Full wwPDB EM Validation Report

Dec 19, 2022 – 01:44 PM EST

PDB ID	:	7R7A
EMDB ID	:	EMD-24296
Title	:	State E1 nucleolar 60S ribosome biogenesis intermediate - Composite model
Authors	:	Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on	:	2021-06-24
Resolution	:	3.04 Å(reported)

This is a Full wwPDB EM Validation 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:

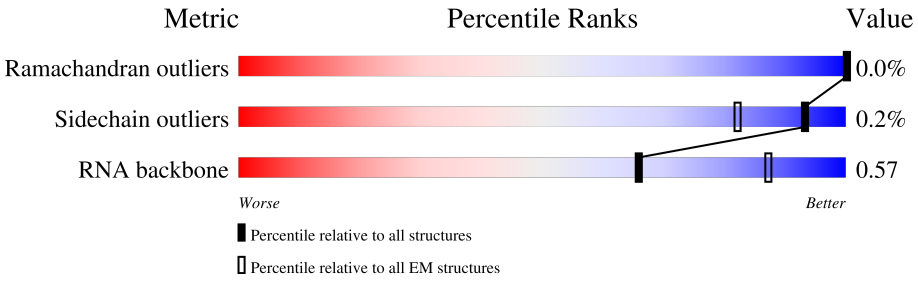
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.04 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	1	3396	9% 60% 15% 24%
2	2	158	83% 17%
3	7	204	5% 63% 37%
4	A	291	15% 91% 9%
5	B	387	86% 13%
6	C	362	99%
7	E	175	5% 94% 6%
8	F	244	91% 9%

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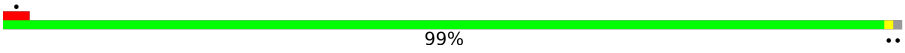
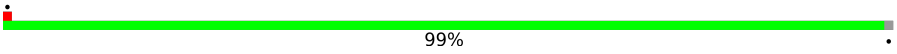
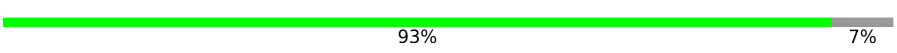
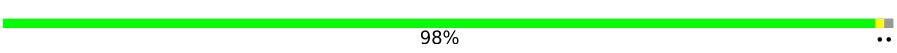
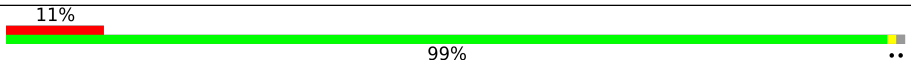
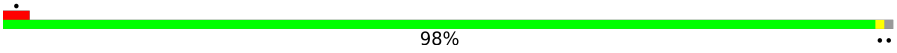
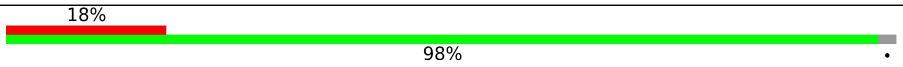
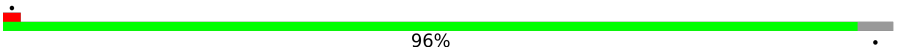
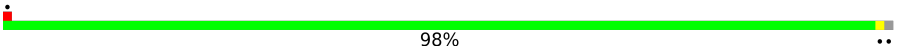
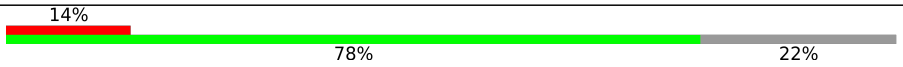
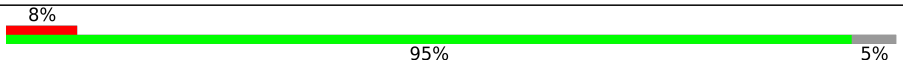
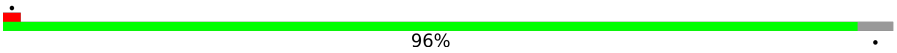
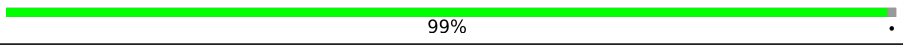
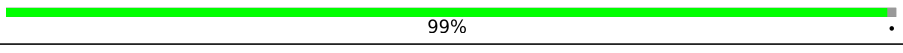
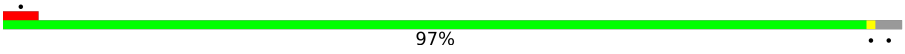
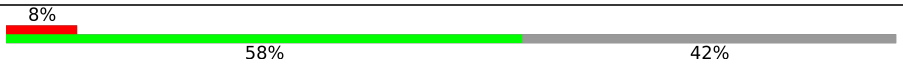
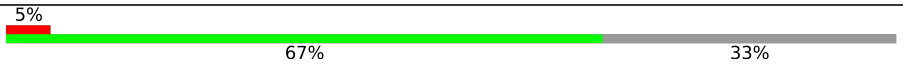
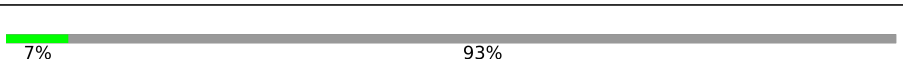
Mol	Chain	Length	Quality of chain
9	H	191	
10	J	427	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	S	172	
18	T	160	
19	W	236	
20	X	142	
21	Y	127	
22	b	647	
23	d	113	
24	e	130	
25	f	107	
26	h	120	
27	i	100	
28	j	88	
29	l	181	
30	m	807	
31	q	618	
32	r	261	
33	s	520	

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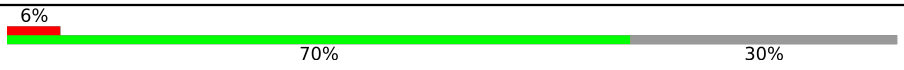
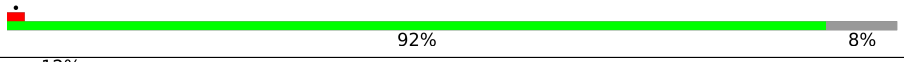
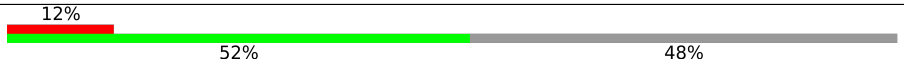
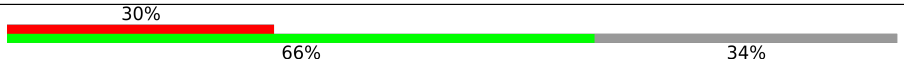
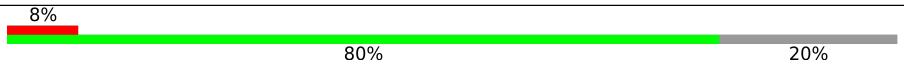
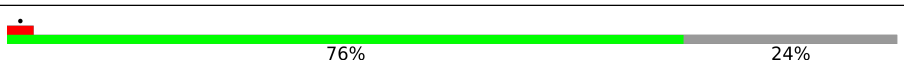
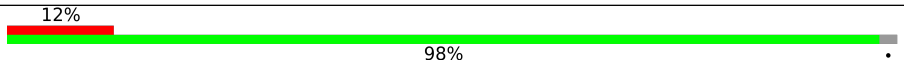
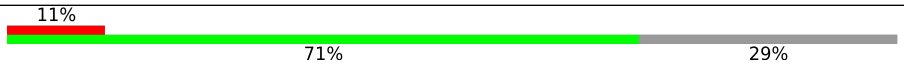
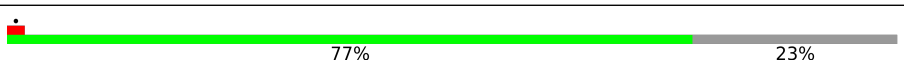
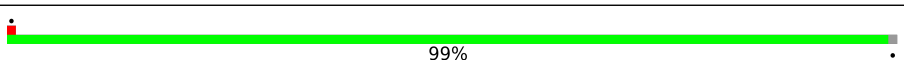
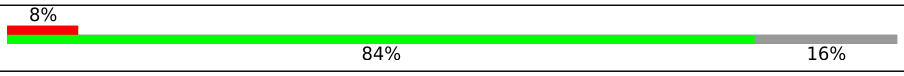
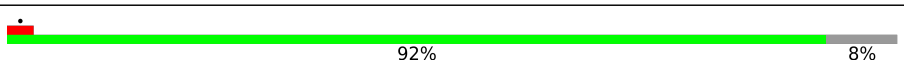
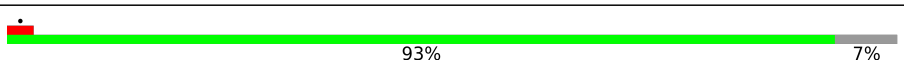
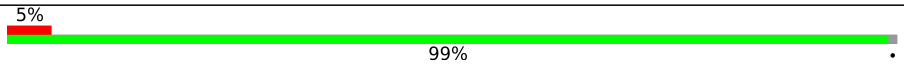
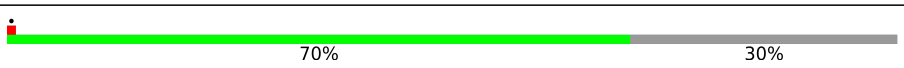
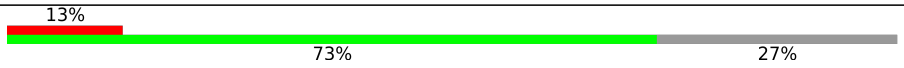
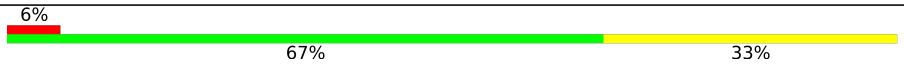
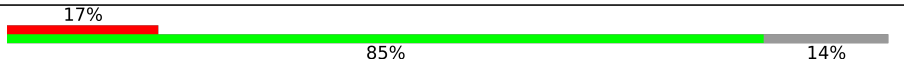
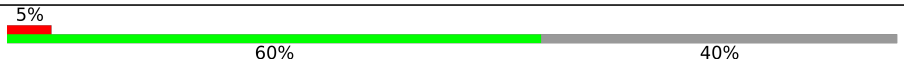
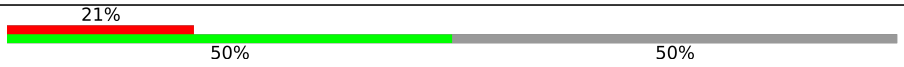
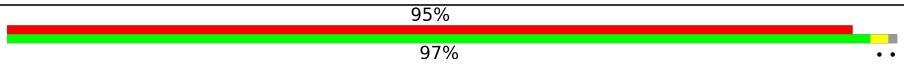
Mol	Chain	Length	Quality of chain
34	u	199	
35	v	231	
36	y	245	
37	z	106	
38	8	710	
39	I	663	
40	K	376	
41	V	137	
42	R	189	
43	G	256	
44	Z	136	
45	U	121	
46	c	105	
47	g	121	
48	k	78	
49	n	605	
50	p	460	
51	t	322	
52	6	87	
53	D	505	
54	o	220	
55	w	841	
56	a	217	
57	x	606	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 153087 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2571	55024	24568	9931	17955	2570	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	7	129	1048	650	204	194	0	0

- Molecule 4 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	266	2174	1382	386	400	6	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	335	2661	1691	492	472	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	359	2731	1720	518	490	3	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	164	Total	C	N	O	S	0	0
			1309	843	235	230	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LEU	deletion	UNP Q02326

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 10 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	145	Total	C	N	O	S	0	0
			1215	759	225	228	3		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	L	121	Total	C	N	O	0	0
			991	623	208	160		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	189	Total	C	N	O	S	0	0
			1621	1015	343	262	1		

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	P	183	Total	C	N	O	0	0
			1442	896	287	259		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 17 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 18 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	52	Total	C	N	O	S	0	0
			401	244	82	74	1		

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	232	Total	C	N	O	S	0	0
			1870	1184	321	360	5		

- Molecule 20 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	137	Total	C	N	O	S	0	0
			1068	682	192	192	2		

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 22 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	502	Total	C	N	O	S	0	0
			4066	2581	710	754	21		

- Molecule 23 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	125	Total	C	N	O	S	0	0
			1009	641	203	164	1		

- Molecule 25 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 27 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	79	Total	C	N	O	S	0	0
			628	388	130	108	2		

- Molecule 28 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	73	Total	C	N	O	S	0	0
			580	353	126	96	5		

- Molecule 29 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	176	Total	C	N	O	S	0	0
			1394	896	244	247	7		

- Molecule 30 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	m	666	Total	C	N	O	S	0	0
			5377	3421	936	1005	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	551	ALA	GLU	conflict	UNP Q04660

- Molecule 31 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	q	358	Total	C	N	O	S	0	0
			2799	1779	490	518	12		

- Molecule 32 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	r	176	Total	C	N	O	S	0	0
			1438	906	279	248	5		

- Molecule 33 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 34 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	140	Total	C	N	O	S	0	0
			1183	742	237	195	9		

- Molecule 35 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	v	130	Total	C	N	O	S	0	0
			1087	678	211	195	3		

- Molecule 36 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	y	225	Total	C	N	O	S	0	0
			1701	1056	295	343	7		

- Molecule 37 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 38 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	8	470	Total	C	N	O	S	0	0
			3567	2269	632	655	11		

- Molecule 39 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	533	Total	C	N	O	S	0	0
			4247	2693	726	808	20		

- Molecule 40 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	K	284	Total	C	N	O	S	0	0
			2274	1462	375	433	4		

- Molecule 41 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	V	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 42 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	R	134	Total	C	N	O	0	0
			1082	679	220	183		

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	198	Total	C	N	O	S	0	0
			1549	998	271	277	3		

- Molecule 44 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 45 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	U	102	Total	C	N	O	0	0
			808	524	132	152		

- Molecule 46 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 47 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 48 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 49 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	n	425	Total	C	N	O	S	0	0
			3470	2241	600	615	14		

- Molecule 50 is a protein called YTM1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	337	Total	C	N	O	S	0	0
			2628	1633	470	518	7		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	285	Total	C	N	O	S	0	0
			2293	1453	425	412	3		

- Molecule 52 is a RNA chain called 5.8S ribosomal RNA gene and internal transcribed spacer 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 53 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	D	432	Total	C	N	O	S	0	0
			3451	2227	591	621	12		

- Molecule 54 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 55 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	422	Total	C	N	O	S	0	0
			3446	2146	633	649	18		

- Molecule 56 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	a	214	Total	C	N	O	S	0	0
			1695	1083	295	308	9		

- Molecule 57 is a protein called ATP-dependent rRNA helicase SPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A7A237

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

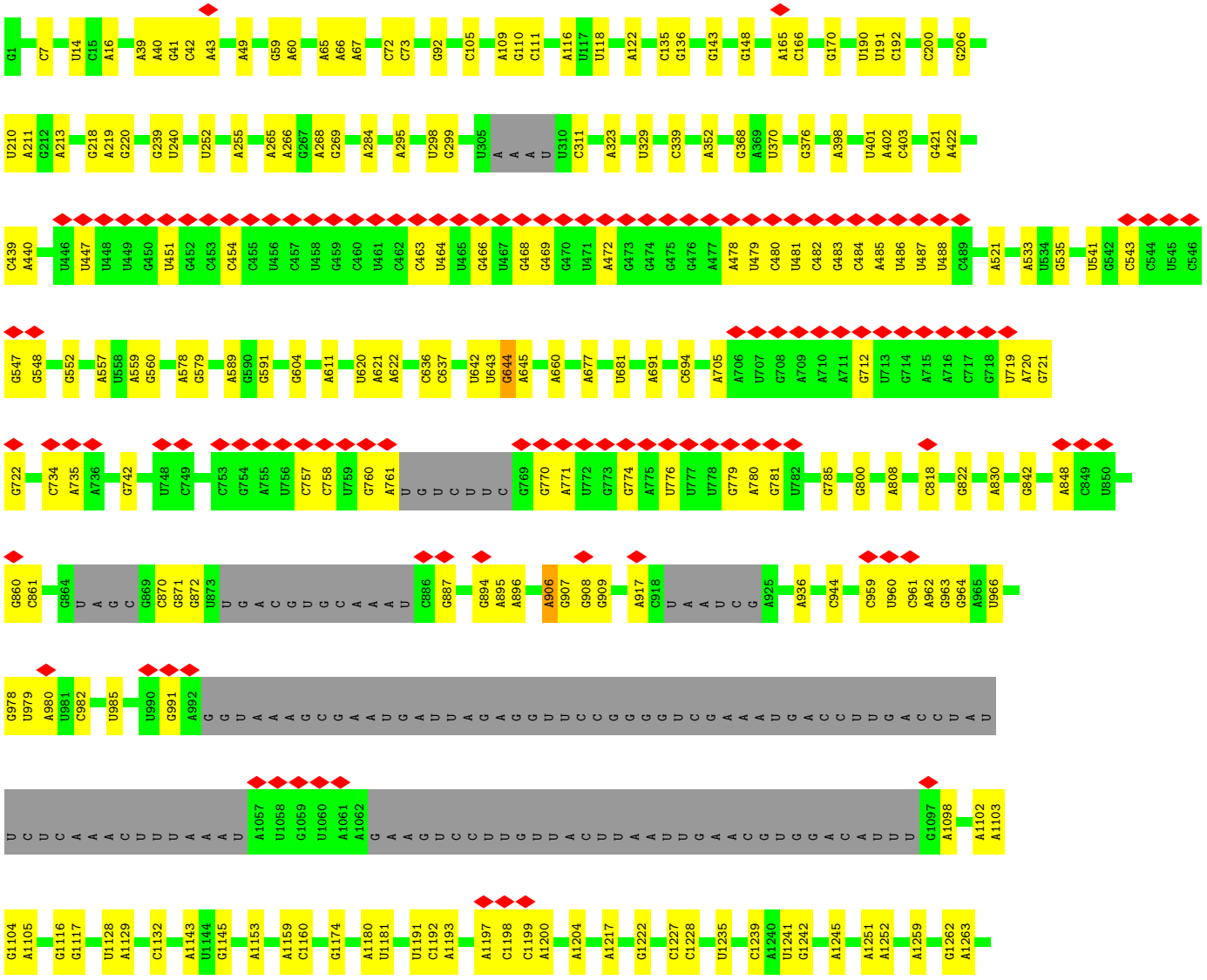
Mol	Chain	Residues	Atoms		AltConf
58	j	1	Total	Zn	0
			1	1	
58	g	1	Total	Zn	0
			1	1	

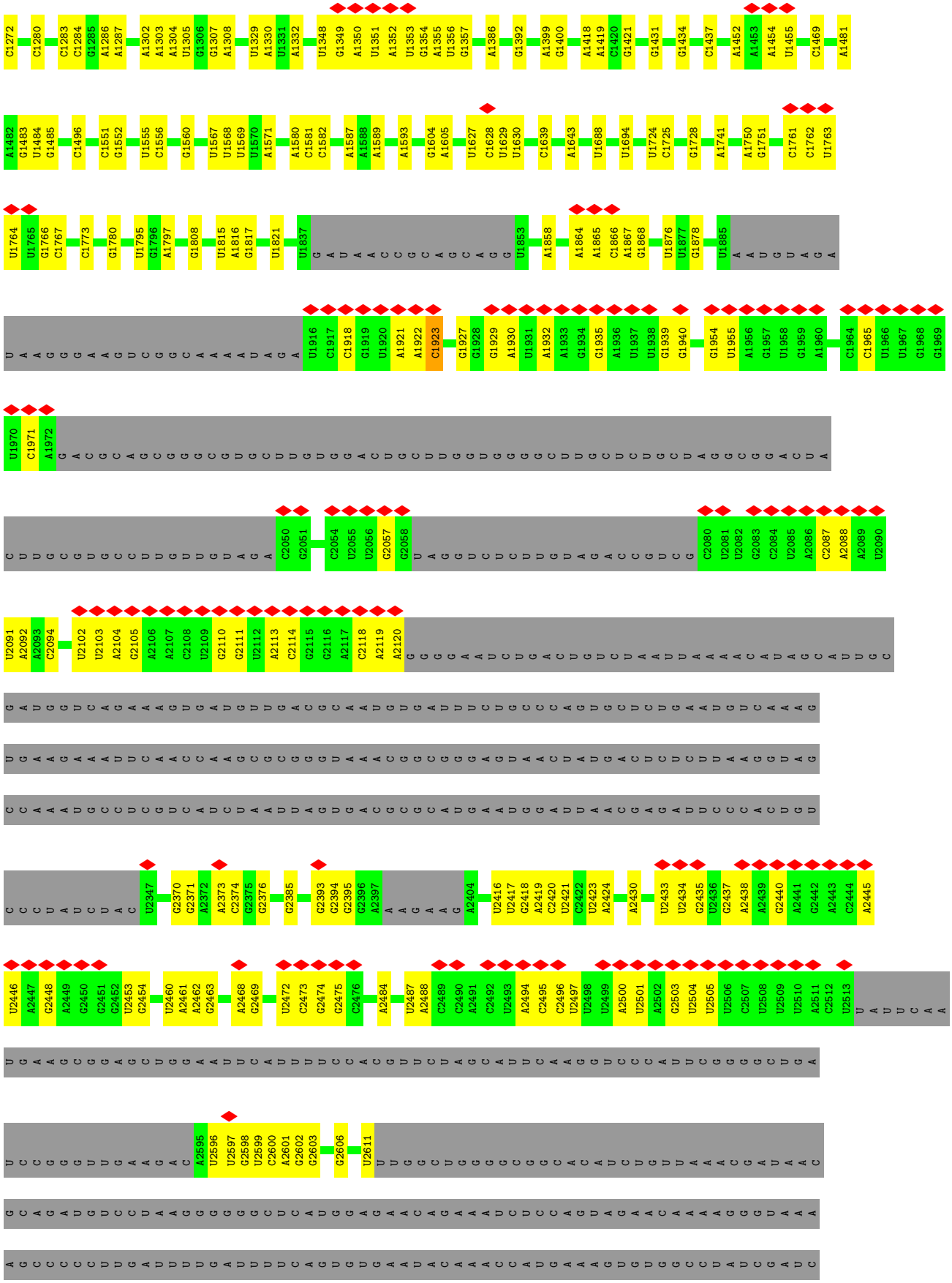
3 Residue-property plots (i)

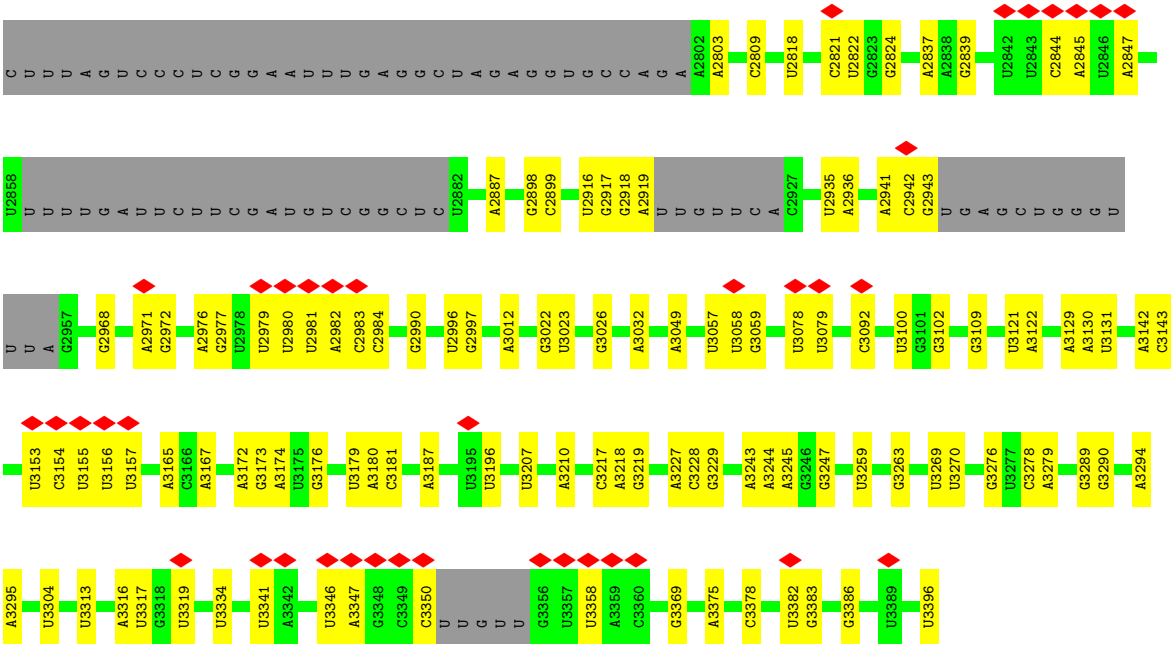
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA

Chain 1:

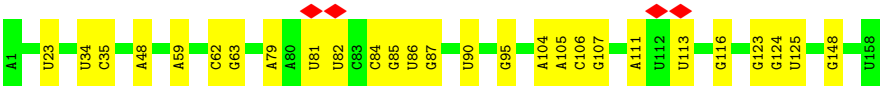






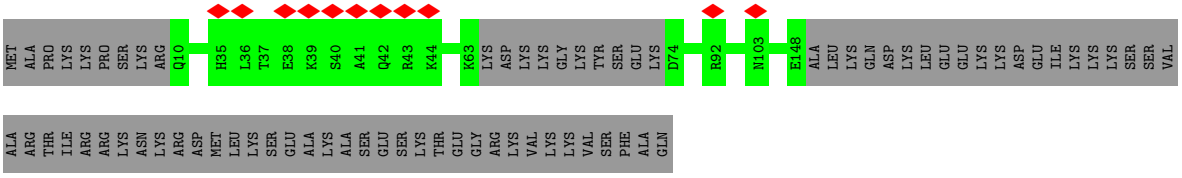
• Molecule 2: 5.8S rRNA

Chain 2:



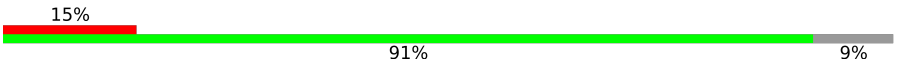
• Molecule 3: 60S ribosomal subunit assembly/export protein LOC1

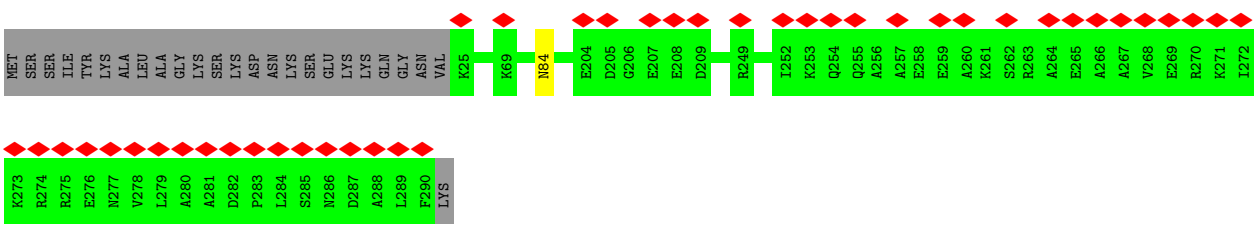
Chain 7:



• Molecule 4: Ribosome biogenesis protein BRX1

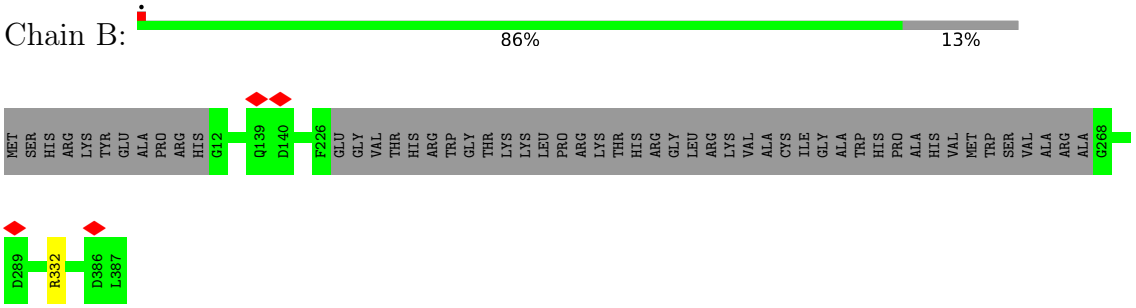
Chain A:





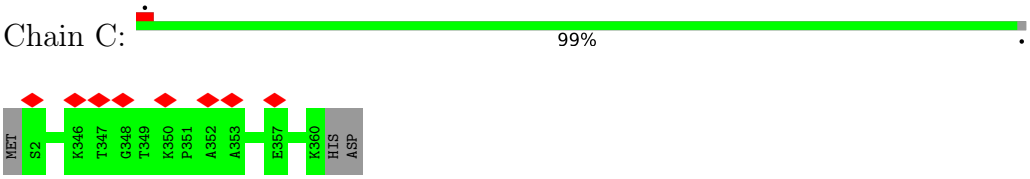
• Molecule 5: 60S ribosomal protein L3

Chain B:



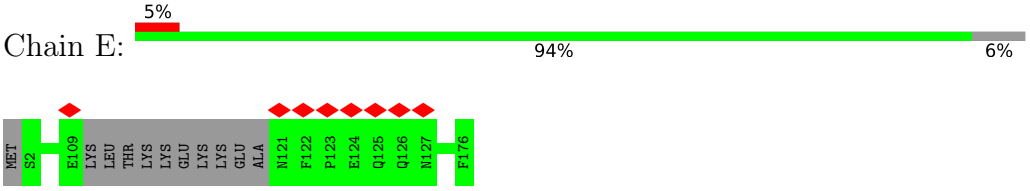
• Molecule 6: 60S ribosomal protein L4-A

Chain C:



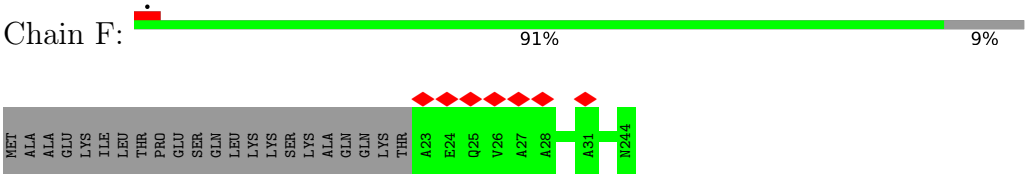
• Molecule 7: 60S ribosomal protein L6-A

Chain E:



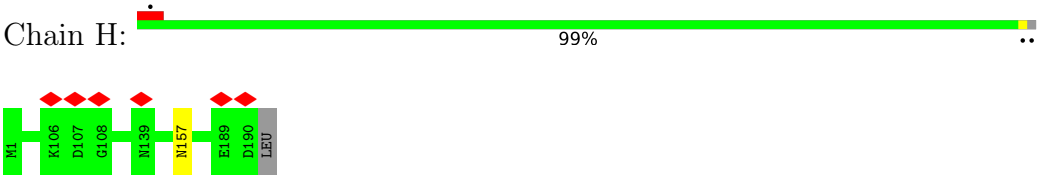
• Molecule 8: 60S ribosomal protein L7-A

Chain F:



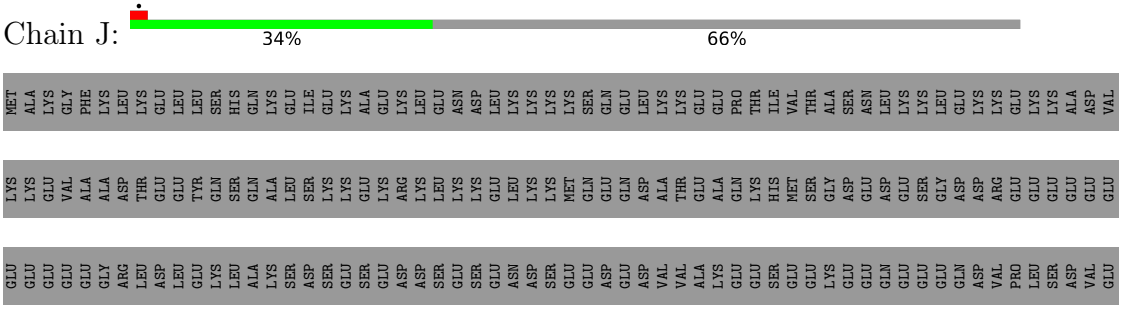
• Molecule 9: 60S ribosomal protein L9-A

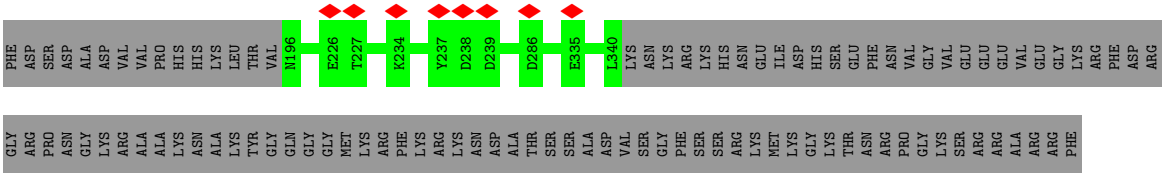
Chain H:



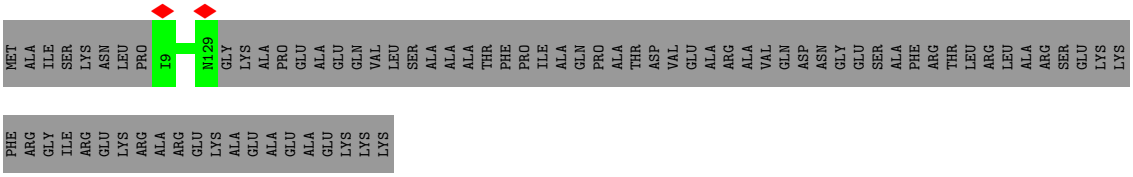
• Molecule 10: rRNA-processing protein EBP2

Chain J:

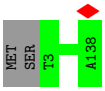




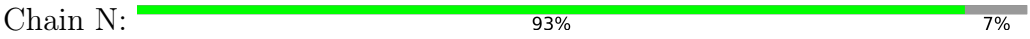
• Molecule 11: 60S ribosomal protein L13-A

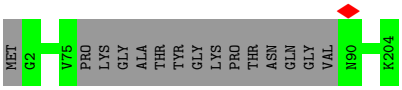


• Molecule 12: 60S ribosomal protein L14-A

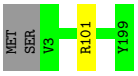


• Molecule 13: 60S ribosomal protein L15-A

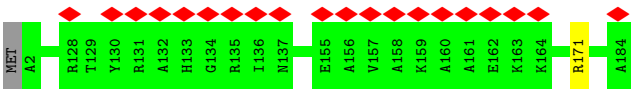




• Molecule 14: 60S ribosomal protein L16-A

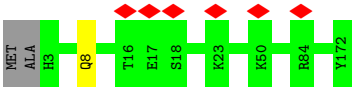


• Molecule 15: 60S ribosomal protein L17-A

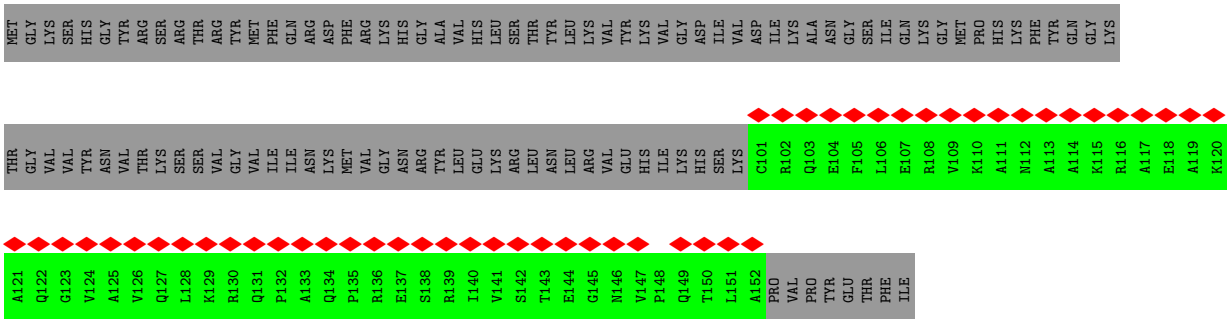


• Molecule 16: 60S ribosomal protein L18-A

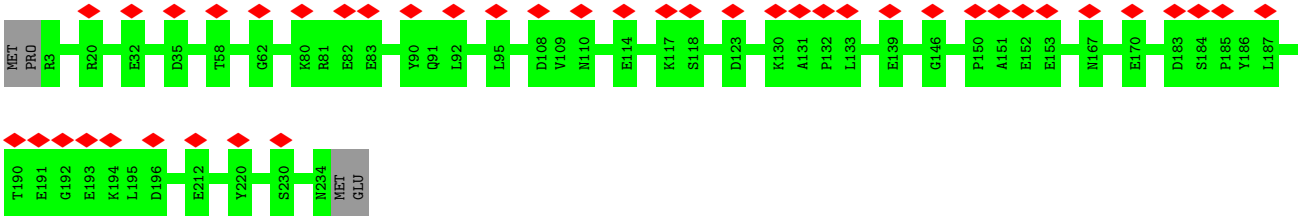
• Molecule 17: 60S ribosomal protein L20-A



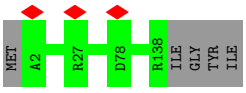
• Molecule 18: 60S ribosomal protein L21-A



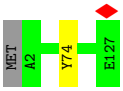
• Molecule 19: Ribosome assembly factor MRT4



• Molecule 20: 60S ribosomal protein L25

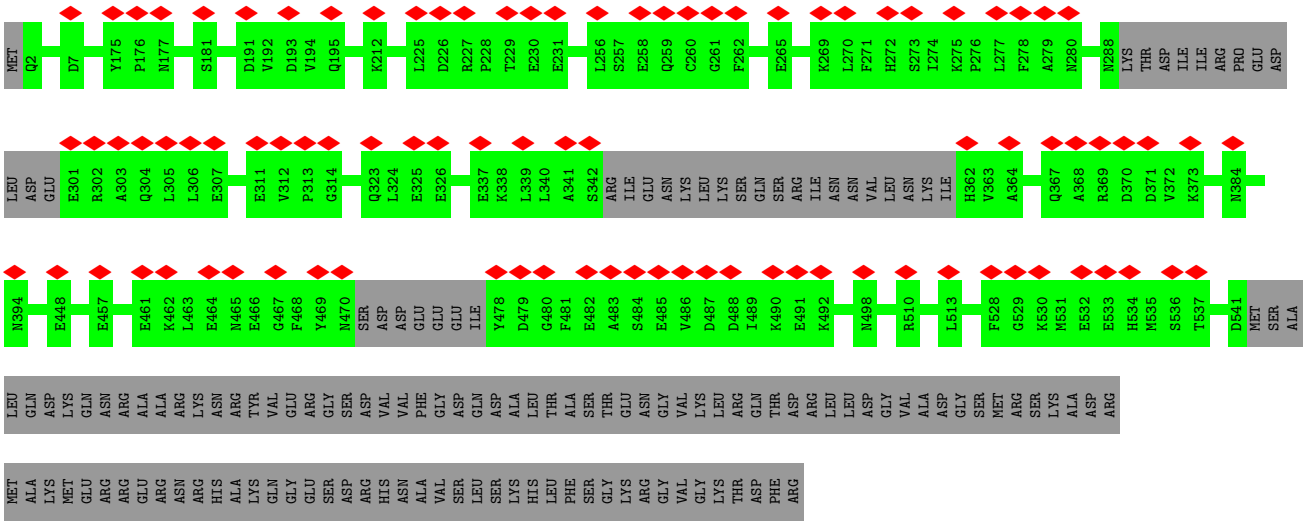


• Molecule 21: 60S ribosomal protein L26-A



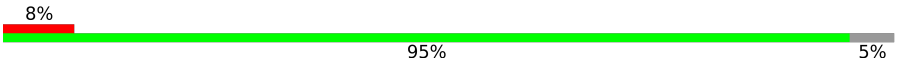
• Molecule 22: Nucleolar GTP-binding protein 1

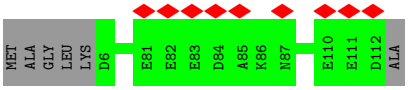
Chain b:



• Molecule 23: 60S ribosomal protein L31-A

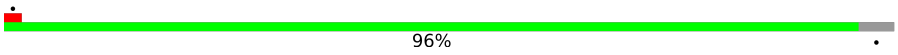
Chain d:

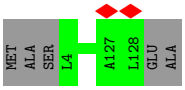




• Molecule 24: 60S ribosomal protein L32

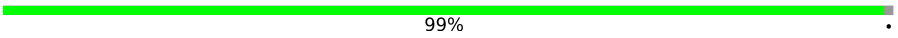
Chain e:





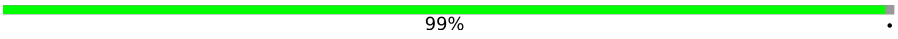
• Molecule 25: 60S ribosomal protein L33-A

Chain f:



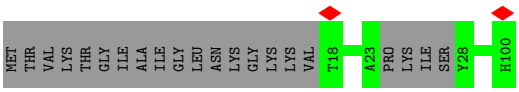
• Molecule 26: 60S ribosomal protein L35-A

Chain h:



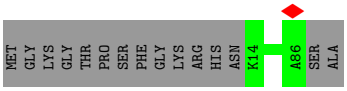
• Molecule 27: 60S ribosomal protein L36-A

Chain i:



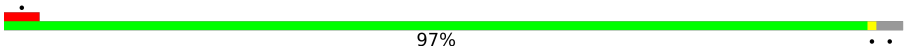
• Molecule 28: 60S ribosomal protein L37-A

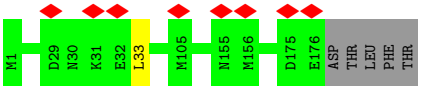
Chain j:



• Molecule 29: 60S ribosome subunit biogenesis protein NIP7

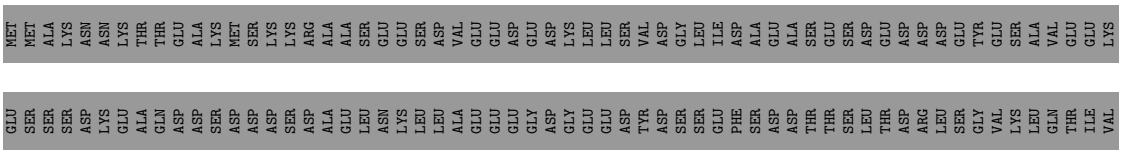
Chain l:

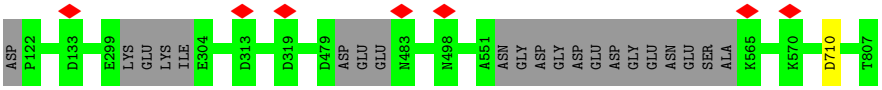




• Molecule 30: Ribosome biogenesis protein ERB1

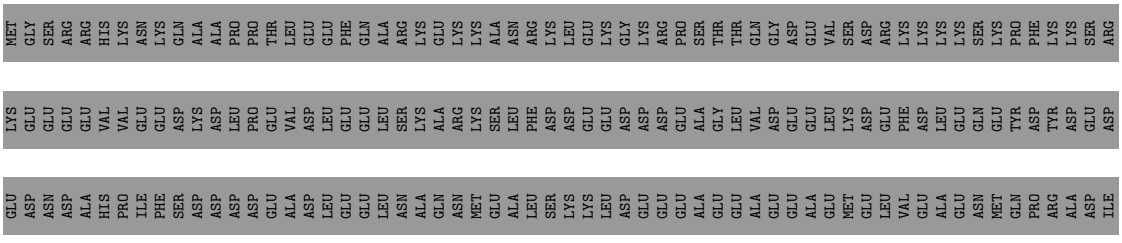
Chain m:

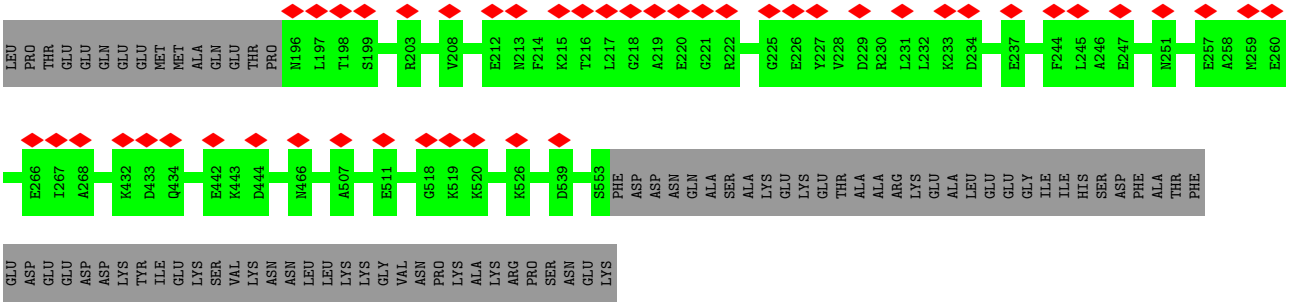




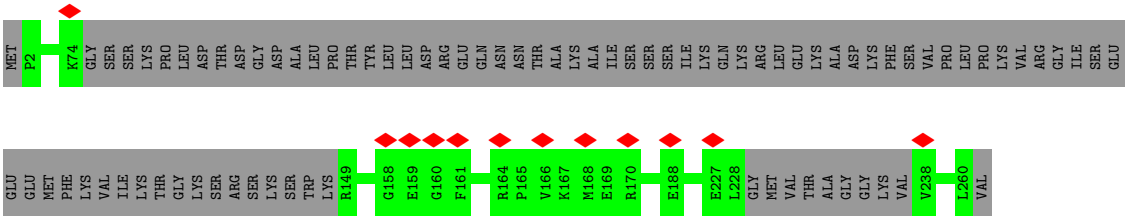
• Molecule 31: 25S rRNA (cytosine(2870)-C(5))-methyltransferase

Chain q:

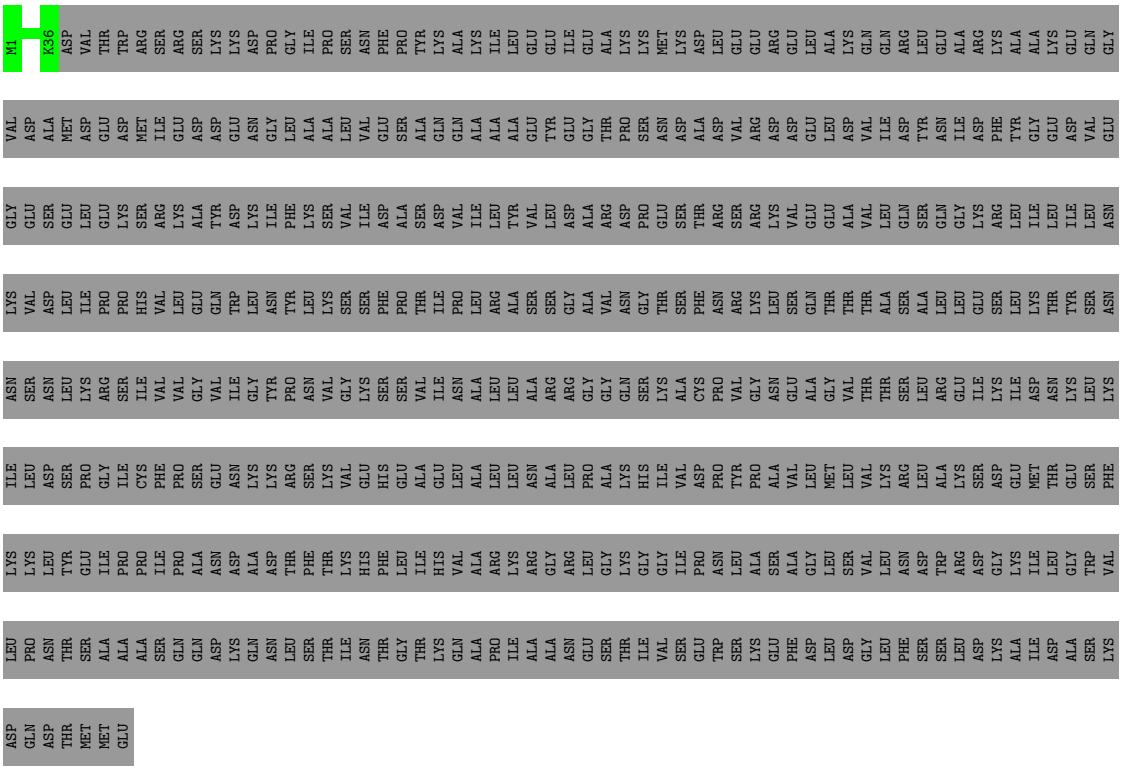




• Molecule 32: Ribosome biogenesis protein NSA2

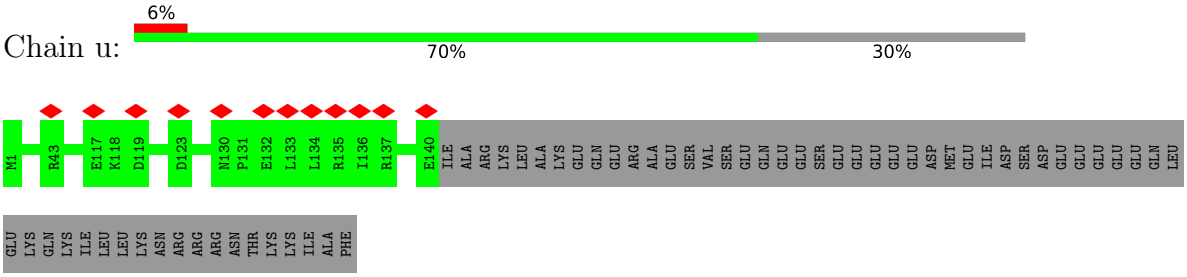


• Molecule 33: Nuclear GTP-binding protein NUG1



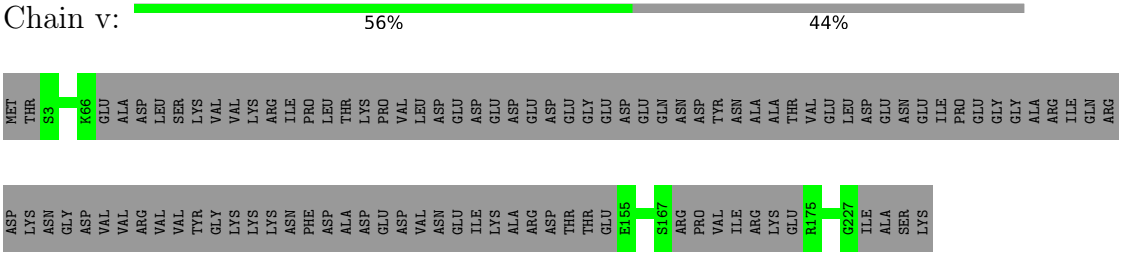
• Molecule 34: Ribosome biogenesis protein RLP24

Chain u:



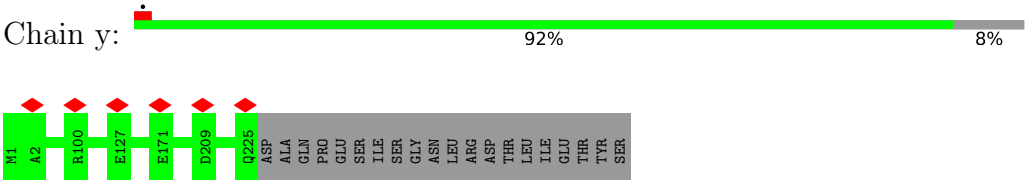
• Molecule 35: Nucleolar protein 16

Chain v:



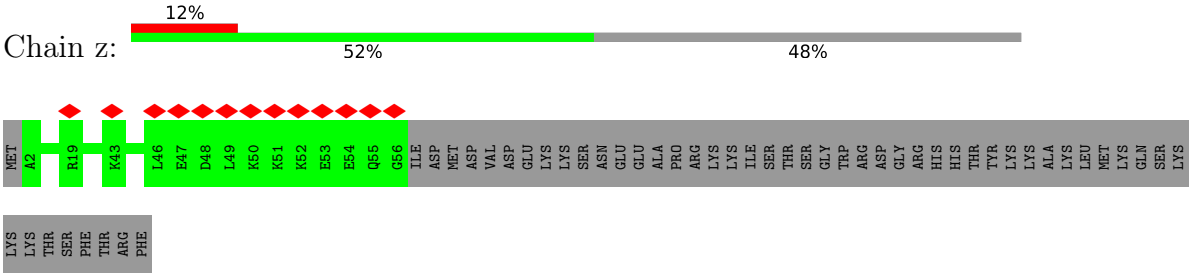
• Molecule 36: Eukaryotic translation initiation factor 6

Chain y:



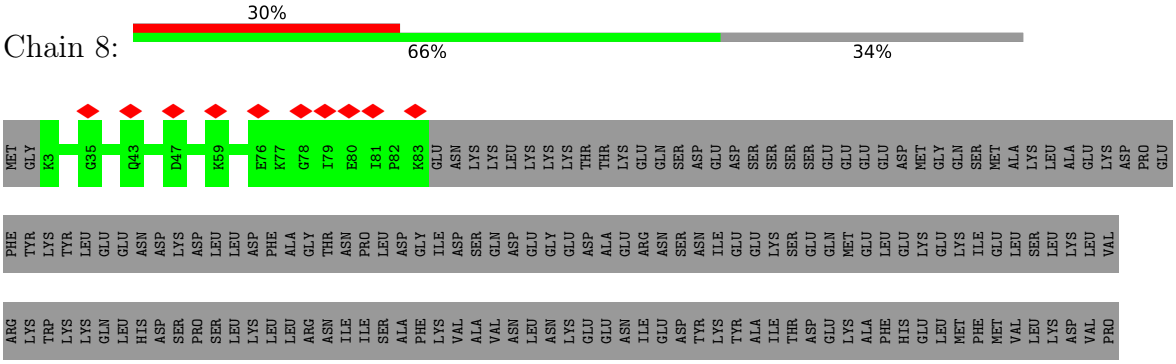
• Molecule 37: UPF0642 protein YBL028C

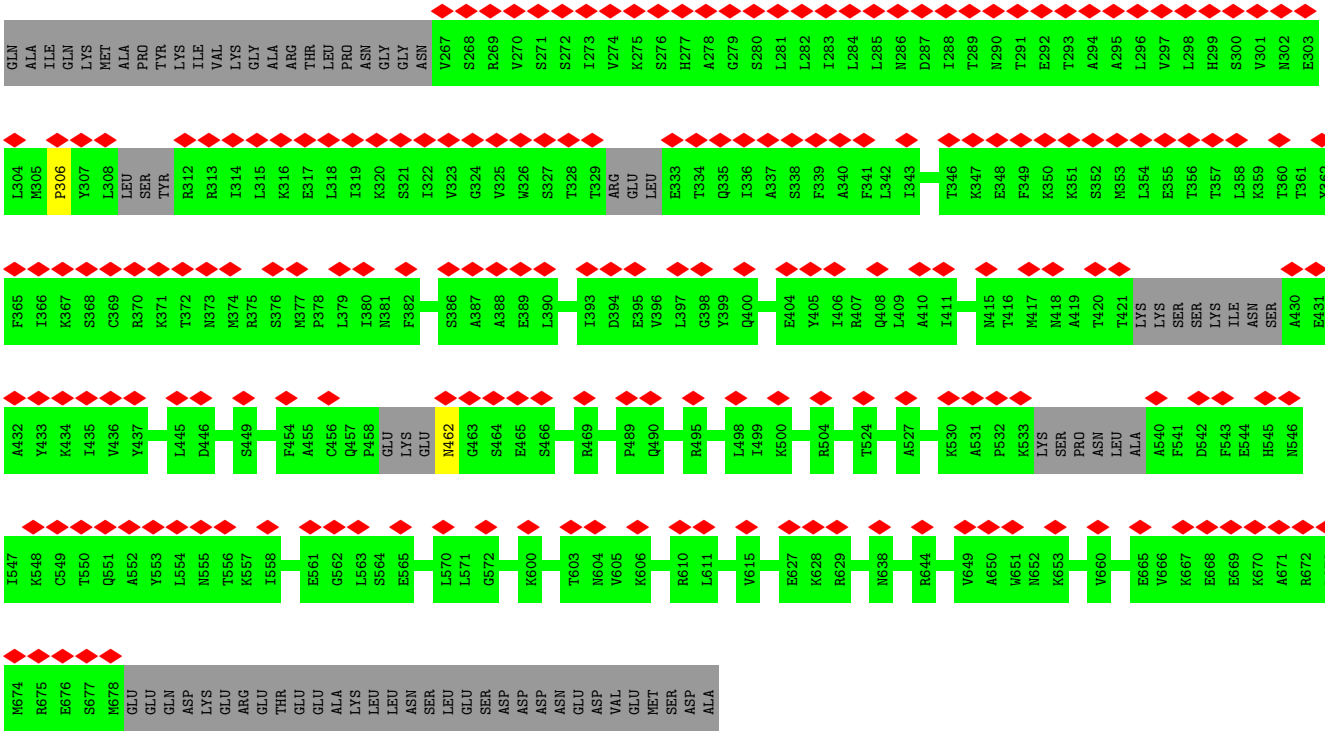
Chain z:



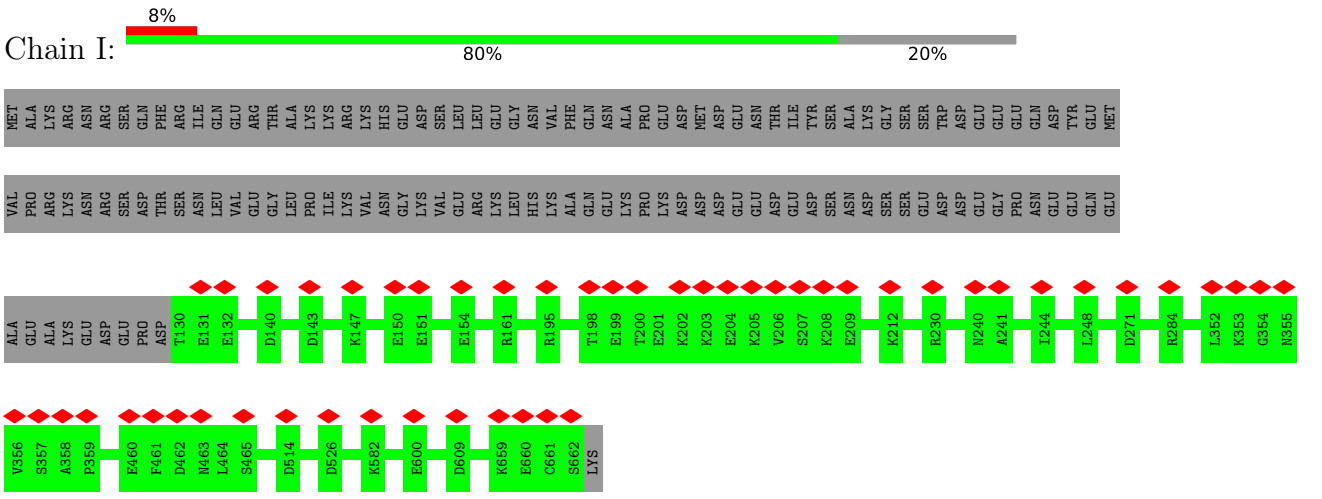
• Molecule 38: Nucleolar complex protein 2

Chain 8:

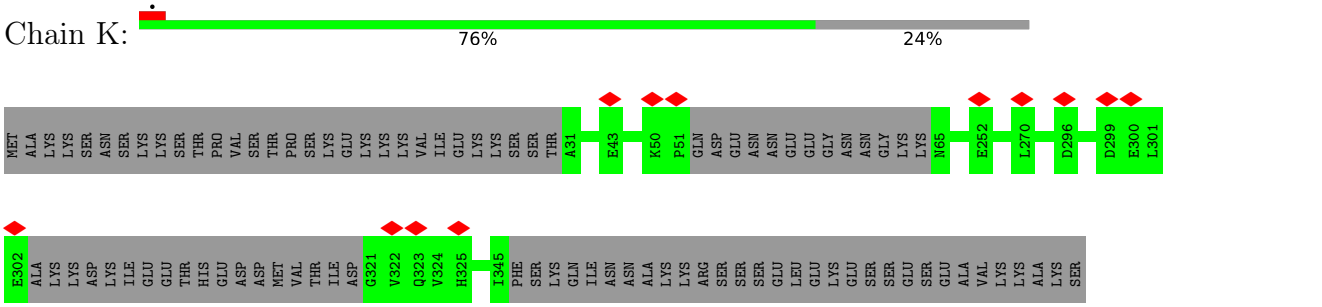




• Molecule 39: Nucleolar complex-associated protein 3

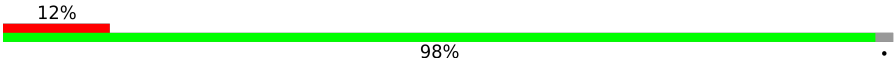


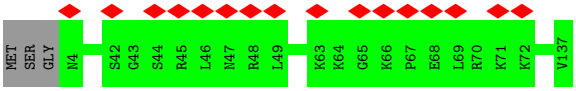
• Molecule 40: Proteasome-interacting protein CIC1



• Molecule 41: 60S ribosomal protein L23-A

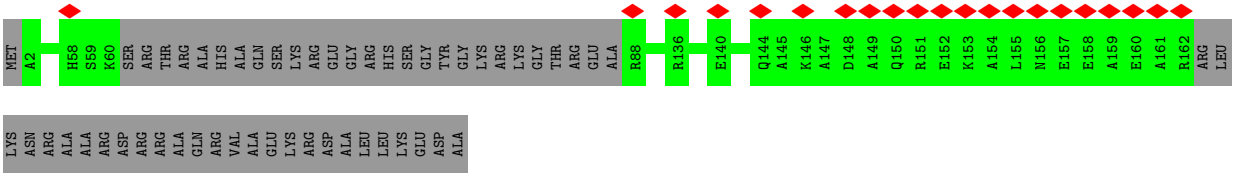
Chain V:





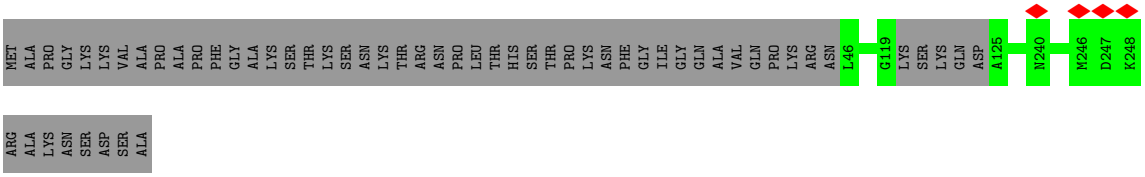
• Molecule 42: 60S ribosomal protein L19-A

Chain R:



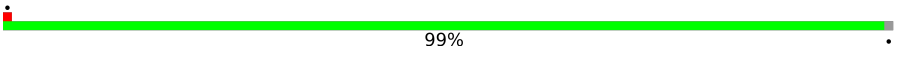
• Molecule 43: 60S ribosomal protein L8-A

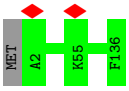
Chain G:



• Molecule 44: 60S ribosomal protein L27-A

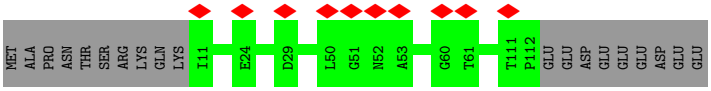
Chain Z:





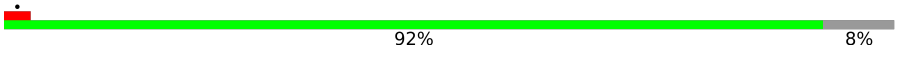
• Molecule 45: 60S ribosomal protein L22-A

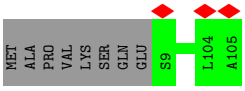
Chain U:



• Molecule 46: 60S ribosomal protein L30

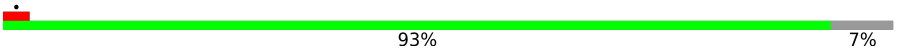
Chain c:

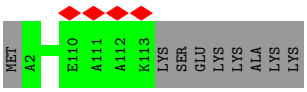




• Molecule 47: 60S ribosomal protein L34-A

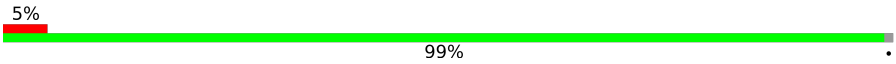
Chain g:

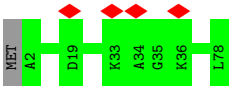




• Molecule 48: 60S ribosomal protein L38

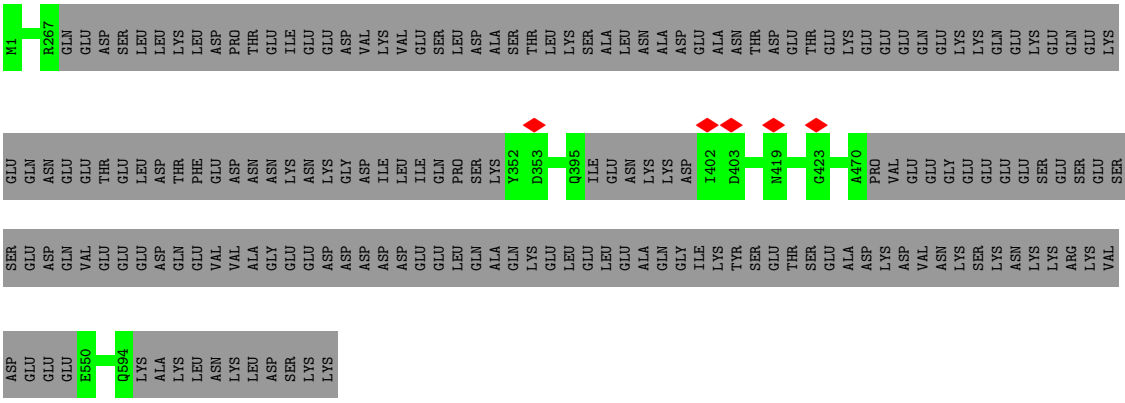
Chain k:





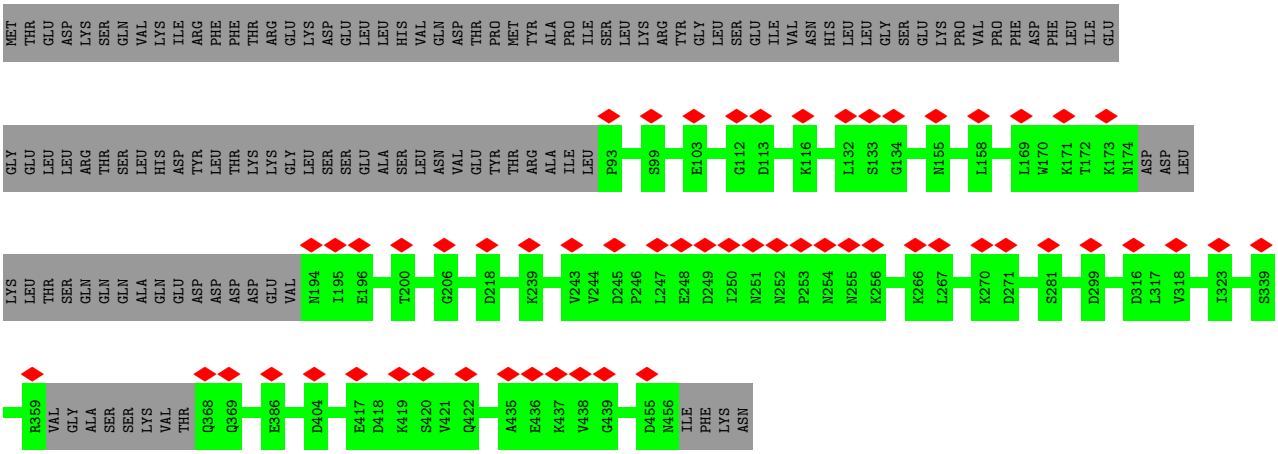
• Molecule 49: Pescadillo homolog

Chain n:



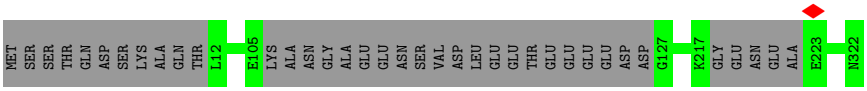
• Molecule 50: YTM1 isoform 1

Chain p:

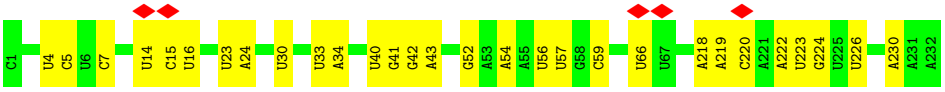


• Molecule 51: Ribosome biogenesis protein RLP7

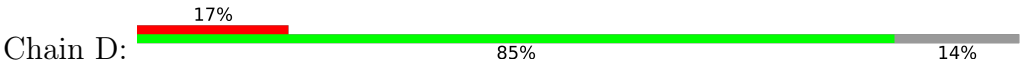
Chain t:

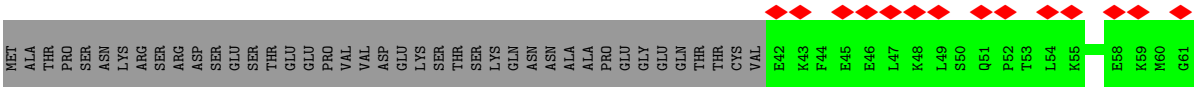


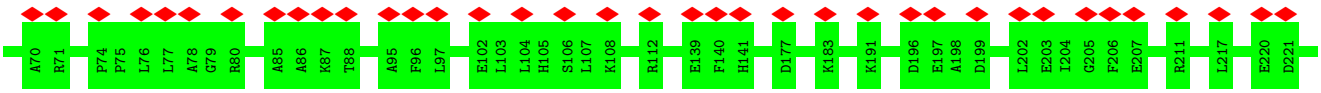
• Molecule 52: 5.8S ribosomal RNA gene and internal transcribed spacer 2

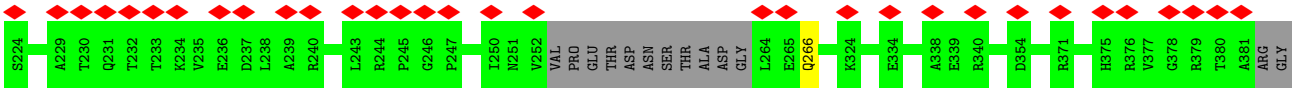


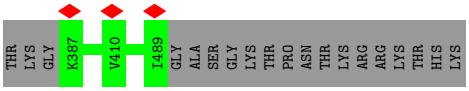
• Molecule 53: ATP-dependent RNA helicase HAS1



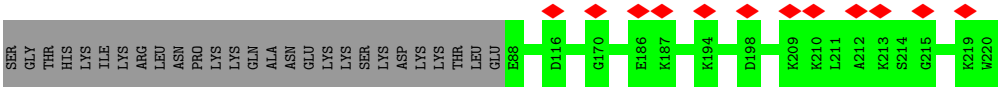




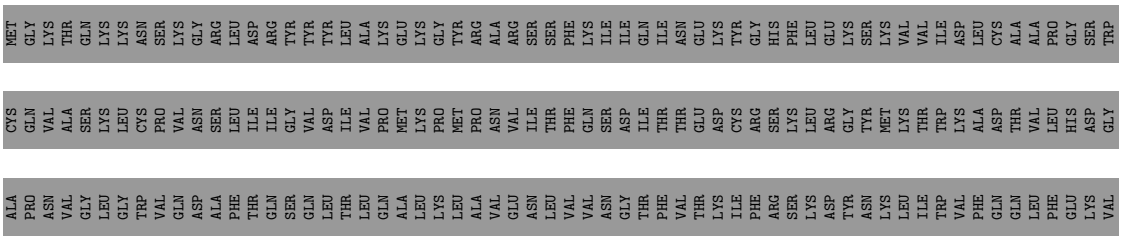


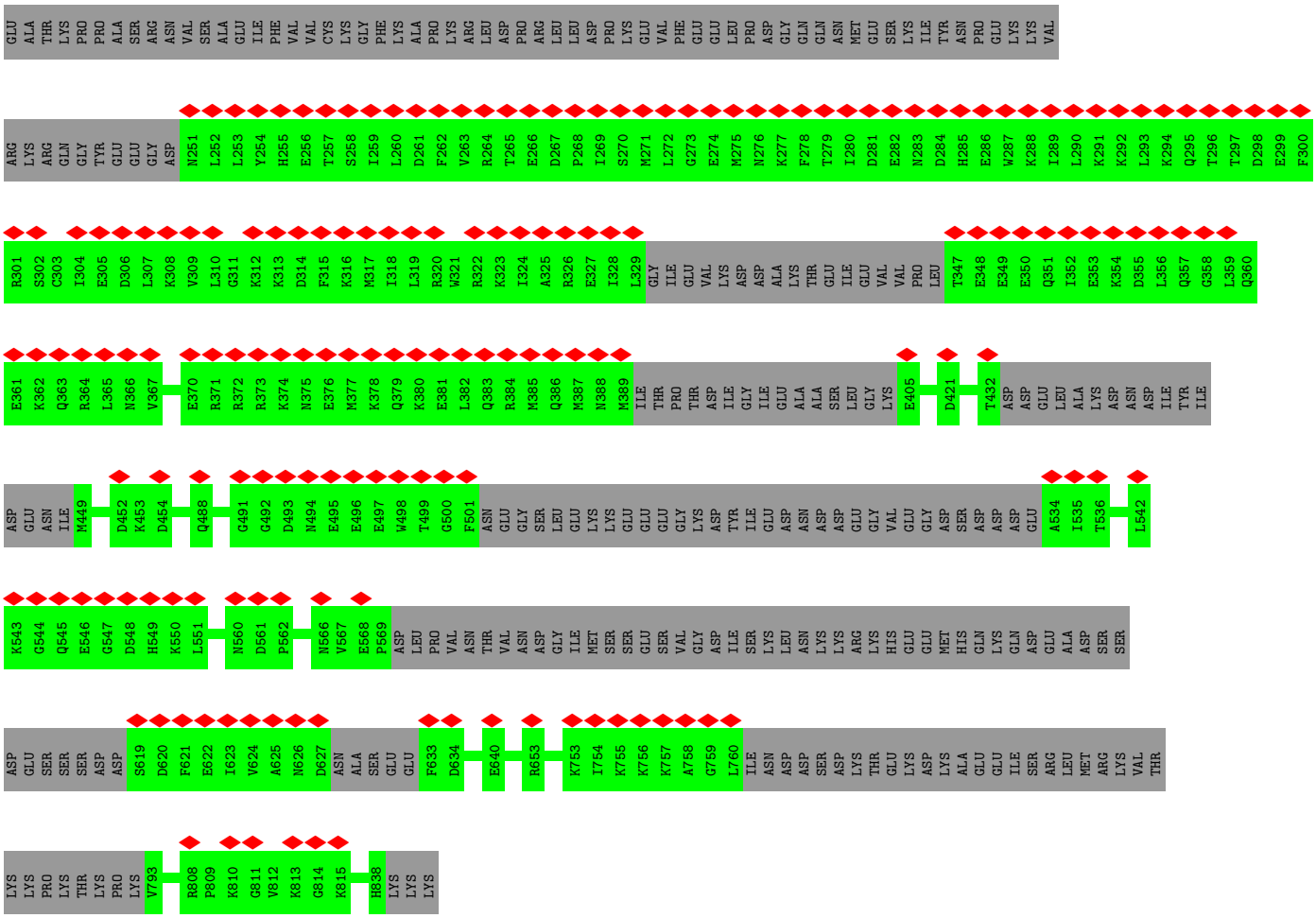


• Molecule 54: Ribosome biogenesis protein 15



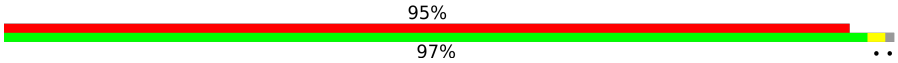
• Molecule 55: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

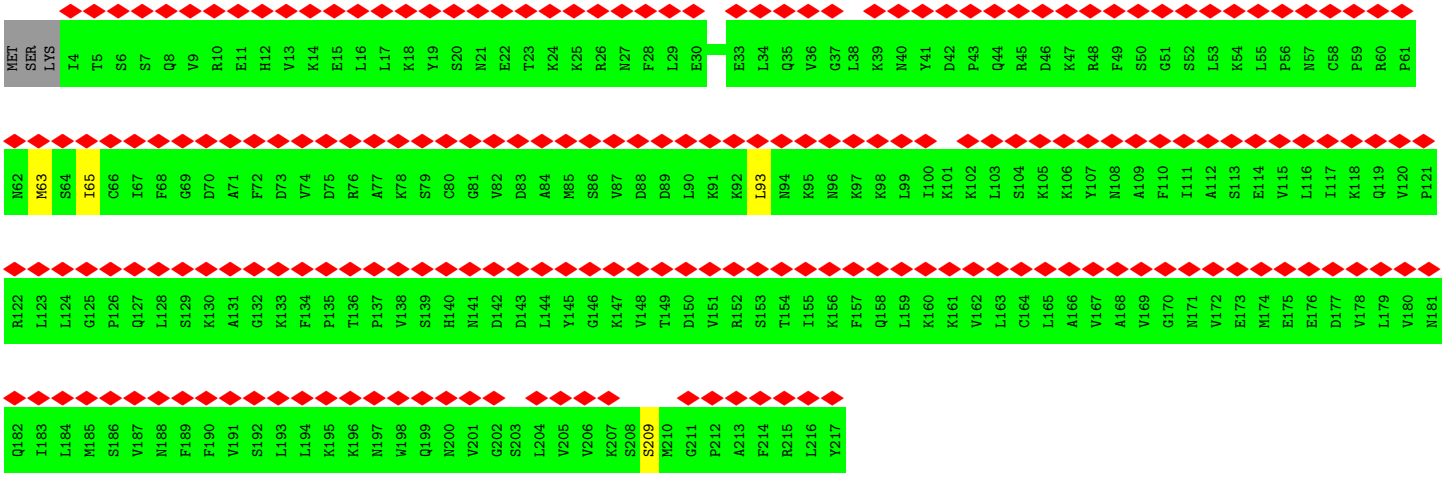




• Molecule 56: Ribosomal protein

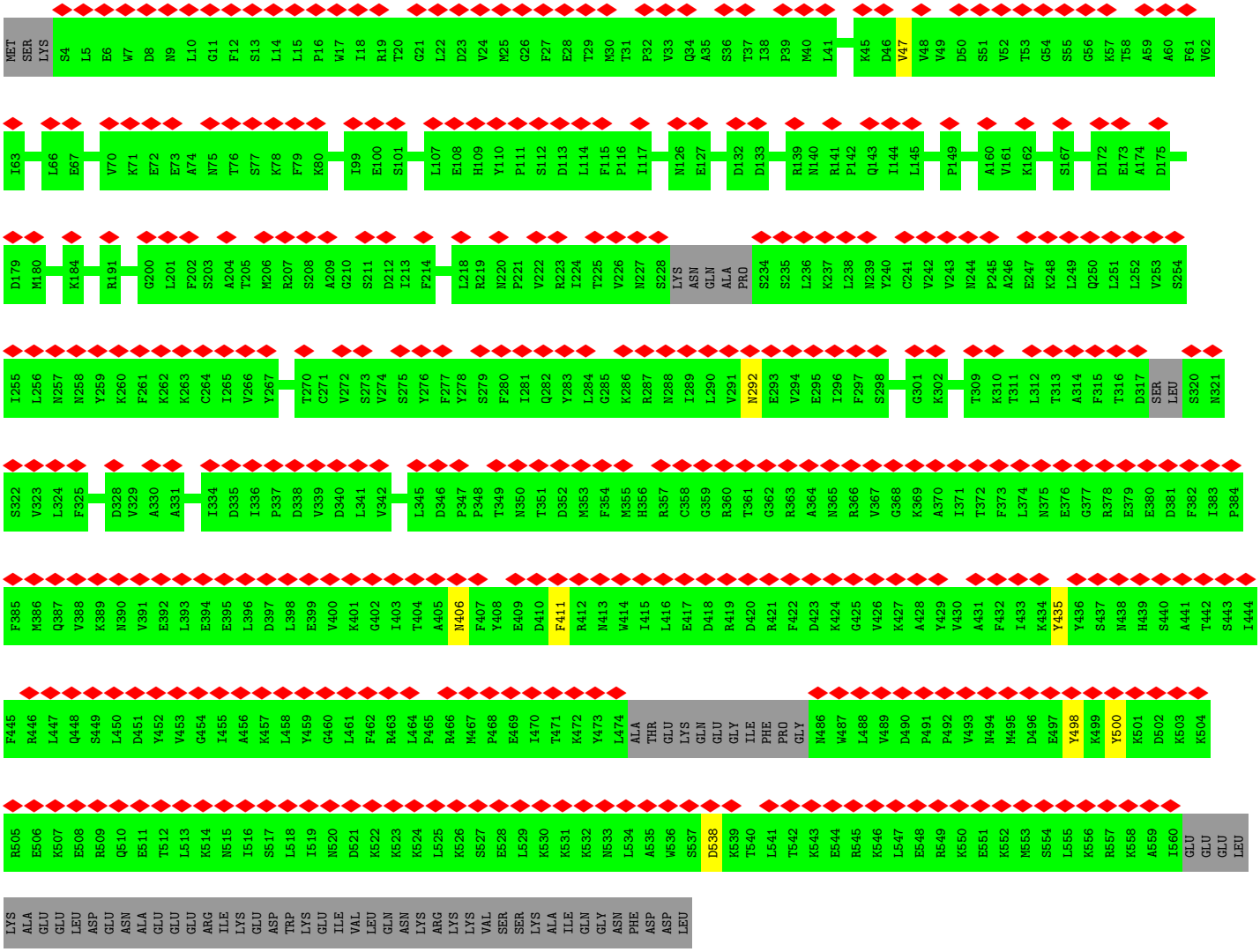
Chain a:





• Molecule 57: ATP-dependent rRNA helicase SPB4

Chain x:


MET SER LYS S4 L5 E6 W7 D8 N9 L10 G11 F12 S13 L14 L15 P16 W17 I18 R19 T20 G21 L22 D23 V24 M25 G26 F27 E28 T29 M30 T31 P32 V33 Q34 A35 S36 T37 I38 P39 M40 L41 K45 D46 V47 V48 V49 D50 S51 V52 T53 G54 S55 G56 K57 T58 A59 A60 F61 V62
I63 L66 E67 V70 K71 E72 E73 A74 N75 T76 S77 K78 F79 K80 I99 E100 S101 L107 E108 H109 Y110 P111 S112 D113 L114 F115 P116 I117 N126 E127 D132 D133 R139 N140 R141 P142 Q143 I144 L145 P149 A160 V161 K162 S167 D172 E173 A174 D175
D179 M180 K184 R191 G200 L201 F202 S203 A204 T205 M206 R207 S208 A209 G210 S211 D212 I213 F214 L218 R219 N220 P221 V222 R223 I224 T225 V226 N227 S228 LYS ASN GLN ALA PRO S234 S235 L236 K237 L238 N239 Y240 C241 V242 V243 N244 P245 A246 E247 K248 L249 Q250 L251 L252 V253 S254
I255 L256 N257 N258 Y259 K260 F261 K262 K263 C264 I265 V266 Y267 T270 C271 V272 S273 V274 S275 Y276 F277 Y278 S279 F280 I281 Q282 Y283 L284 G285 K286 R287 N288 I289 L290 V291 N292 E293 V294 E295 I296 F297 S298 G301 K302 T309 K310 T311 L312 T313 A314 F315 T316 D317 SER LEU S320 N321
S322 V323 L324 F325 D328 V329 A330 A331 I334 D335 I336 P337 D338 V339 D340 L341 V342 L345 D346 P347 P348 T349 N350 T351 D352 M353 F354 M355 H356 R357 C358 G359 R360 T361 G362 R363 A364 N365 R366 V367 G368 K369 A370 I371 T372 F373 L374 N375 E376 G377 R378 E379 E380 D381 F382 I383 P384
F385 M386 Q387 V388 K389 N390 V391 E392 L393 E394 E395 L396 D397 L398 E399 V400 K401 G402 I403 T404 A405 N406 F407 Y408 E409 D410 F411 R412 N413 W414 I415 L416 E417 D418 R419 D420 R421 F422 D423 K424 G425 V426 K427 A428 Y429 V430 A431 F432 I433 K434 Y435 Y436 S437 N438 H439 S440 A441 T442 S443 I444
F445 R446 L447 Q448 S449 L450 D451 Y452 V453 G454 I455 A456 K457 L458 Y459 G460 L461 F462 R463 L464 P465 R466 M467 P468 E469 I470 T471 K472 Y473 L474 ALA THR GLU LYS GLN GLU GLY ILE PHE PRO GLY N486 W487 L488 V489 D490 P491 P492 V493 N494 M495 D496 E497 Y498 K499 Y500 K501 D502 K503 K504
R505 E506 K507 E508 R509 Q510 E511 T512 L513 K514 N515 I516 S517 L518 I519 N520 D521 K522 K523 K524 L525 K526 S527 E528 L529 K530 K531 K532 N533 L534 A535 W536 S537 D538 K539 T540 L541 T542 K543 E544 R545 K546 L547 E548 R549 K550 E551 K552 M553 S554 L555 K556 R557 K558 A559 I560 GLU GLU GLU LEU
LYS ALA GLU GLU LEU ASP GLU ASN ALA GLU GLU GLU ARG ILE LYS GLU ASP TRP LYS GLU ILE VAL LEU GLN ASN LYS ARG LYS LYS VAL SER SER LYS ALA ILE GLN GLY ASN PHE ASP ASP LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	211000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.2	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.169	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.29	0/61575	0.77	3/95973 (0.0%)
2	2	0.33	0/3746	0.76	0/5832
3	7	0.24	0/1056	0.52	0/1408
4	A	0.26	0/2222	0.49	0/2998
5	B	0.27	0/2715	0.53	0/3647
6	C	0.27	0/2782	0.50	0/3766
7	E	0.26	0/1332	0.49	0/1791
8	F	0.26	0/1821	0.47	0/2451
9	H	0.26	0/1531	0.50	0/2062
10	J	0.24	0/1232	0.46	0/1642
11	L	0.26	0/1009	0.56	0/1355
12	M	0.25	0/1068	0.50	0/1438
13	N	0.27	0/1654	0.58	0/2212
14	O	0.27	0/1585	0.49	0/2128
15	P	0.25	0/1465	0.53	0/1968
16	Q	0.26	0/1050	0.52	0/1419
17	S	0.27	0/1468	0.51	0/1973
18	T	0.23	0/404	0.53	0/542
19	W	0.25	0/1902	0.51	0/2564
20	X	0.27	0/1083	0.49	0/1458
21	Y	0.26	0/1004	0.54	0/1341
22	b	0.25	0/4141	0.48	0/5575
23	d	0.25	0/887	0.54	0/1191
24	e	0.25	0/1030	0.51	0/1379
25	f	0.29	0/868	0.52	0/1168
26	h	0.26	0/978	0.50	0/1301
27	i	0.26	0/633	0.55	0/839
28	j	0.27	0/592	0.58	0/785
29	l	0.26	0/1425	0.54	1/1922 (0.1%)
30	m	0.25	0/5511	0.50	0/7471
31	q	0.25	0/2854	0.52	0/3860
32	r	0.25	0/1462	0.51	0/1952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	s	0.23	0/301	0.55	0/386
34	u	0.25	0/1205	0.53	0/1603
35	v	0.26	0/1100	0.50	0/1456
36	y	0.25	0/1722	0.53	0/2343
37	z	0.23	0/445	0.46	0/585
38	8	0.25	0/3624	0.46	1/4891 (0.0%)
39	I	0.24	0/4310	0.46	0/5807
40	K	0.25	0/2310	0.46	0/3118
41	V	0.26	0/1008	0.54	0/1356
42	R	0.23	0/1095	0.48	0/1465
43	G	0.28	0/1575	0.46	0/2125
44	Z	0.27	0/1118	0.45	0/1497
45	U	0.26	0/825	0.46	0/1120
46	c	0.25	0/751	0.43	0/1008
47	g	0.26	0/891	0.55	0/1191
48	k	0.26	0/618	0.51	0/826
49	n	0.27	0/3544	0.46	0/4766
50	p	0.24	0/2674	0.50	0/3623
51	t	0.24	0/2319	0.50	0/3108
52	6	0.24	0/2050	0.76	0/3186
53	D	0.25	0/3516	0.48	0/4741
54	o	0.26	0/1129	0.48	0/1502
55	w	0.24	0/3483	0.47	0/4628
56	a	0.25	0/1722	0.51	1/2313 (0.0%)
57	x	0.26	0/4419	0.49	0/5958
All	All	0.27	0/161839	0.64	6/232013 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	644	G	C2'-C3'-O3'	7.93	126.95	109.50
1	1	906	A	C2'-C3'-O3'	6.74	124.49	113.70
29	l	33	LEU	CA-CB-CG	5.58	128.12	115.30
38	8	306	PRO	N-CA-CB	5.57	109.98	103.30
1	1	1923	C	C2-N1-C1'	5.13	124.44	118.80
56	a	93	LEU	CA-CB-CG	5.07	126.97	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	7	125/204 (61%)	120 (96%)	5 (4%)	0	100	100
4	A	264/291 (91%)	249 (94%)	15 (6%)	0	100	100
5	B	331/387 (86%)	321 (97%)	10 (3%)	0	100	100
6	C	357/362 (99%)	346 (97%)	11 (3%)	0	100	100
7	E	160/175 (91%)	149 (93%)	11 (7%)	0	100	100
8	F	220/244 (90%)	216 (98%)	4 (2%)	0	100	100
9	H	188/191 (98%)	177 (94%)	11 (6%)	0	100	100
10	J	143/427 (34%)	138 (96%)	5 (4%)	0	100	100
11	L	119/199 (60%)	115 (97%)	4 (3%)	0	100	100
12	M	134/138 (97%)	126 (94%)	8 (6%)	0	100	100
13	N	185/204 (91%)	181 (98%)	4 (2%)	0	100	100
14	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
15	P	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
16	Q	132/186 (71%)	132 (100%)	0	0	100	100
17	S	168/172 (98%)	162 (96%)	6 (4%)	0	100	100
18	T	50/160 (31%)	48 (96%)	2 (4%)	0	100	100
19	W	230/236 (98%)	220 (96%)	10 (4%)	0	100	100
20	X	135/142 (95%)	128 (95%)	7 (5%)	0	100	100
21	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
22	b	494/647 (76%)	474 (96%)	20 (4%)	0	100	100
23	d	105/113 (93%)	101 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	e	123/130 (95%)	121 (98%)	2 (2%)	0	100	100
25	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
26	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
27	i	75/100 (75%)	68 (91%)	7 (9%)	0	100	100
28	j	71/88 (81%)	69 (97%)	2 (3%)	0	100	100
29	l	174/181 (96%)	160 (92%)	14 (8%)	0	100	100
30	m	658/807 (82%)	633 (96%)	24 (4%)	1 (0%)	47	80
31	q	356/618 (58%)	323 (91%)	33 (9%)	0	100	100
32	r	170/261 (65%)	166 (98%)	4 (2%)	0	100	100
33	s	34/520 (6%)	34 (100%)	0	0	100	100
34	u	138/199 (69%)	135 (98%)	3 (2%)	0	100	100
35	v	124/231 (54%)	122 (98%)	2 (2%)	0	100	100
36	y	223/245 (91%)	214 (96%)	9 (4%)	0	100	100
37	z	53/106 (50%)	53 (100%)	0	0	100	100
38	8	456/710 (64%)	431 (94%)	25 (6%)	0	100	100
39	I	531/663 (80%)	509 (96%)	22 (4%)	0	100	100
40	K	278/376 (74%)	266 (96%)	12 (4%)	0	100	100
41	V	132/137 (96%)	129 (98%)	3 (2%)	0	100	100
42	R	130/189 (69%)	129 (99%)	1 (1%)	0	100	100
43	G	194/256 (76%)	191 (98%)	3 (2%)	0	100	100
44	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
45	U	100/121 (83%)	92 (92%)	8 (8%)	0	100	100
46	c	95/105 (90%)	95 (100%)	0	0	100	100
47	g	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
48	k	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
49	n	417/605 (69%)	402 (96%)	15 (4%)	0	100	100
50	p	331/460 (72%)	305 (92%)	26 (8%)	0	100	100
51	t	279/322 (87%)	272 (98%)	7 (2%)	0	100	100
53	D	426/505 (84%)	415 (97%)	11 (3%)	0	100	100
54	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
55	w	406/841 (48%)	390 (96%)	16 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
56	a	212/217 (98%)	195 (92%)	14 (7%)	3 (1%)	11 40
57	x	531/606 (88%)	509 (96%)	21 (4%)	1 (0%)	47 80
All	All	11427/15369 (74%)	10966 (96%)	456 (4%)	5 (0%)	100 100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	m	710	ASP
56	a	209	SER
57	x	406	ASN
56	a	63	MET
56	a	65	ILE

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	7	114/181 (63%)	114 (100%)	0	100 100
4	A	242/263 (92%)	241 (100%)	1 (0%)	91 96
5	B	281/323 (87%)	280 (100%)	1 (0%)	91 96
6	C	286/289 (99%)	286 (100%)	0	100 100
7	E	142/152 (93%)	142 (100%)	0	100 100
8	F	186/205 (91%)	186 (100%)	0	100 100
9	H	170/171 (99%)	169 (99%)	1 (1%)	86 94
10	J	133/383 (35%)	133 (100%)	0	100 100
11	L	100/159 (63%)	100 (100%)	0	100 100
12	M	107/109 (98%)	107 (100%)	0	100 100
13	N	165/176 (94%)	165 (100%)	0	100 100
14	O	160/162 (99%)	159 (99%)	1 (1%)	86 94
15	P	145/146 (99%)	144 (99%)	1 (1%)	84 93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	110/151 (73%)	110 (100%)	0	100	100
17	S	155/156 (99%)	154 (99%)	1 (1%)	86	94
18	T	41/137 (30%)	41 (100%)	0	100	100
19	W	209/213 (98%)	209 (100%)	0	100	100
20	X	114/118 (97%)	114 (100%)	0	100	100
21	Y	109/110 (99%)	108 (99%)	1 (1%)	78	91
22	b	447/573 (78%)	447 (100%)	0	100	100
23	d	94/97 (97%)	94 (100%)	0	100	100
24	e	108/111 (97%)	108 (100%)	0	100	100
25	f	90/91 (99%)	90 (100%)	0	100	100
26	h	104/105 (99%)	104 (100%)	0	100	100
27	i	65/82 (79%)	65 (100%)	0	100	100
28	j	60/71 (84%)	60 (100%)	0	100	100
29	l	151/156 (97%)	151 (100%)	0	100	100
30	m	599/722 (83%)	599 (100%)	0	100	100
31	q	304/535 (57%)	304 (100%)	0	100	100
32	r	156/229 (68%)	156 (100%)	0	100	100
33	s	32/445 (7%)	32 (100%)	0	100	100
34	u	125/180 (69%)	125 (100%)	0	100	100
35	v	116/205 (57%)	116 (100%)	0	100	100
36	y	193/211 (92%)	193 (100%)	0	100	100
37	z	48/95 (50%)	48 (100%)	0	100	100
38	8	351/647 (54%)	350 (100%)	1 (0%)	92	97
39	I	484/602 (80%)	484 (100%)	0	100	100
40	K	261/346 (75%)	261 (100%)	0	100	100
41	V	103/105 (98%)	103 (100%)	0	100	100
42	R	112/154 (73%)	112 (100%)	0	100	100
43	G	161/208 (77%)	161 (100%)	0	100	100
44	Z	115/116 (99%)	115 (100%)	0	100	100
45	U	89/107 (83%)	89 (100%)	0	100	100
46	c	81/88 (92%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
47	g	95/103 (92%)	95 (100%)	0	100 100
48	k	68/69 (99%)	68 (100%)	0	100 100
49	n	381/548 (70%)	381 (100%)	0	100 100
50	p	300/413 (73%)	300 (100%)	0	100 100
51	t	256/287 (89%)	256 (100%)	0	100 100
53	D	378/440 (86%)	377 (100%)	1 (0%)	92 97
54	o	118/199 (59%)	118 (100%)	0	100 100
55	w	371/745 (50%)	371 (100%)	0	100 100
56	a	195/198 (98%)	195 (100%)	0	100 100
57	x	489/548 (89%)	482 (99%)	7 (1%)	67 86
All	All	10069/13435 (75%)	10053 (100%)	16 (0%)	93 98

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	84	ASN
5	B	332	ARG
9	H	157	ASN
14	O	101	ARG
15	P	171	ARG
17	S	8	GLN
21	Y	74	TYR
38	8	462	ASN
53	D	266	GLN
57	x	47	VAL
57	x	292	ASN
57	x	411	PHE
57	x	435	TYR
57	x	498	TYR
57	x	500	TYR
57	x	538	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	198	HIS
9	H	139	ASN

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Mol	Chain	Res	Type
11	L	120	GLN
24	e	104	ASN
32	r	203	ASN
34	u	101	GLN
34	u	115	ASN
35	v	33	ASN
39	I	218	GLN
40	K	295	GLN
53	D	323	GLN
55	w	420	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2551/3396 (75%)	504 (19%)	35 (1%)
2	2	157/158 (99%)	26 (16%)	1 (0%)
52	6	85/87 (97%)	27 (31%)	3 (3%)
All	All	2793/3641 (76%)	557 (19%)	39 (1%)

All (557) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	C
1	1	14	U
1	1	16	A
1	1	39	A
1	1	40	A
1	1	41	G
1	1	42	C
1	1	43	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	72	C
1	1	73	C
1	1	92	G
1	1	105	C
1	1	109	A

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Mol	Chain	Res	Type
1	1	110	G
1	1	111	C
1	1	116	A
1	1	118	U
1	1	122	A
1	1	135	C
1	1	136	G
1	1	143	G
1	1	148	G
1	1	165	A
1	1	166	C
1	1	170	G
1	1	190	U
1	1	191	U
1	1	192	C
1	1	200	C
1	1	206	G
1	1	210	U
1	1	211	A
1	1	213	A
1	1	218	G
1	1	219	A
1	1	220	G
1	1	240	U
1	1	252	U
1	1	255	A
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	284	A
1	1	295	A
1	1	298	U
1	1	299	G
1	1	311	C
1	1	323	A
1	1	329	U
1	1	339	C
1	1	352	A
1	1	368	G
1	1	370	U
1	1	376	G

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Mol	Chain	Res	Type
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	421	G
1	1	422	A
1	1	439	C
1	1	440	A
1	1	447	U
1	1	451	U
1	1	454	C
1	1	463	C
1	1	464	U
1	1	466	G
1	1	468	G
1	1	469	G
1	1	472	A
1	1	478	A
1	1	479	U
1	1	480	C
1	1	481	U
1	1	482	C
1	1	483	G
1	1	485	A
1	1	486	U
1	1	487	U
1	1	488	U
1	1	521	A
1	1	533	A
1	1	535	G
1	1	541	U
1	1	543	C
1	1	547	G
1	1	548	G
1	1	552	G
1	1	557	A
1	1	559	A
1	1	560	G
1	1	578	A
1	1	579	G
1	1	589	A
1	1	591	G

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Mol	Chain	Res	Type
1	1	604	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	622	A
1	1	636	C
1	1	637	C
1	1	642	U
1	1	643	U
1	1	644	G
1	1	645	A
1	1	660	A
1	1	677	A
1	1	681	U
1	1	691	A
1	1	694	C
1	1	705	A
1	1	712	G
1	1	719	U
1	1	721	G
1	1	722	G
1	1	734	C
1	1	735	A
1	1	742	G
1	1	757	C
1	1	758	C
1	1	760	G
1	1	761	A
1	1	770	G
1	1	771	A
1	1	774	G
1	1	776	U
1	1	779	G
1	1	780	A
1	1	781	G
1	1	785	G
1	1	800	G
1	1	808	A
1	1	818	C
1	1	822	G
1	1	830	A
1	1	842	G

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Mol	Chain	Res	Type
1	1	848	A
1	1	860	G
1	1	861	C
1	1	871	G
1	1	872	G
1	1	887	G
1	1	894	G
1	1	895	A
1	1	896	A
1	1	906	A
1	1	907	G
1	1	908	G
1	1	909	G
1	1	917	A
1	1	936	A
1	1	944	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	962	A
1	1	963	G
1	1	964	G
1	1	966	U
1	1	978	G
1	1	979	U
1	1	980	A
1	1	982	C
1	1	985	U
1	1	991	G
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1105	A
1	1	1116	G
1	1	1117	G
1	1	1129	A
1	1	1132	C
1	1	1143	A
1	1	1145	G
1	1	1153	A
1	1	1159	A
1	1	1160	C

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Mol	Chain	Res	Type
1	1	1174	G
1	1	1180	A
1	1	1181	U
1	1	1191	U
1	1	1192	C
1	1	1193	A
1	1	1197	A
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1204	A
1	1	1217	A
1	1	1222	G
1	1	1228	C
1	1	1235	U
1	1	1239	C
1	1	1241	U
1	1	1242	G
1	1	1245	A
1	1	1251	A
1	1	1252	A
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1272	C
1	1	1280	C
1	1	1284	C
1	1	1286	A
1	1	1287	A
1	1	1303	A
1	1	1304	A
1	1	1305	U
1	1	1307	G
1	1	1308	A
1	1	1330	A
1	1	1332	A
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U

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Mol	Chain	Res	Type
1	1	1354	G
1	1	1356	U
1	1	1357	G
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1418	A
1	1	1419	A
1	1	1421	G
1	1	1431	G
1	1	1434	G
1	1	1437	C
1	1	1452	A
1	1	1454	A
1	1	1455	U
1	1	1469	C
1	1	1481	A
1	1	1483	G
1	1	1484	U
1	1	1485	G
1	1	1496	C
1	1	1552	G
1	1	1555	U
1	1	1556	C
1	1	1560	G
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1587	A
1	1	1589	A
1	1	1593	A
1	1	1604	G
1	1	1605	A
1	1	1627	U
1	1	1628	C
1	1	1629	U
1	1	1630	U

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Mol	Chain	Res	Type
1	1	1639	C
1	1	1643	A
1	1	1688	U
1	1	1694	U
1	1	1724	U
1	1	1725	C
1	1	1728	G
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1761	C
1	1	1762	C
1	1	1763	U
1	1	1764	U
1	1	1766	G
1	1	1767	C
1	1	1773	C
1	1	1780	G
1	1	1795	U
1	1	1797	A
1	1	1808	G
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1821	U
1	1	1858	A
1	1	1864	A
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1868	G
1	1	1876	U
1	1	1878	G
1	1	1918	C
1	1	1921	A
1	1	1922	A
1	1	1923	C
1	1	1927	G
1	1	1929	G
1	1	1930	A
1	1	1932	A
1	1	1935	G

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Mol	Chain	Res	Type
1	1	1939	G
1	1	1940	G
1	1	1954	G
1	1	1955	U
1	1	1965	C
1	1	1971	C
1	1	2057	G
1	1	2087	C
1	1	2088	A
1	1	2091	U
1	1	2092	A
1	1	2094	C
1	1	2102	U
1	1	2103	U
1	1	2104	A
1	1	2105	G
1	1	2110	G
1	1	2111	G
1	1	2113	A
1	1	2114	C
1	1	2118	C
1	1	2119	A
1	1	2120	A
1	1	2370	G
1	1	2371	G
1	1	2373	A
1	1	2374	C
1	1	2376	G
1	1	2385	G
1	1	2393	G
1	1	2394	G
1	1	2395	G
1	1	2416	U
1	1	2418	G
1	1	2419	A
1	1	2420	C
1	1	2421	U
1	1	2423	U
1	1	2424	A
1	1	2430	A
1	1	2433	U
1	1	2434	U

Continued on next page...

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Mol	Chain	Res	Type
1	1	2435	G
1	1	2437	G
1	1	2438	A
1	1	2440	G
1	1	2446	U
1	1	2448	G
1	1	2453	U
1	1	2454	G
1	1	2460	U
1	1	2461	A
1	1	2462	A
1	1	2463	G
1	1	2468	A
1	1	2469	G
1	1	2472	U
1	1	2473	C
1	1	2474	G
1	1	2475	G
1	1	2484	A
1	1	2487	U
1	1	2488	A
1	1	2494	A
1	1	2495	C
1	1	2497	U
1	1	2501	U
1	1	2503	G
1	1	2504	U
1	1	2505	U
1	1	2596	U
1	1	2598	G
1	1	2599	U
1	1	2601	A
1	1	2602	G
1	1	2603	G
1	1	2606	G
1	1	2611	U
1	1	2803	A
1	1	2809	C
1	1	2818	U
1	1	2821	C
1	1	2822	U
1	1	2824	G

Continued on next page...

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Mol	Chain	Res	Type
1	1	2837	A
1	1	2839	G
1	1	2844	C
1	1	2845	A
1	1	2847	A
1	1	2887	A
1	1	2898	G
1	1	2899	C
1	1	2916	U
1	1	2917	G
1	1	2918	G
1	1	2919	A
1	1	2935	U
1	1	2936	A
1	1	2941	A
1	1	2942	C
1	1	2943	G
1	1	2968	G
1	1	2971	A
1	1	2972	G
1	1	2976	A
1	1	2977	G
1	1	2979	U
1	1	2980	U
1	1	2981	U
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2990	G
1	1	2996	U
1	1	2997	G
1	1	3012	A
1	1	3022	G
1	1	3023	U
1	1	3026	G
1	1	3032	A
1	1	3049	A
1	1	3057	U
1	1	3058	U
1	1	3059	G
1	1	3078	U
1	1	3079	U

Continued on next page...

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Mol	Chain	Res	Type
1	1	3092	C
1	1	3100	U
1	1	3102	G
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3153	U
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3165	A
1	1	3167	A
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3207	U
1	1	3210	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3227	A
1	1	3229	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3259	U
1	1	3263	G
1	1	3270	U
1	1	3276	G
1	1	3278	C

Continued on next page...

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Mol	Chain	Res	Type
1	1	3279	A
1	1	3289	G
1	1	3290	G
1	1	3294	A
1	1	3295	A
1	1	3304	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3319	U
1	1	3334	U
1	1	3341	U
1	1	3346	U
1	1	3347	A
1	1	3350	C
1	1	3358	U
1	1	3369	G
1	1	3375	A
1	1	3378	C
1	1	3382	U
1	1	3383	G
1	1	3386	G
1	1	3396	U
2	2	23	U
2	2	34	U
2	2	35	C
2	2	48	A
2	2	59	A
2	2	62	C
2	2	63	G
2	2	79	A
2	2	81	U
2	2	82	U
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	104	A
2	2	105	A
2	2	106	C

Continued on next page...

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Mol	Chain	Res	Type
2	2	107	G
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	148	G
52	6	4	U
52	6	5	C
52	6	7	C
52	6	14	U
52	6	15	C
52	6	16	U
52	6	23	U
52	6	24	A
52	6	30	U
52	6	33	U
52	6	34	A
52	6	40	U
52	6	41	G
52	6	43	A
52	6	52	G
52	6	54	A
52	6	56	U
52	6	57	U
52	6	59	C
52	6	66	U
52	6	218	A
52	6	219	A
52	6	220	C
52	6	223	U
52	6	224	G
52	6	226	U
52	6	230	A

All (39) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	165	A
1	1	239	G
1	1	480	C
1	1	484	C

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Mol	Chain	Res	Type
1	1	644	G
1	1	720	A
1	1	734	C
1	1	870	C
1	1	906	A
1	1	908	G
1	1	1102	A
1	1	1104	G
1	1	1128	U
1	1	1159	A
1	1	1227	C
1	1	1241	U
1	1	1283	C
1	1	1302	A
1	1	1307	G
1	1	1329	U
1	1	1355	A
1	1	1551	C
1	1	1954	G
1	1	2417	U
1	1	2419	A
1	1	2445	A
1	1	2496	C
1	1	2500	A
1	1	2597	U
1	1	2600	C
1	1	2602	G
1	1	3121	U
1	1	3217	C
1	1	3228	C
1	1	3269	U
2	2	123	G
52	6	42	G
52	6	56	U
52	6	222	A

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
52	6	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	6	67:U	O3'	213:A	P	14.70

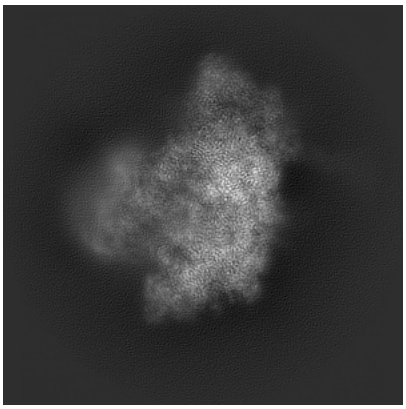
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24296. These allow visual inspection of the internal detail of the map and identification of artifacts.

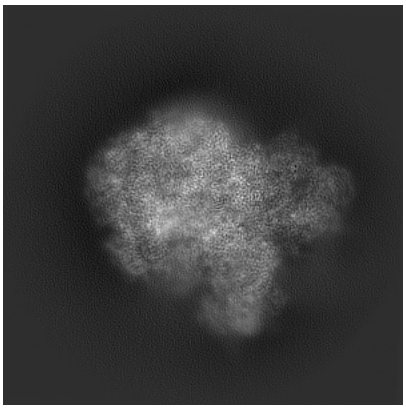
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

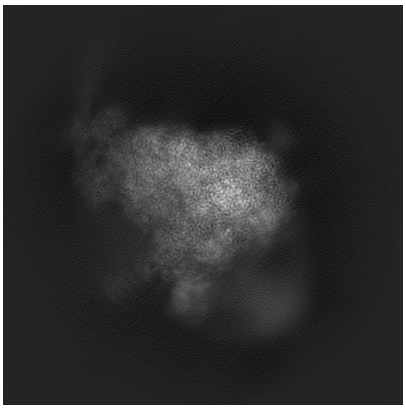
6.1.1 Primary map



X

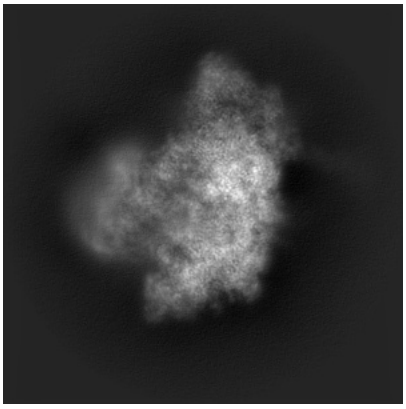


Y

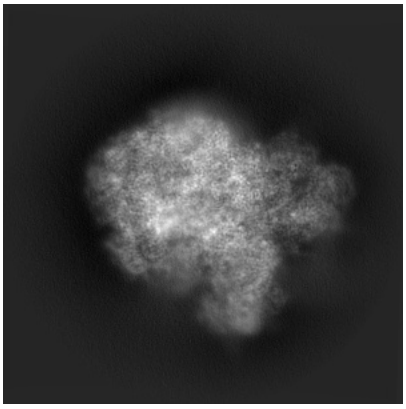


Z

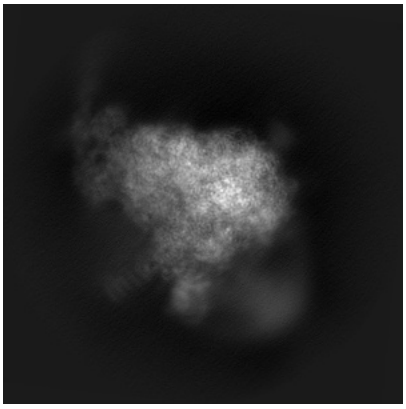
6.1.2 Raw map



X



Y

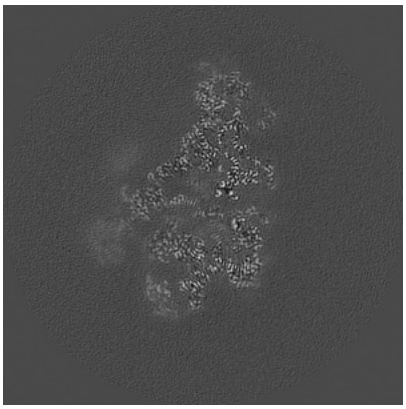


Z

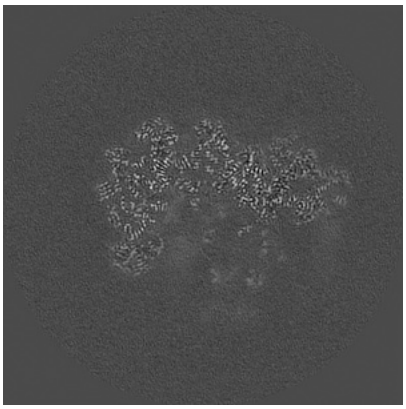
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

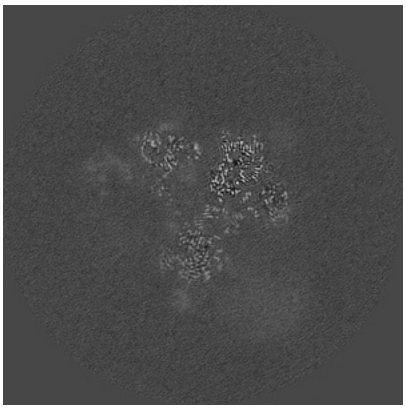
6.2.1 Primary map



X Index: 210

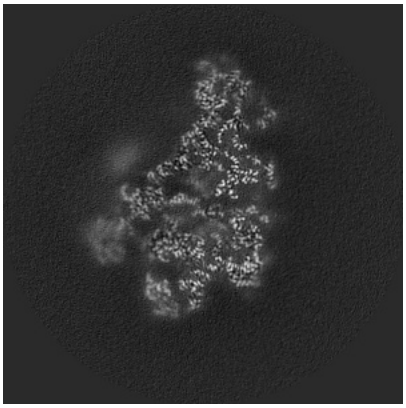


Y Index: 210

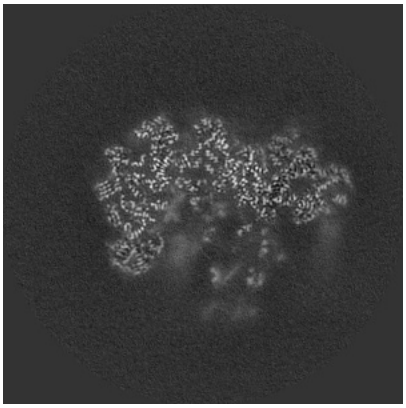


Z Index: 210

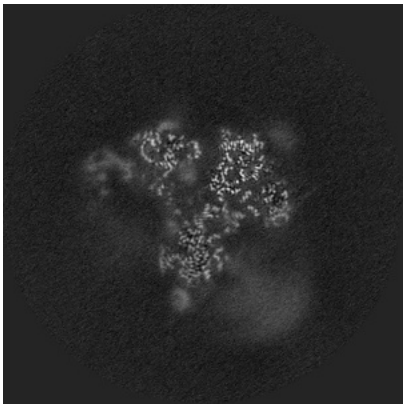
6.2.2 Raw map



X Index: 210



Y Index: 210

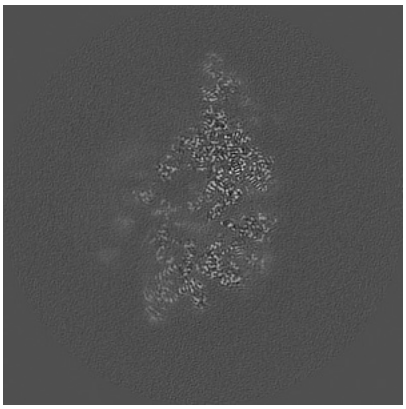


Z Index: 210

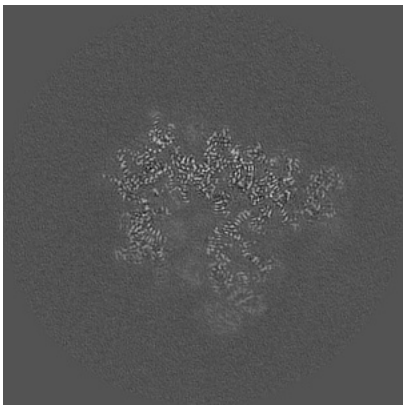
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

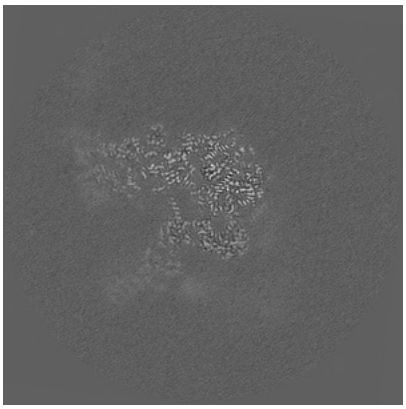
6.3.1 Primary map



X Index: 219

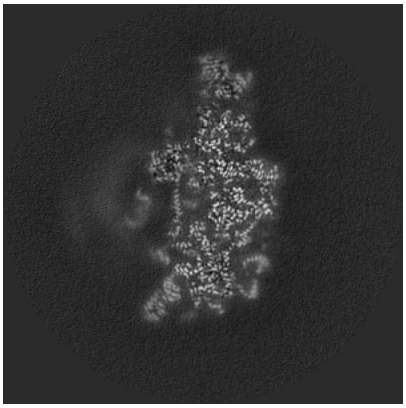


Y Index: 233

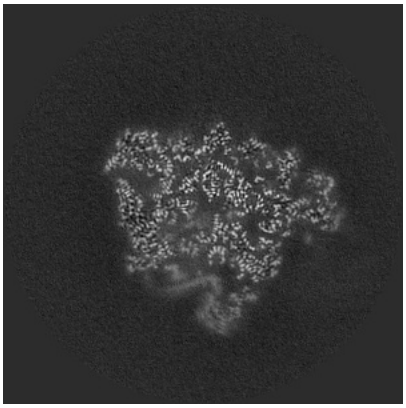


Z Index: 247

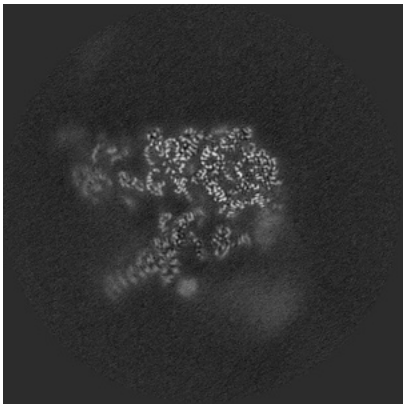
6.3.2 Raw map



X Index: 236



Y Index: 247



Z Index: 235

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

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

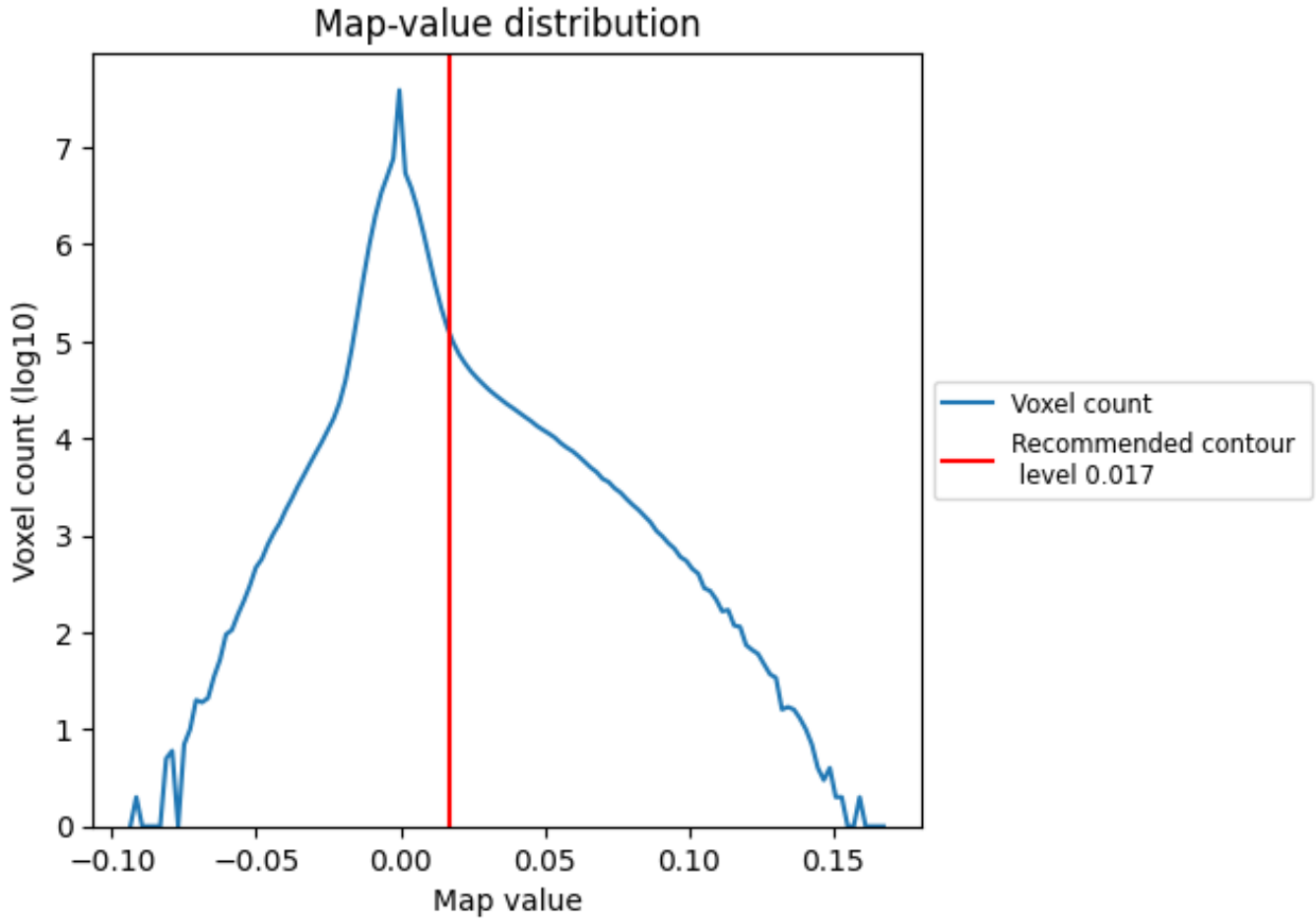
6.5 Mask visualisation (i)

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

7 Map analysis

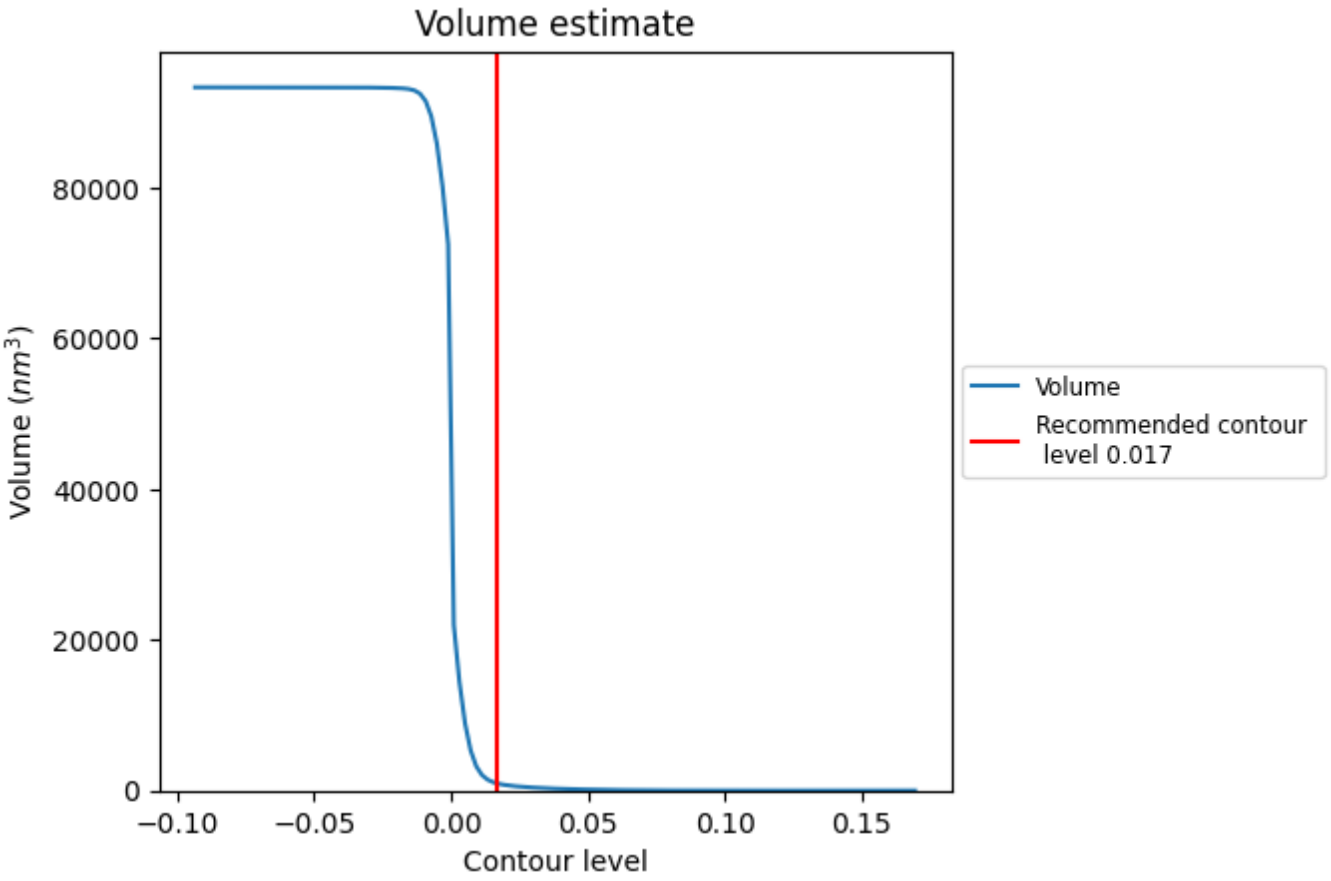
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

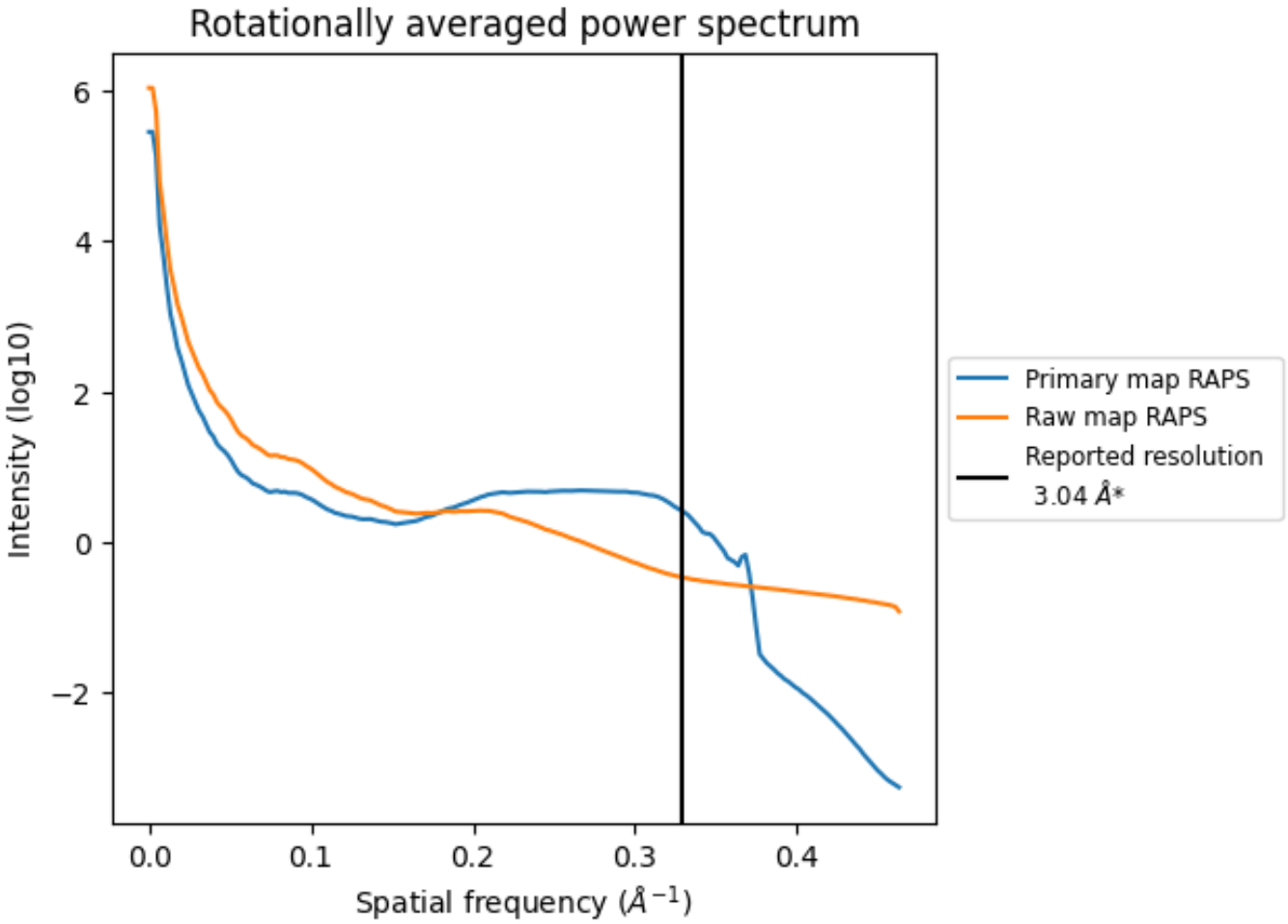
7.2 Volume estimate



The volume at the recommended contour level is 937 nm^3; this corresponds to an approximate mass of 846 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)

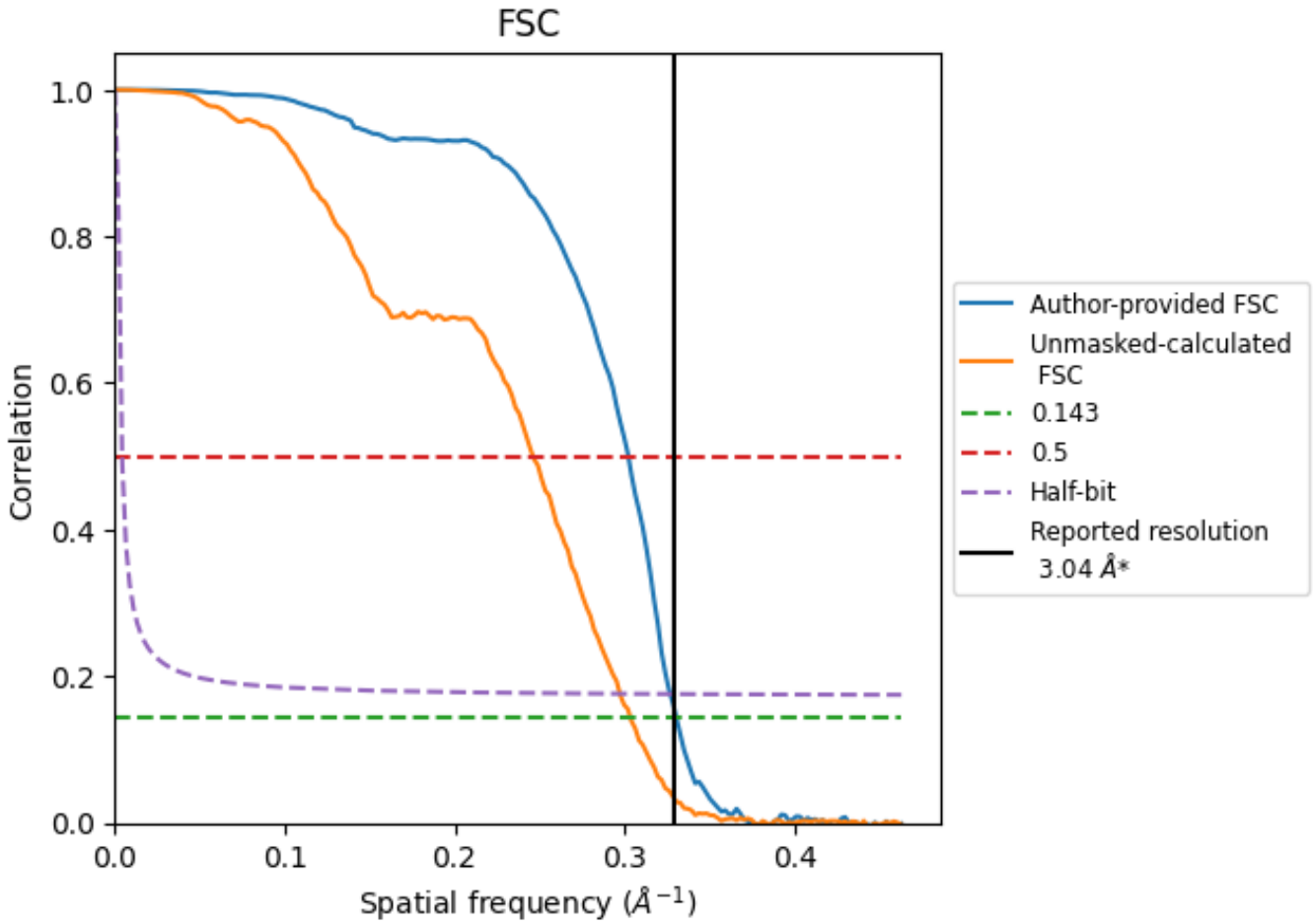


*Reported resolution corresponds to spatial frequency of 0.329 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.329 Å^{-1}

8.2 Resolution estimates (i)

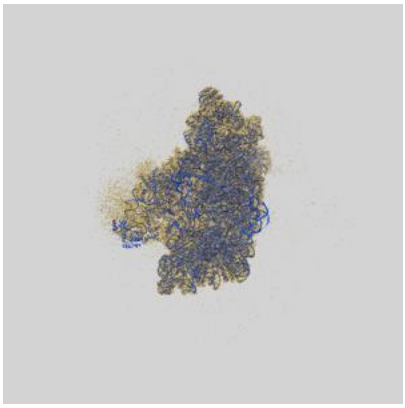
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	3.02	3.31	3.06
Unmasked-calculated*	3.29	4.06	3.36

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

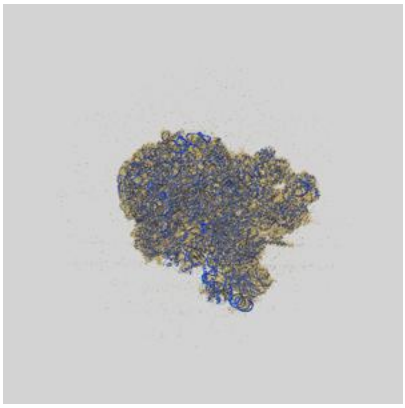
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24296 and PDB model 7R7A. Per-residue inclusion information can be found in section 3 on page 14.

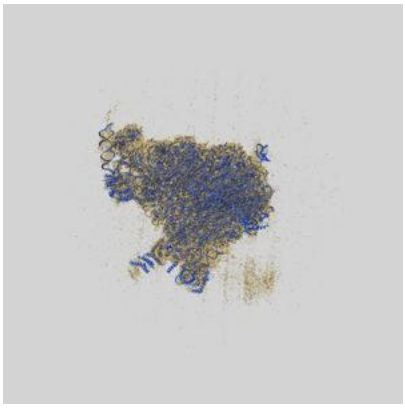
9.1 Map-model overlay



X



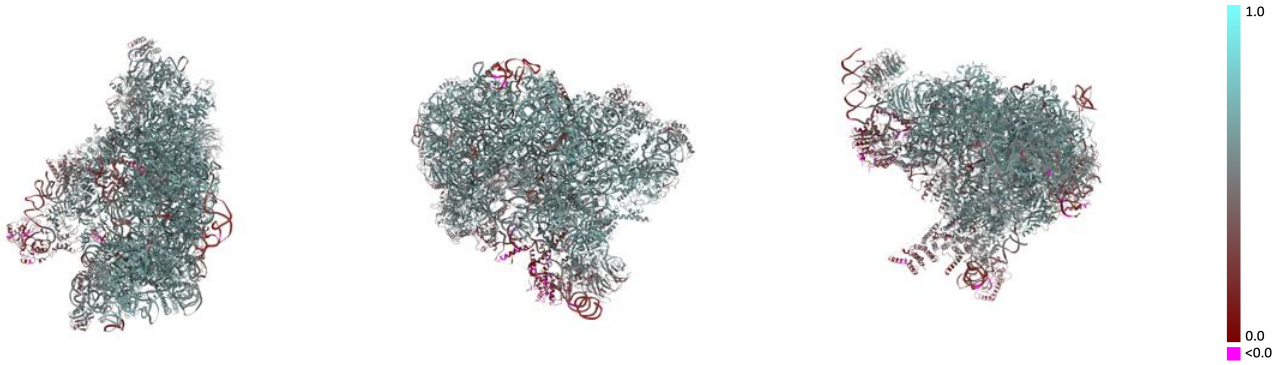
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.017 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.

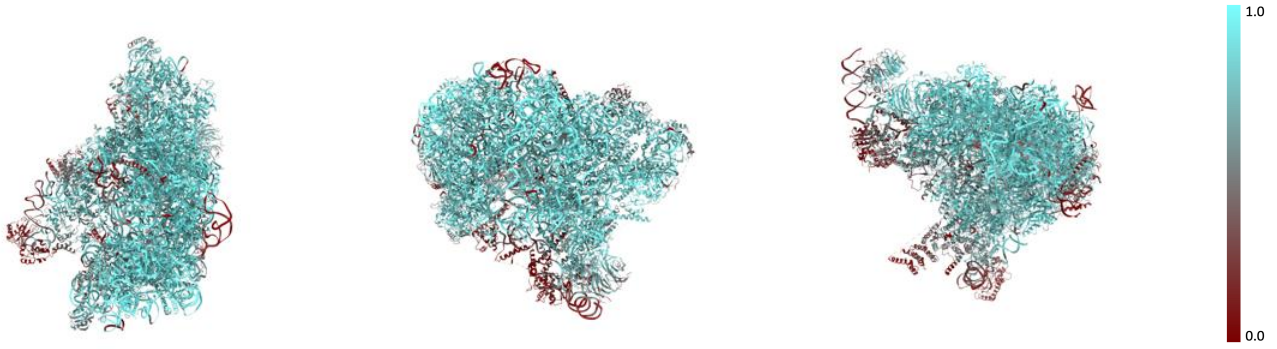
9.2 Q-score mapped to coordinate model



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.

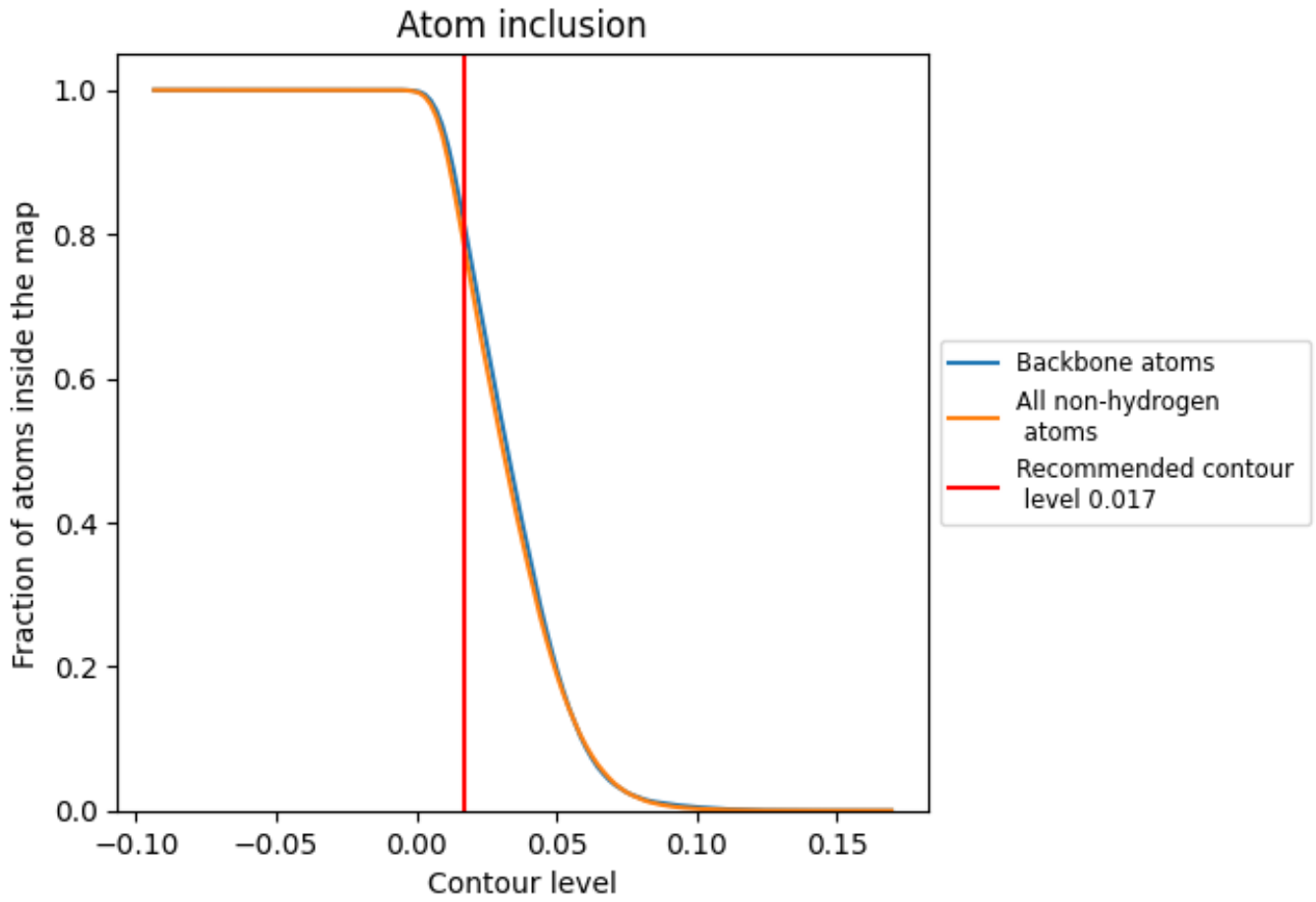
9.3 Atom inclusion mapped to coordinate model



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 (0.017).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 78% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7839	0.5270
1	0.8408	0.5280
2	0.9493	0.5970
6	0.8536	0.5320
7	0.7407	0.5380
8	0.4626	0.4010
A	0.7536	0.5180
B	0.9067	0.5800
C	0.9131	0.6090
D	0.6566	0.5010
E	0.8418	0.5610
F	0.8944	0.5950
G	0.8941	0.5980
H	0.8731	0.5790
I	0.7411	0.5150
J	0.7502	0.5300
K	0.7656	0.5280
L	0.9211	0.6040
M	0.9123	0.6000
N	0.9643	0.6310
O	0.9353	0.6110
P	0.8231	0.5610
Q	0.8659	0.5820
R	0.7545	0.5340
S	0.8495	0.5750
T	0.0566	0.2370
U	0.7292	0.5110
V	0.7193	0.5190
W	0.6305	0.4540
X	0.8978	0.6020
Y	0.9265	0.6000
Z	0.8609	0.5920
a	0.0981	0.2300
b	0.6775	0.4900
c	0.7770	0.5480

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Chain	Atom inclusion	Q-score
d	0.7816	0.5440
e	0.9400	0.6160
f	0.9720	0.6300
g	0.8933	0.6010
h	0.9226	0.6070
i	0.8555	0.5630
j	0.9551	0.6340
k	0.8130	0.5620
l	0.8218	0.5640
m	0.8540	0.5820
n	0.8881	0.5950
o	0.7779	0.5270
p	0.6233	0.4630
q	0.6826	0.4860
r	0.7871	0.5570
s	0.8789	0.6070
t	0.8495	0.5830
u	0.7782	0.5280
v	0.8936	0.5890
w	0.4956	0.4480
x	0.2631	0.2640
y	0.8128	0.5240
z	0.5553	0.4810