	11 (17%)	0	100	100
71	Bu	96/195 (49%)	78 (81%)	18 (19%)	0	100	100
72	Bv	147/195 (75%)	119 (81%)	28 (19%)	0	100	100
73	By	74/142 (52%)	62 (84%)	12 (16%)	0	100	100
74	BB	21/137 (15%)	20 (95%)	1 (5%)	0	100	100
75	BC	66/112 (59%)	53 (80%)	13 (20%)	0	100	100
76	BD	208/420 (50%)	164 (79%)	43 (21%)	1 (0%)	25	60
77	BE	346/409 (85%)	277 (80%)	69 (20%)	0	100	100
78	BI	264/266 (99%)	227 (86%)	37 (14%)	0	100	100
79	BJ	347/349 (99%)	301 (87%)	46 (13%)	0	100	100
80	BH	204/390 (52%)	176 (86%)	24 (12%)	4 (2%)	6	34
81	BN	67/69 (97%)	57 (85%)	10 (15%)	0	100	100
82	BM	77/79 (98%)	67 (87%)	10 (13%)	0	100	100
83	BO	28/30 (93%)	28 (100%)	0	0	100	100
84	BL	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
86	Az	80/109 (73%)	73 (91%)	6 (8%)	1 (1%)	10	41
87	Ah	135/171 (79%)	126 (93%)	7 (5%)	2 (2%)	8	39
88	BK	314/316 (99%)	289 (92%)	23 (7%)	2 (1%)	22	57
89	Bk	119/125 (95%)	114 (96%)	4 (3%)	1 (1%)	16	51
All	All	11835/18772 (63%)	9765 (82%)	2029 (17%)	41 (0%)	38	70

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	BG	89	VAL
57	BG	277	SER
57	BG	278	PRO
87	Ah	91	PRO
1	Aa	81	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Aa	82/284 (29%)	81 (99%)	1 (1%)	67	78
2	Ab	121/169 (72%)	121 (100%)	0	100	100
3	Ac	174/267 (65%)	174 (100%)	0	100	100
4	AD	54/158 (34%)	54 (100%)	0	100	100
5	Ad	181/260 (70%)	180 (99%)	1 (1%)	84	88
6	Ae	133/168 (79%)	133 (100%)	0	100	100
7	Af	84/86 (98%)	84 (100%)	0	100	100
8	Ag	43/196 (22%)	43 (100%)	0	100	100
9	Ai	116/128 (91%)	113 (97%)	3 (3%)	41	62
10	Aj	135/170 (79%)	132 (98%)	3 (2%)	47	65
11	Ak	103/138 (75%)	100 (97%)	3 (3%)	37	59
12	Al	147/236 (62%)	147 (100%)	0	100	100
13	Am	111/146 (76%)	110 (99%)	1 (1%)	75	83
14	An	119/137 (87%)	119 (100%)	0	100	100
15	Ao	91/98 (93%)	90 (99%)	1 (1%)	70	79
16	Ap	103/199 (52%)	101 (98%)	2 (2%)	52	70
17	Aq	93/110 (84%)	93 (100%)	0	100	100
18	Ar	122/244 (50%)	122 (100%)	0	100	100
19	As	98/233 (42%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	At	92/146 (63%)	92 (100%)	0	100	100
21	Au	121/132 (92%)	119 (98%)	2 (2%)	56	72
22	Av	175/216 (81%)	174 (99%)	1 (1%)	84	88
23	Aw	64/126 (51%)	63 (98%)	1 (2%)	58	73
24	Ax	83/173 (48%)	82 (99%)	1 (1%)	67	78
25	Ay	105/127 (83%)	105 (100%)	0	100	100
26	AA	28/65 (43%)	28 (100%)	0	100	100
27	AB	36/116 (31%)	36 (100%)	0	100	100
28	AC	46/52 (88%)	46 (100%)	0	100	100
29	AE	35/87 (40%)	35 (100%)	0	100	100
30	AF	70/206 (34%)	69 (99%)	1 (1%)	62	75
31	AG	55/82 (67%)	54 (98%)	1 (2%)	54	71
32	AH	98/130 (75%)	98 (100%)	0	100	100
33	AI	185/209 (88%)	183 (99%)	2 (1%)	70	79
34	AJ	71/111 (64%)	70 (99%)	1 (1%)	62	75
35	AK	76/109 (70%)	76 (100%)	0	100	100
36	AL	42/63 (67%)	41 (98%)	1 (2%)	44	63
37	AM	73/130 (56%)	73 (100%)	0	100	100
38	AN	69/163 (42%)	69 (100%)	0	100	100
39	AO	388/424 (92%)	387 (100%)	1 (0%)	91	92
41	AQ	311/461 (68%)	309 (99%)	2 (1%)	84	88
45	Bb	243/495 (49%)	241 (99%)	2 (1%)	79	84
46	Bf	116/125 (93%)	116 (100%)	0	100	100
47	Bh	99/360 (28%)	99 (100%)	0	100	100
48	Bi	94/211 (44%)	94 (100%)	0	100	100
49	Bl	78/129 (60%)	78 (100%)	0	100	100
50	Bm	84/144 (58%)	84 (100%)	0	100	100
51	Br	73/180 (41%)	65 (89%)	8 (11%)	5	21
52	Bw	289/404 (72%)	288 (100%)	1 (0%)	91	92
53	Bx	68/85 (80%)	65 (96%)	3 (4%)	24	49
54	Bz	107/368 (29%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	BA	35/81 (43%)	35 (100%)	0	100	100
56	Bt	25/81 (31%)	25 (100%)	0	100	100
60	Ba	173/191 (91%)	171 (99%)	2 (1%)	67	78
61	Bc	310/343 (90%)	308 (99%)	2 (1%)	84	88
62	Bd	185/463 (40%)	185 (100%)	0	100	100
63	Be	90/126 (71%)	90 (100%)	0	100	100
64	Bg	112/113 (99%)	112 (100%)	0	100	100
65	Bj	103/264 (39%)	103 (100%)	0	100	100
66	Bn	94/378 (25%)	94 (100%)	0	100	100
67	Bo	82/113 (73%)	81 (99%)	1 (1%)	67	78
68	Bp	71/99 (72%)	71 (100%)	0	100	100
69	Bq	51/224 (23%)	50 (98%)	1 (2%)	50	68
70	Bs	61/92 (66%)	61 (100%)	0	100	100
71	Bu	86/170 (51%)	86 (100%)	0	100	100
72	Bv	132/173 (76%)	131 (99%)	1 (1%)	79	84
73	By	61/115 (53%)	59 (97%)	2 (3%)	33	56
74	BB	22/127 (17%)	22 (100%)	0	100	100
75	BC	58/94 (62%)	57 (98%)	1 (2%)	56	72
76	BD	188/368 (51%)	187 (100%)	1 (0%)	86	90
77	BE	296/351 (84%)	295 (100%)	1 (0%)	91	92
86	Az	73/96 (76%)	67 (92%)	6 (8%)	9	33
87	Ah	119/144 (83%)	115 (97%)	4 (3%)	32	55
89	Bk	104/108 (96%)	97 (93%)	7 (7%)	13	39
All	All	8115/13570 (60%)	8043 (99%)	72 (1%)	74	83

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
86	Az	37	THR
89	Bk	121	LYS
86	Az	77	TYR
89	Bk	34	CYS
34	AJ	29	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
61	Bc	135	ASN
73	By	68	HIS
61	Bc	219	GLN
64	Bg	123	GLN
77	BE	265	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	1	2836/2842 (99%)	1125 (39%)	66 (2%)
44	3	118/118 (100%)	49 (41%)	7 (5%)
85	2	1733/1743 (99%)	757 (43%)	66 (3%)
All	All	4687/4703 (99%)	1931 (41%)	139 (2%)

5 of 1931 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	1	17	A
43	1	27	A
43	1	37	G
43	1	38	G
43	1	45	A

5 of 139 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	2	1428	G
85	2	1478	C
85	2	1795	A
43	1	2051	U
43	1	2050	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
85	2	39
43	1	5
58	BP	3
45	Bb	1

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	120:C	O3'	128:C	P	28.73
1	BP	204:ALA	C	205:ALA	N	21.29
1	2	1193:G	O3'	1202:C	P	17.46
1	2	1220:G	O3'	1368:C	P	17.36
1	2	98:G	O3'	111:C	P	17.08

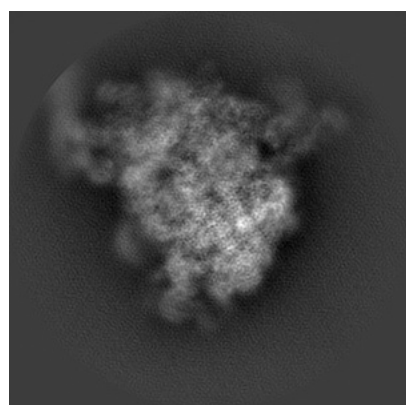
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10654. These allow visual inspection of the internal detail of the map and identification of artifacts.

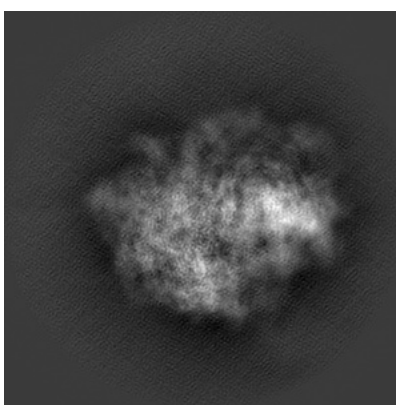
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

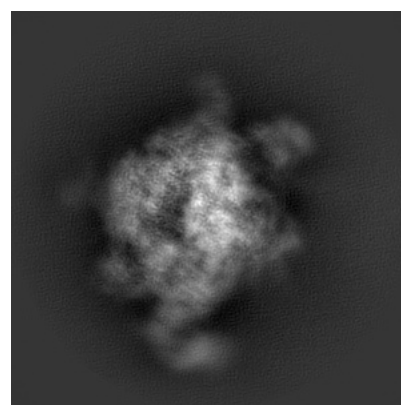
6.1.1 Primary map



X



Y

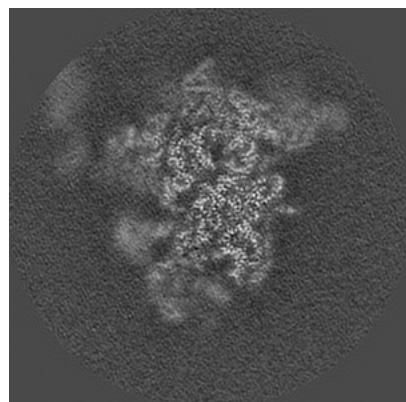


Z

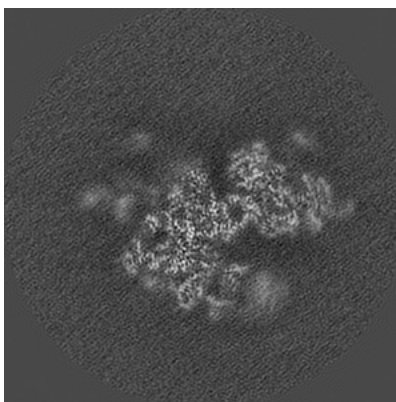
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

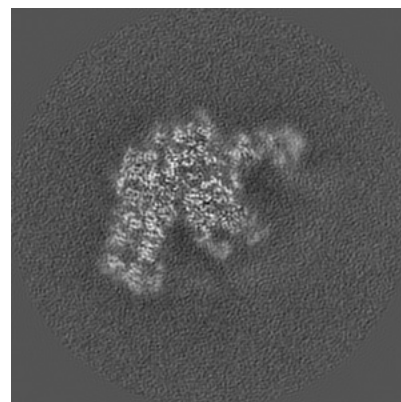
6.2.1 Primary map



X Index: 200



Y Index: 200

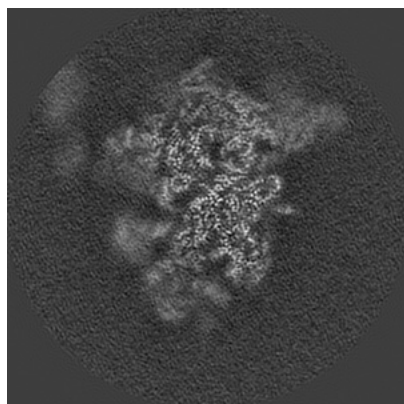


Z Index: 200

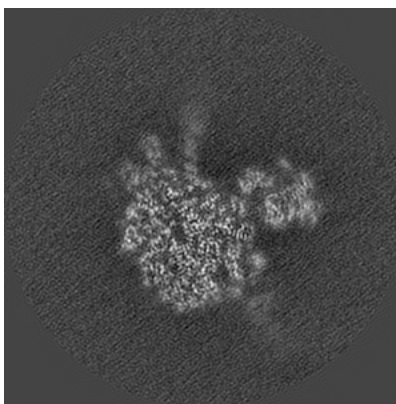
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

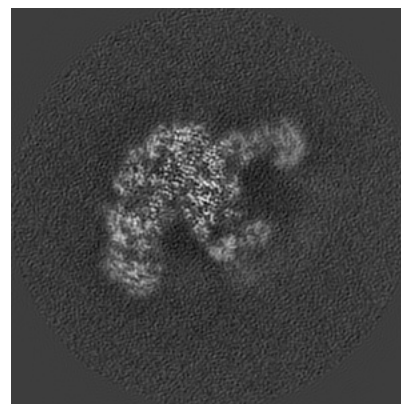
6.3.1 Primary map



X Index: 201



Y Index: 229

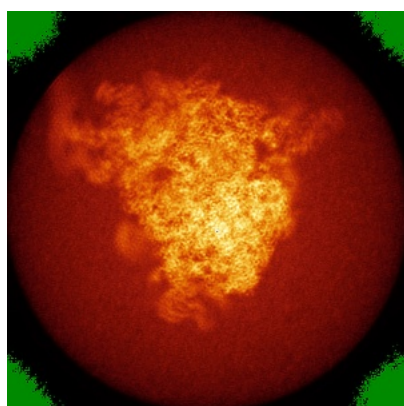


Z Index: 205

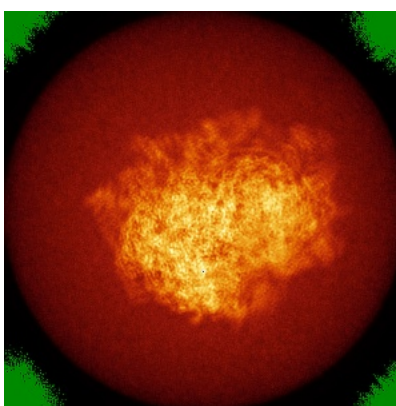
The images above show the largest variance slices of the map in three orthogonal directions.

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

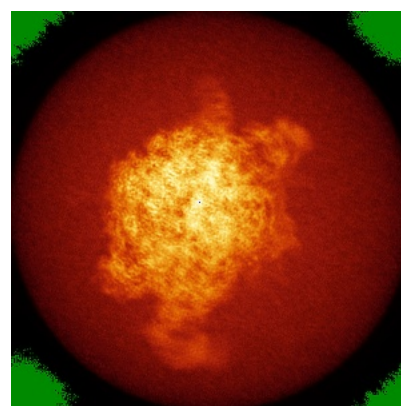
6.4.1 Primary map



X



Y

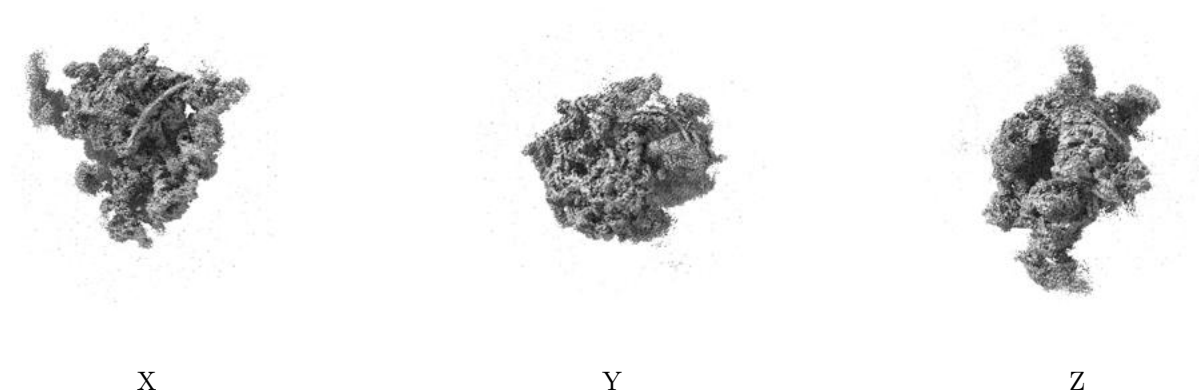


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

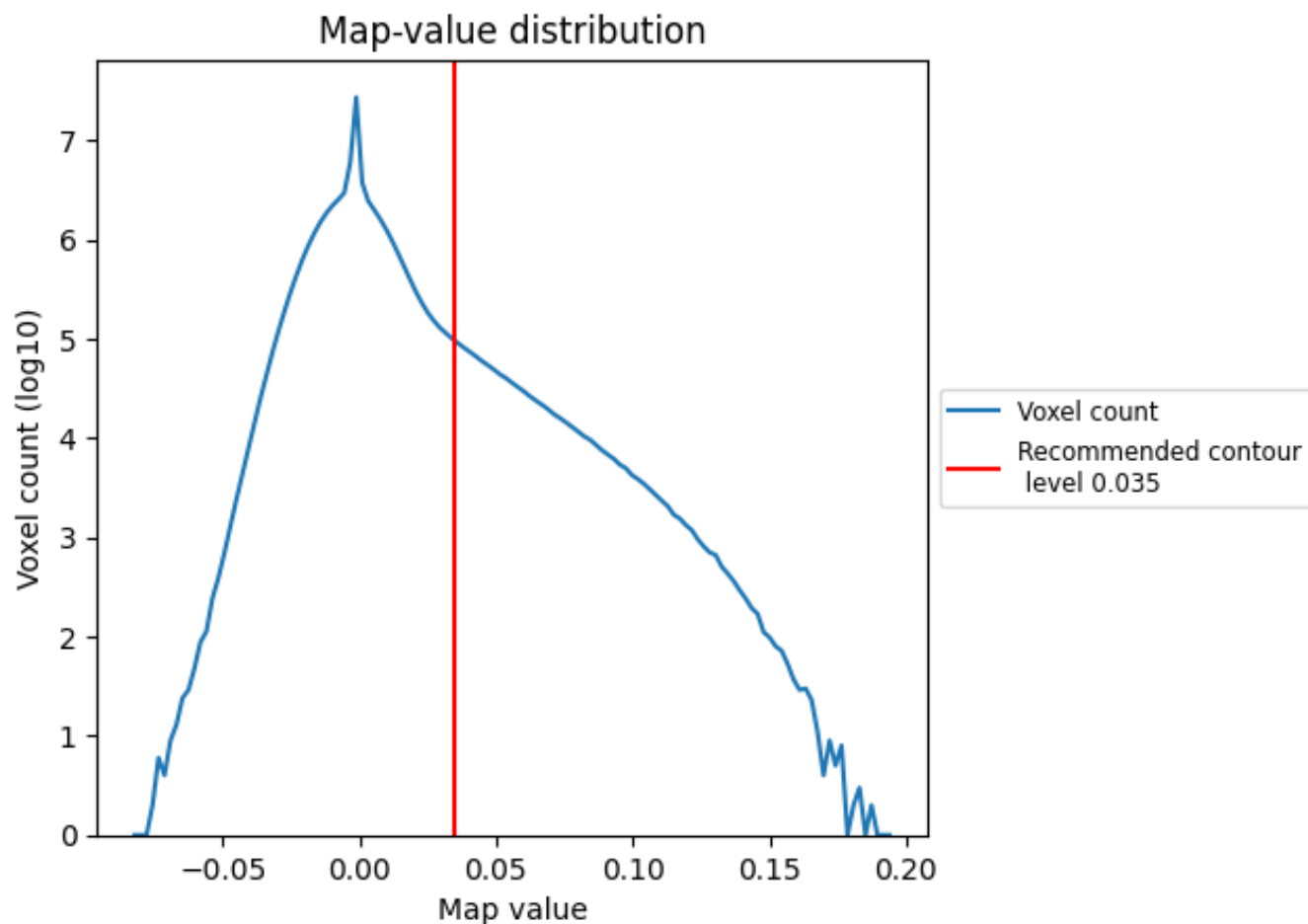
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

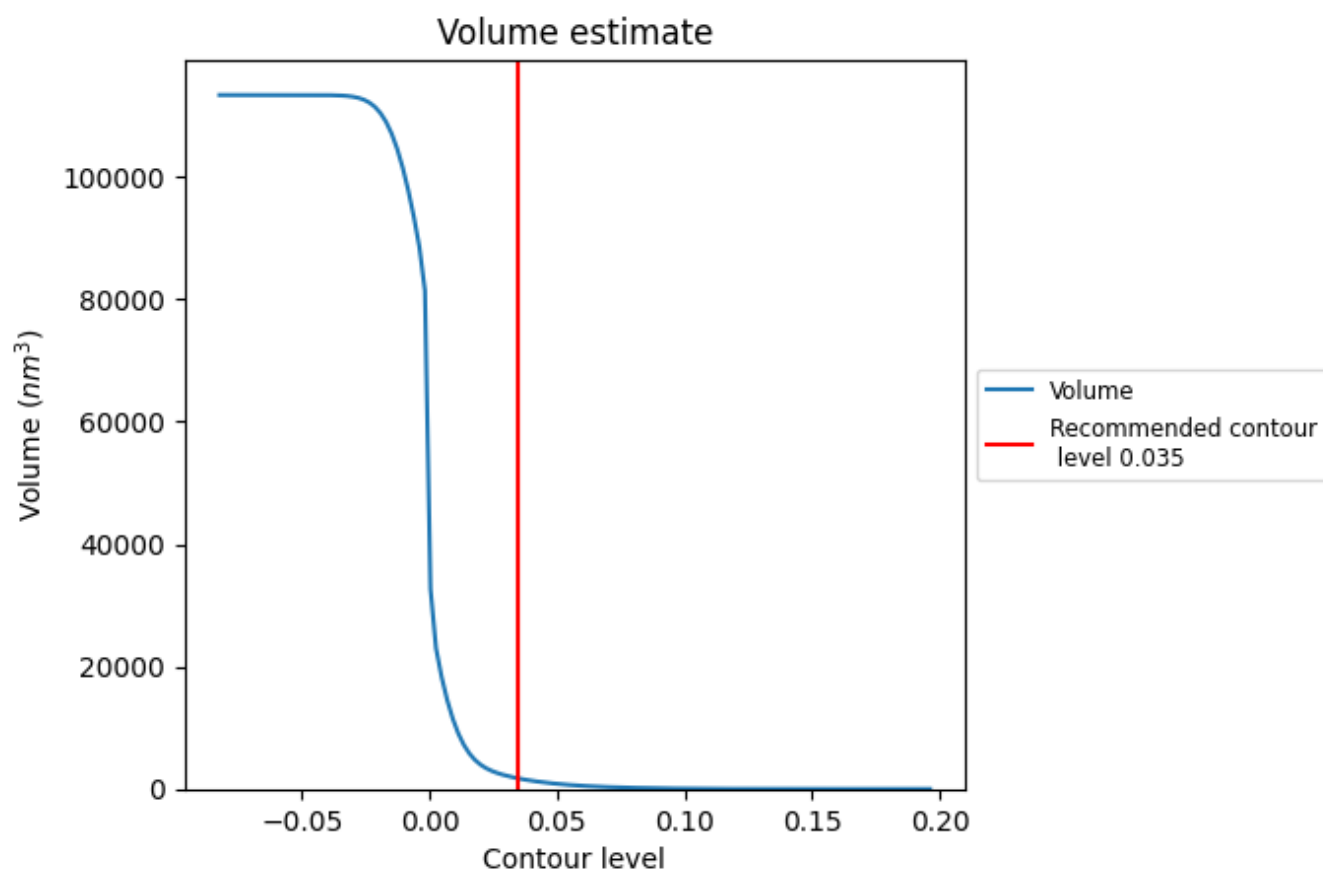
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

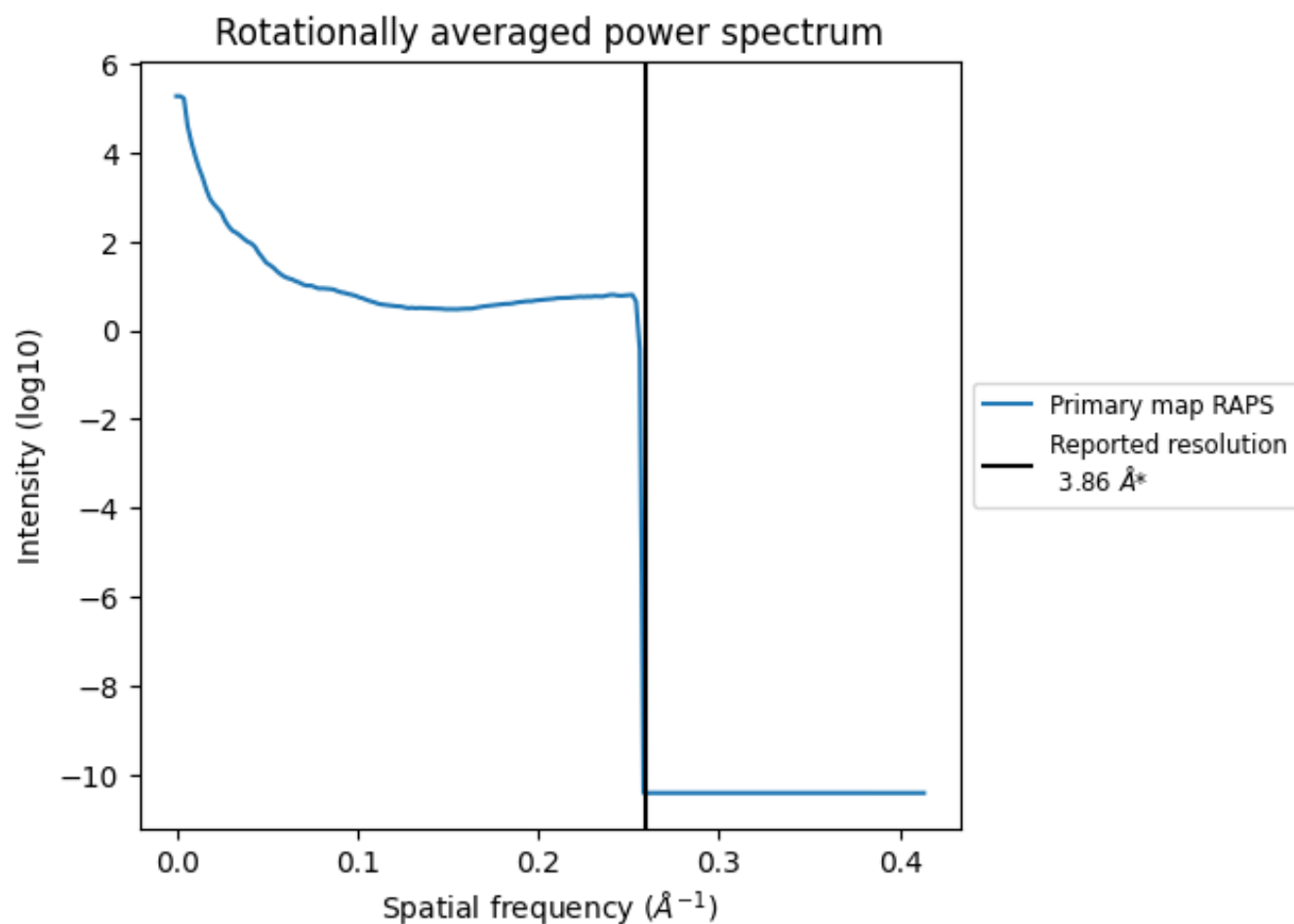
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1711 nm^3 ; this corresponds to an approximate mass of 1546 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.259 Å⁻¹

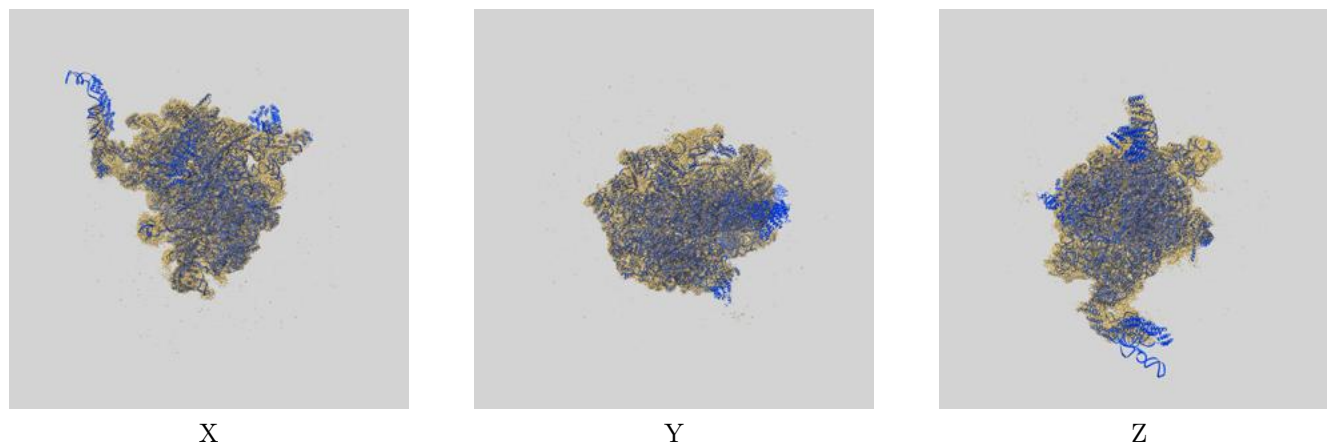
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

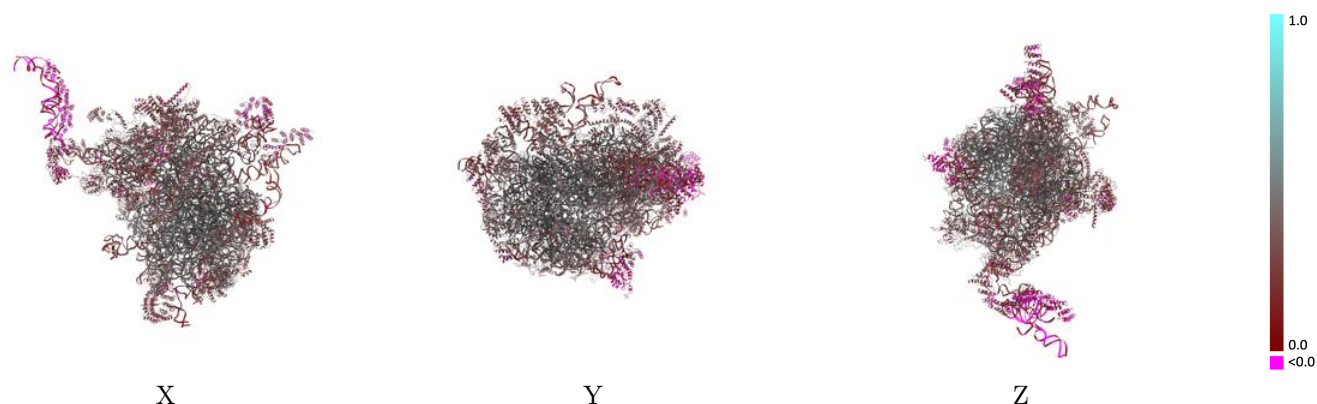
This section contains information regarding the fit between EMDB map EMD-10654 and PDB model 6XYW. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



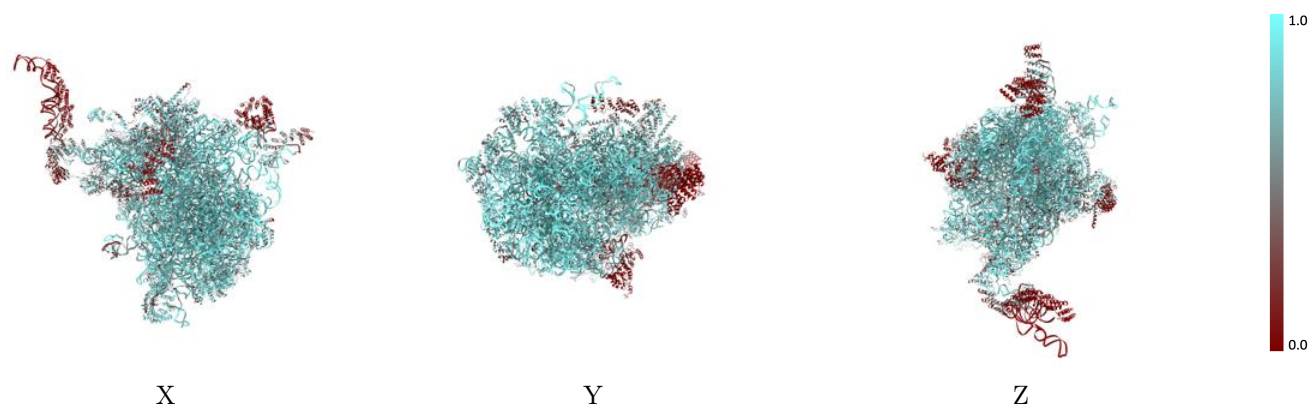
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



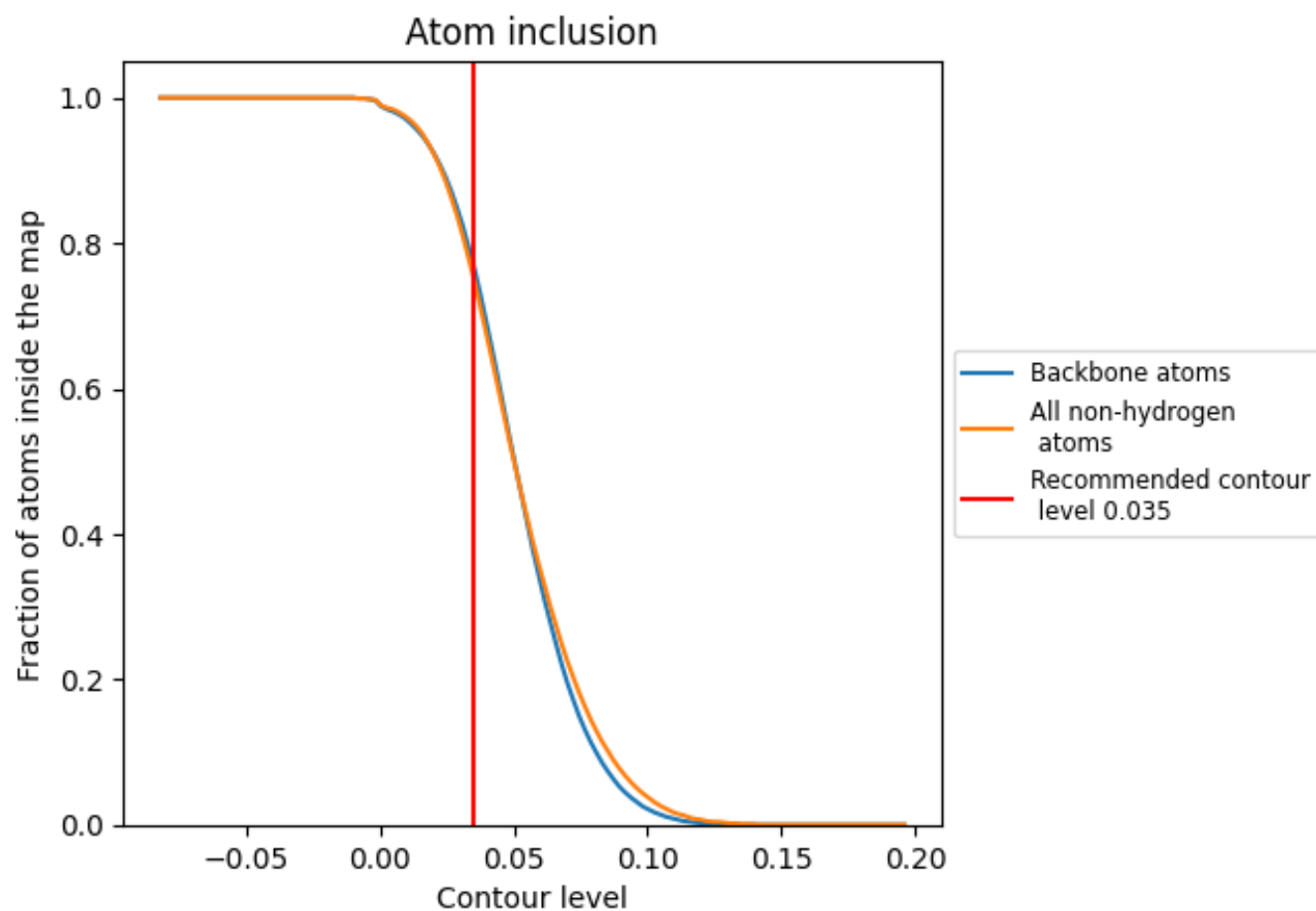
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7510	 0.3590
1	 0.8950	 0.3950
2	 0.8180	 0.3350
3	 0.9540	 0.3880
AA	 0.7600	 0.3460
AB	 0.8160	 0.4630
AC	 0.8330	 0.4390
AD	 0.8080	 0.4600
AE	 0.6680	 0.4590
AF	 0.7150	 0.3070
AG	 0.7700	 0.4460
AH	 0.8200	 0.4400
AI	 0.6970	 0.3330
AJ	 0.0550	 0.1150
AK	 0.7830	 0.4140
AL	 0.8420	 0.4370
AM	 0.7880	 0.4290
AN	 0.7230	 0.4140
AO	 0.7120	 0.3420
AP	 0.6910	 0.2700
AQ	 0.6640	 0.3290
AR	 0.9030	 0.3810
Aa	 0.7230	 0.4570
Ab	 0.7970	 0.4760
Ac	 0.8150	 0.4450
Ad	 0.7900	 0.4370
Ae	 0.6480	 0.3580
Af	 0.3760	 0.3710
Ag	 0.7510	 0.4030
Ah	 0.0080	 -0.0030
Ai	 0.1070	 0.1780
Aj	 0.8210	 0.4370
Ak	 0.6510	 0.4550
Al	 0.7710	 0.4360
Am	 0.5370	 0.4340





























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Chain	Atom inclusion	Q-score
An	 0.8230	 0.4470
Ao	 0.8350	 0.4090
Ap	 0.7600	 0.4430
Aq	 0.8180	 0.4250
Ar	 0.8070	 0.4250
As	 0.7920	 0.4550
At	 0.7480	 0.4530
Au	 0.7810	 0.3890
Av	 0.6890	 0.3670
Aw	 0.8370	 0.4560
Ax	 0.7880	 0.4540
Ay	 0.7520	 0.3860
Az	 0.7420	 0.3300
BA	 0.2150	 0.2410
BB	 0.5100	 0.4510
BC	 0.6500	 0.3240
BD	 0.6820	 0.3430
BE	 0.5400	 0.3120
BF	 0.6710	 0.3470
BG	 0.3520	 0.2080
BH	 0.0540	 0.2250
BI	 0.4170	 0.2170
BJ	 0.0160	 0.1570
BK	 0.0230	 0.0260
BL	 0.5840	 0.2630
BM	 0.6560	 0.3030
BN	 0.7940	 0.3430
BO	 0.7870	 0.3040
BP	 0.7630	 0.2640
Ba	 0.5290	 0.3400
Bb	 0.6210	 0.3850
Bc	 0.6580	 0.3540
Bd	 0.6630	 0.4100
Be	 0.6500	 0.3760
Bf	 0.4270	 0.3190
Bg	 0.6420	 0.4110
Bh	 0.6490	 0.3370
Bi	 0.6690	 0.3420
Bj	 0.6290	 0.3770
Bk	 0.5830	 0.3110
Bl	 0.5260	 0.3330
Bm	 0.7070	 0.4040

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Chain	Atom inclusion	Q-score
Bn	 0.7270	 0.3950
Bo	 0.7430	 0.4110
Bp	 0.7440	 0.4300
Bq	 0.6130	 0.3900
Br	 0.3840	 0.0570
Bs	 0.5450	 0.3960
Bt	 0.7590	 0.4240
Bu	 0.4110	 0.3400
Bv	 0.6360	 0.3060
Bw	 0.5520	 0.3120
Bx	 0.5350	 0.3790
By	 0.6640	 0.3250
Bz	 0.5720	 0.3380