



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 04:38 PM UTC

PDB ID : 6ZQE / pdb_00006zqe
EMDB ID : EMD-11361
Title : Cryo-EM structure of the 90S pre-ribosome from *Saccharomyces cerevisiae*, state Dis-A (Poly-Ala)
Authors : Cheng, J.; Lau, B.; Venuta, G.L.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2020-07-09
Resolution : 7.10 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:

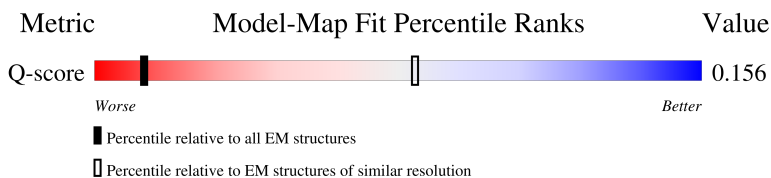
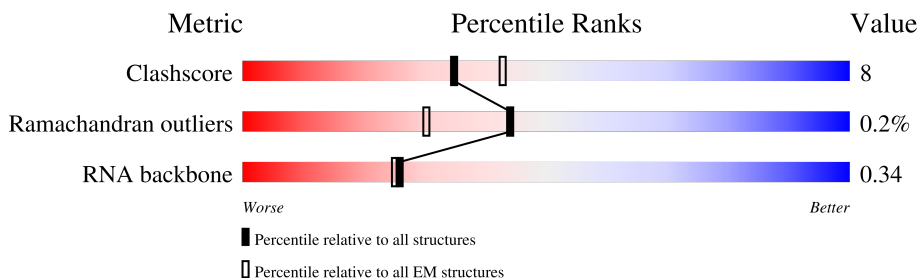
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 7.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	464 (6.60 - 7.60)

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	UA	923	
2	UB	810	
3	UC	610	
4	UD	776	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	UE	575	
6	UH	713	
7	UI	643	
8	UJ	1769	
9	UK	250	
10	UL	943	
11	UM	817	
12	UN	15	
13	UO	513	
14	UP	214	
15	UQ	896	
16	UR	594	
17	US	552	
18	UT	2493	
19	UU	939	
20	UV	1237	
21	UX	189	
22	CA	327	
22	CB	327	
23	CD	504	
24	CE	511	
25	CF	126	
25	CG	126	
26	CH	573	
27	CI	183	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	CJ	290	
29	CK	593	
30	CL	1183	
31	CM	367	
32	CN	297	
33	JD	1267	
34	JF	252	
34	JG	252	
35	JH	483	
36	JL	318	
37	JM	217	
38	Db	82	
39	JJ	274	
40	DA	255	
41	DE	261	
42	DF	225	
43	DG	236	
44	DH	190	
45	DI	200	
46	DJ	197	
47	DL	156	
48	DN	151	
49	DO	137	
50	DQ	143	
51	DS	146	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	DT	144	
53	DW	130	
54	DX	145	
55	DY	135	
56	Dc	67	
57	D2	81	
58	D3	1802	
59	D4	333	

2 Entry composition [i](#)

There are 60 unique types of molecules in this entry. The entry contains 139051 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 Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	UA	792	Total	C	N	O	0	0
			3916	2332	792	792		

- Molecule 2 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	UB	553	Total	C	N	O	0	0
			2754	1648	553	553		

- Molecule 3 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	UC	86	Total	C	N	O	0	0
			421	249	86	86		

- Molecule 4 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	UD	663	Total	C	N	O	0	0
			3280	1954	663	663		

- Molecule 5 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	UE	88	Total	C	N	O	0	0
			437	261	88	88		

- Molecule 6 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	UH	479	Total	C	N	O	0	0
			2372	1414	479	479		

- Molecule 7 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	UI	475	Total	C	N	O	0	0
			2353	1403	475	475		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	UJ	1117	Total	C	N	O	0	0
			5567	3333	1117	1117		

- Molecule 9 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	UK	219	Total	C	N	O	0	0
			1090	652	219	219		

- Molecule 10 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	UL	778	Total	C	N	O	0	0
			3846	2290	778	778		

- Molecule 11 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	UM	762	Total	C	N	O	0	0
			3763	2239	762	762		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	UN	15	Total	C	N	O	0	0
			71	41	15	15		

- Molecule 13 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	UO	493	Total	C	N	O	0	0
			2441	1455	493	493		

- Molecule 14 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	UP	60	Total	C	N	O	0	0
			298	178	60	60		

- Molecule 15 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	UQ	820	Total	C	N	O	0	0
			4062	2422	820	820		

- Molecule 16 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	UR	481	Total	C	N	O	0	0
			2372	1410	481	481		

- Molecule 17 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	US	494	Total	C	N	O	0	0
			2462	1474	494	494		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	UT	1089	Total	C	N	O	0	0
			5419	3241	1089	1089		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	UU	878	Total	C	N	O	0	0
			4328	2572	878	878		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	UV	1098	Total	C	N	O	0	0
			5442	3246	1098	1098		

- Molecule 21 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	UX	167	Total	C	N	O	0	0
			827	493	167	167		

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	CA	242	Total	C	N	O	0	0
			1190	706	242	242		
22	CB	228	Total	C	N	O	0	0
			1122	666	228	228		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	CD	380	Total	C	N	O	0	0
			1880	1120	380	380		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	CE	435	Total	C	N	O	0	0
			2155	1285	435	435		

- Molecule 25 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	CF	121	Total	C	N	O	0	0
			601	359	121	121		
25	CG	121	Total	C	N	O	0	0
			601	359	121	121		

- Molecule 26 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	CH	467	Total	C	N	O	0	0
			2302	1368	467	467		

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	CI	175	Total	C	N	O	0	0
			871	521	175	175		

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	CJ	256	Total	C	N	O	0	0
			1268	756	256	256		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	CK	222	Total	C	N	O	0	0
			1106	662	222	222		

- Molecule 30 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	CL	808	Total	C	N	O	0	0
			3995	2380	808	807		

- Molecule 31 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	CM	360	Total	C	N	O	0	0
			1767	1047	360	360		

- Molecule 32 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	CN	211	Total	C	N	O	0	0
			1049	627	211	211		

- Molecule 33 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	JD	810	Total	C	N	O	0	0
			4010	2390	810	810		

- Molecule 34 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	JF	216	Total	C	N	O	0	0
			1071	639	216	216		
34	JG	230	Total	C	N	O	0	0
			1141	681	230	230		

- Molecule 35 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	JH	261	Total	C	N	O	0	0
			1295	773	261	261		

- Molecule 36 is a protein called Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	JL	283	Total	C	N	O	0	0
			1401	835	283	283		

- Molecule 37 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	JM	134	Total	C	N	O	0	0
			667	399	134	134		

- Molecule 38 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Db	81	Total	C	N	O	0	0
			400	238	81	81		

- Molecule 39 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	JJ	199	Total	C	N	O	0	0
			982	584	199	199		

- Molecule 40 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	DA	240	Total	C	N	O	0	0
			1187	707	240	240		

- Molecule 41 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	DE	246	Total	C	N	O	0	0
			1207	715	246	246		

- Molecule 42 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	DF	213	Total	C	N	O	0	0
			1055	629	213	213		

- Molecule 43 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	DG	218	Total	C	N	O	0	0
			1073	637	218	218		

- Molecule 44 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	DH	170	Total	C	N	O	0	0
			843	503	170	170		

- Molecule 45 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	DI	177	Total	C	N	O	0	0
			869	515	177	177		

- Molecule 46 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	DJ	185	Total	C	N	O	0	0
			915	545	185	185		

- Molecule 47 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	DL	140	Total	C	N	O	0	0
			692	412	140	140		

- Molecule 48 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	DN	150	Total	C	N	O	0	0
			742	442	150	150		

- Molecule 49 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	DO	127	Total	C	N	O	0	0
			620	366	127	127		

- Molecule 50 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	DQ	125	Total	C	N	O	0	0
			616	366	125	125		

- Molecule 51 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	DS	105	Total	C	N	O	0	0
			521	311	105	105		

- Molecule 52 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	DT	143	Total	C	N	O	0	0
			700	414	143	143		

- Molecule 53 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	DW	129	Total	C	N	O	0	0
			634	376	129	129		

- Molecule 54 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	DX	143	Total	C	N	O	0	0
			699	413	143	143		

- Molecule 55 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	DY	134	Total	C	N	O	0	0
			661	393	134	134		

- Molecule 56 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	Dc	63	Total	C	N	O	0	0
			310	184	63	63		

- Molecule 57 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	D2	81	Total	C	N	O	P	0	0
			1741	777	319	564	81		

- Molecule 58 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	D3	1447	Total	C	N	O	P	0	0
			30846	13790	5477	10132	1447		

- Molecule 59 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	D4	223	Total	C	N	O	P	0	0
			4723	2114	819	1567	223		

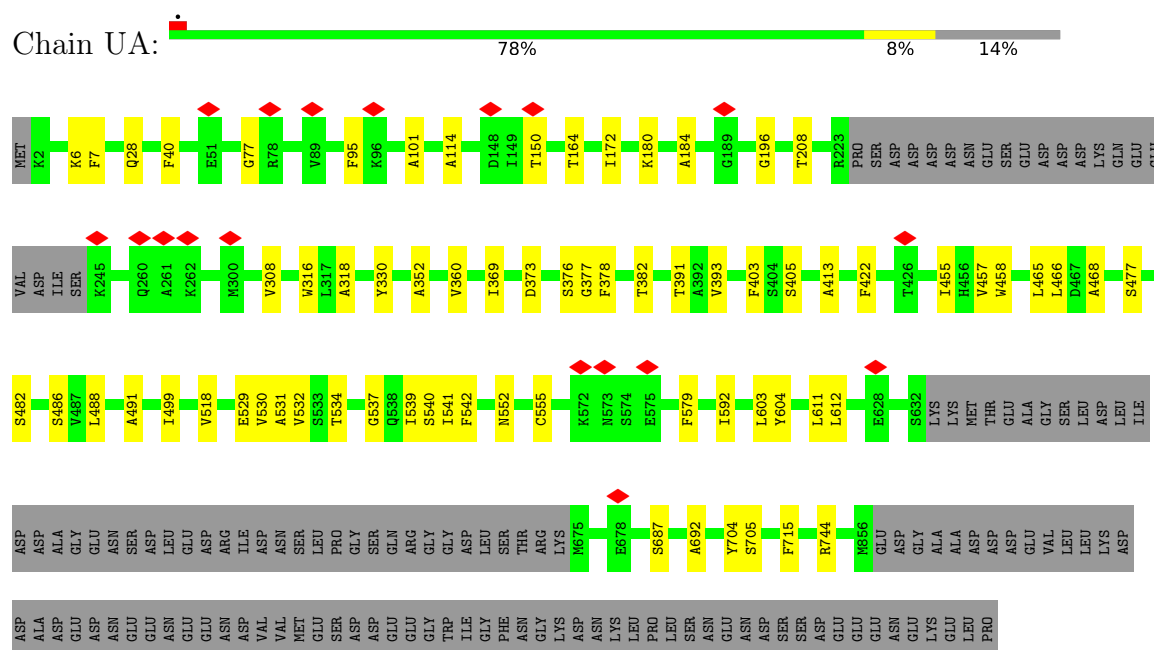
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	UX	1	Total	Zn	0
			1	1	
60	Db	1	Total	Zn	0
			1	1	

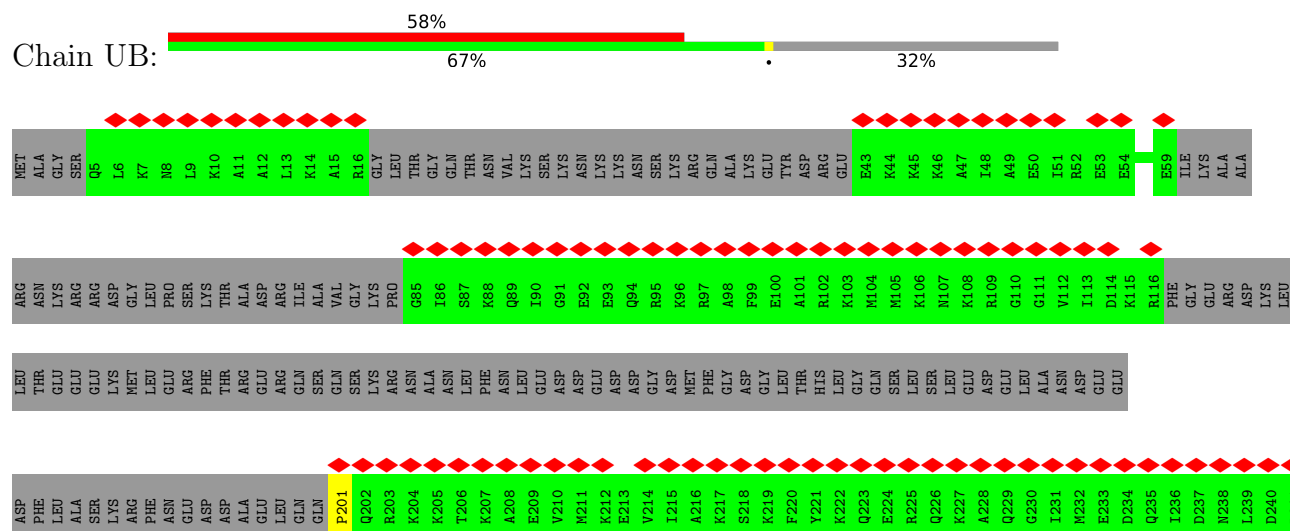
3 Residue-property plots

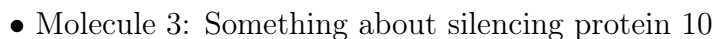
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Periodic tryptophan protein 2



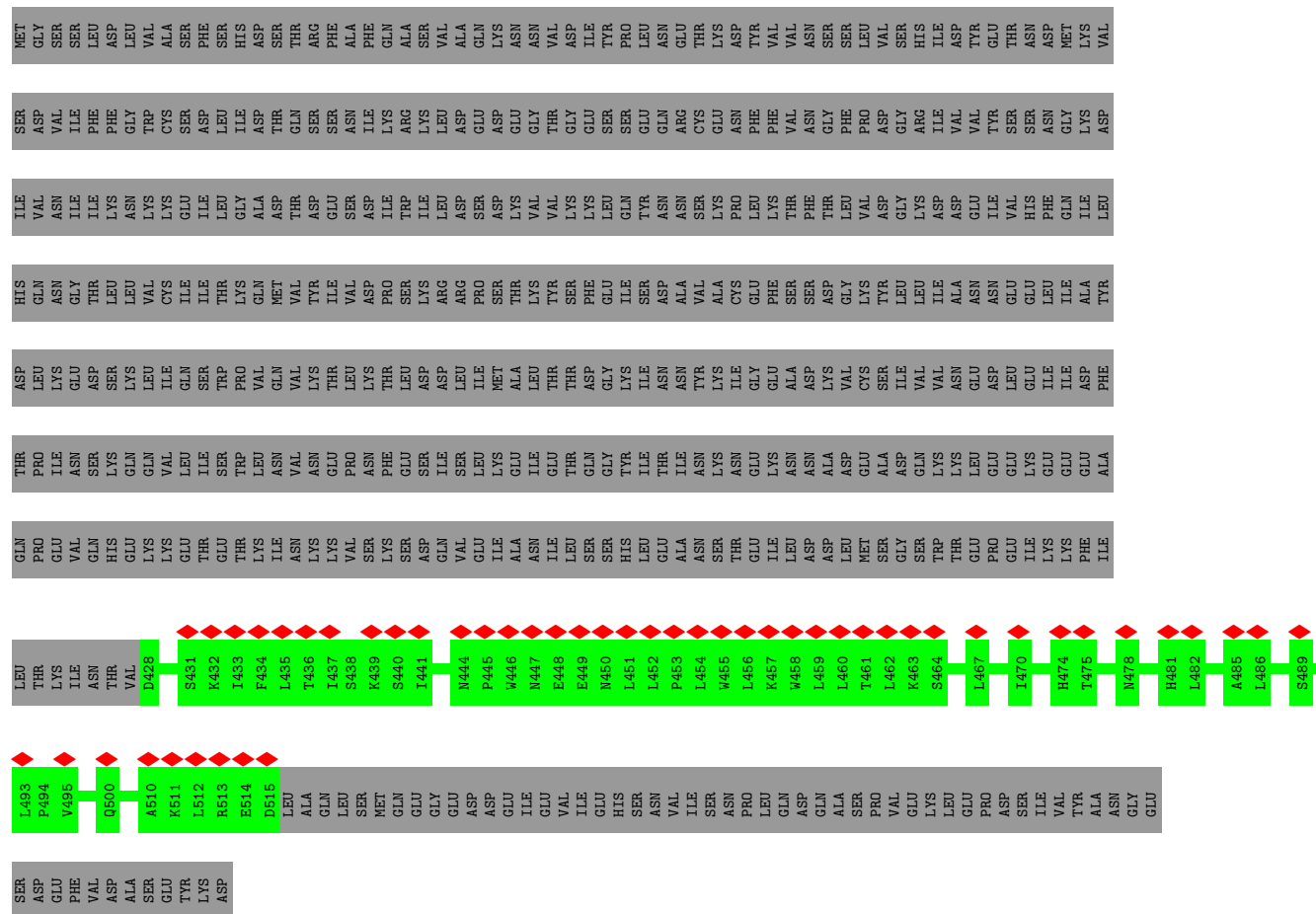
• Molecule 2: Nucleolar complex protein 14



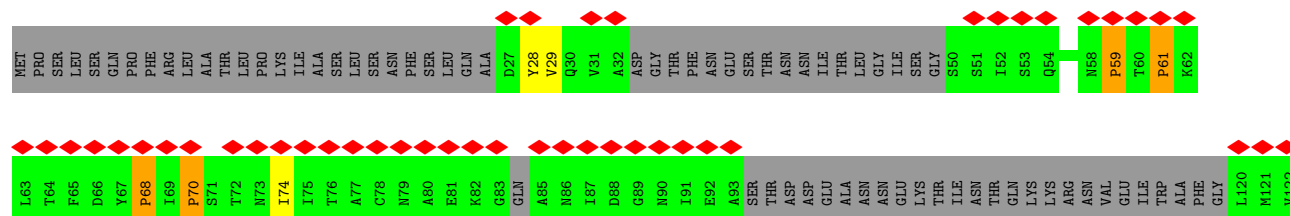


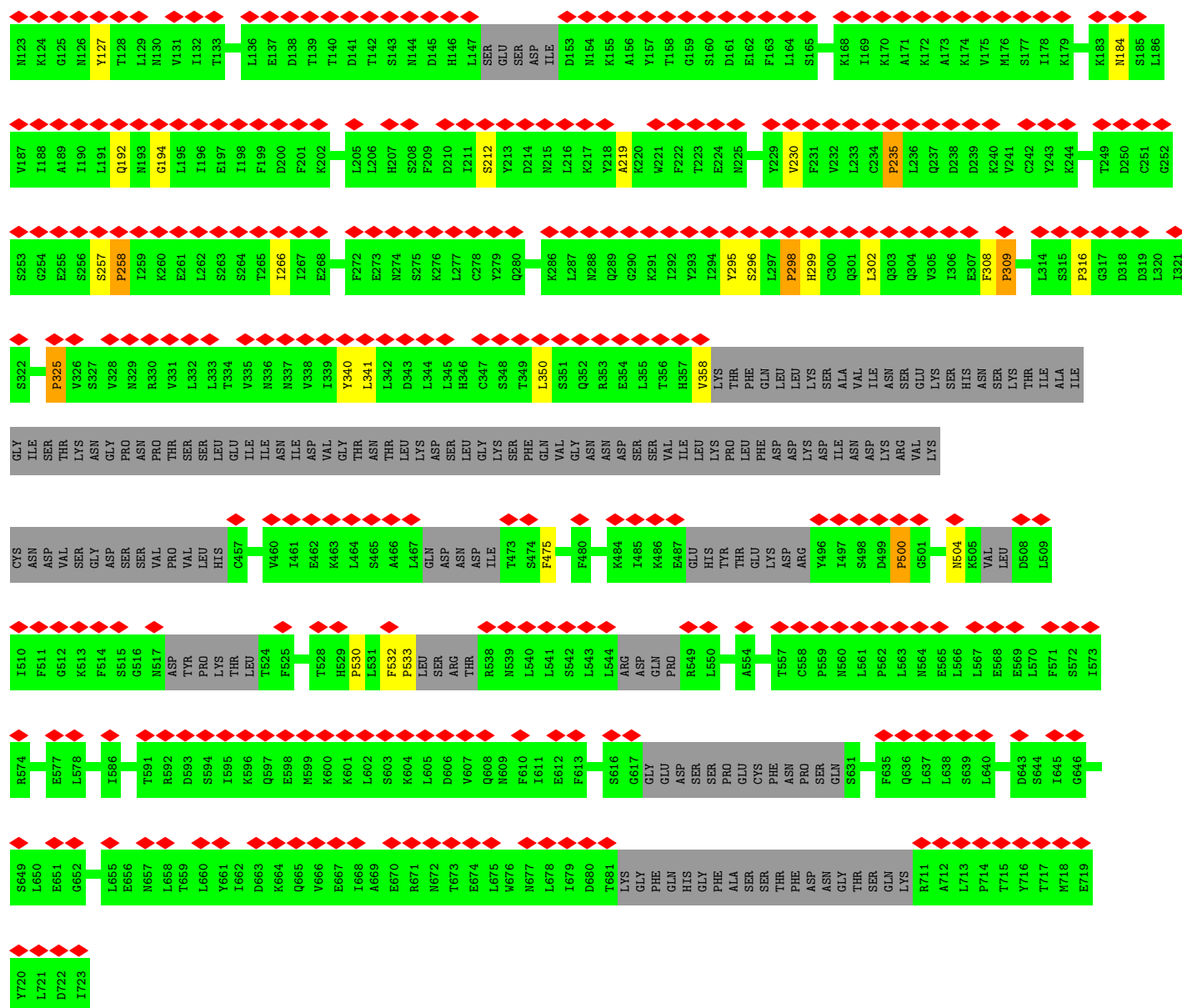


• Molecule 5: U3 small nucleolar RNA-associated protein 9

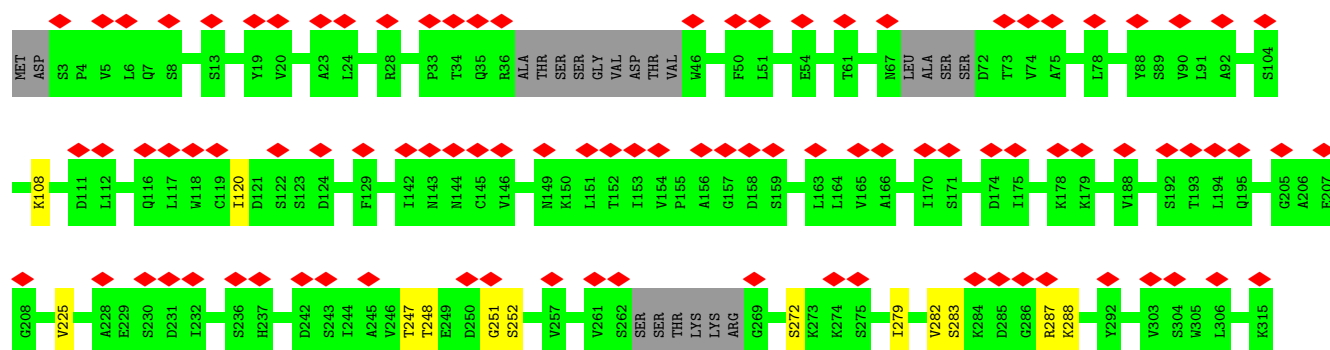
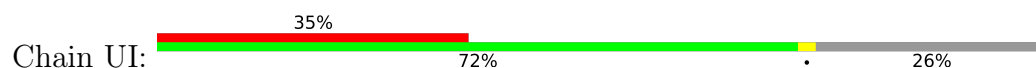


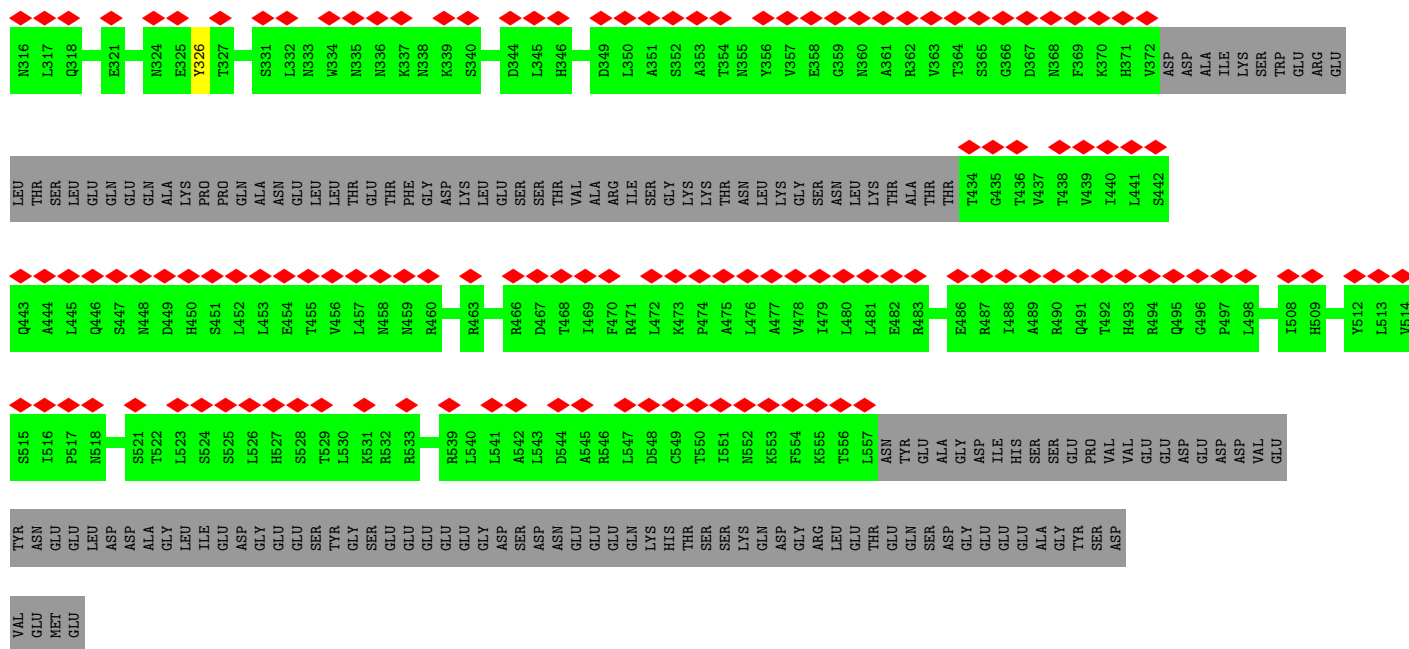
• Molecule 6: U3 small nucleolar RNA-associated protein 8



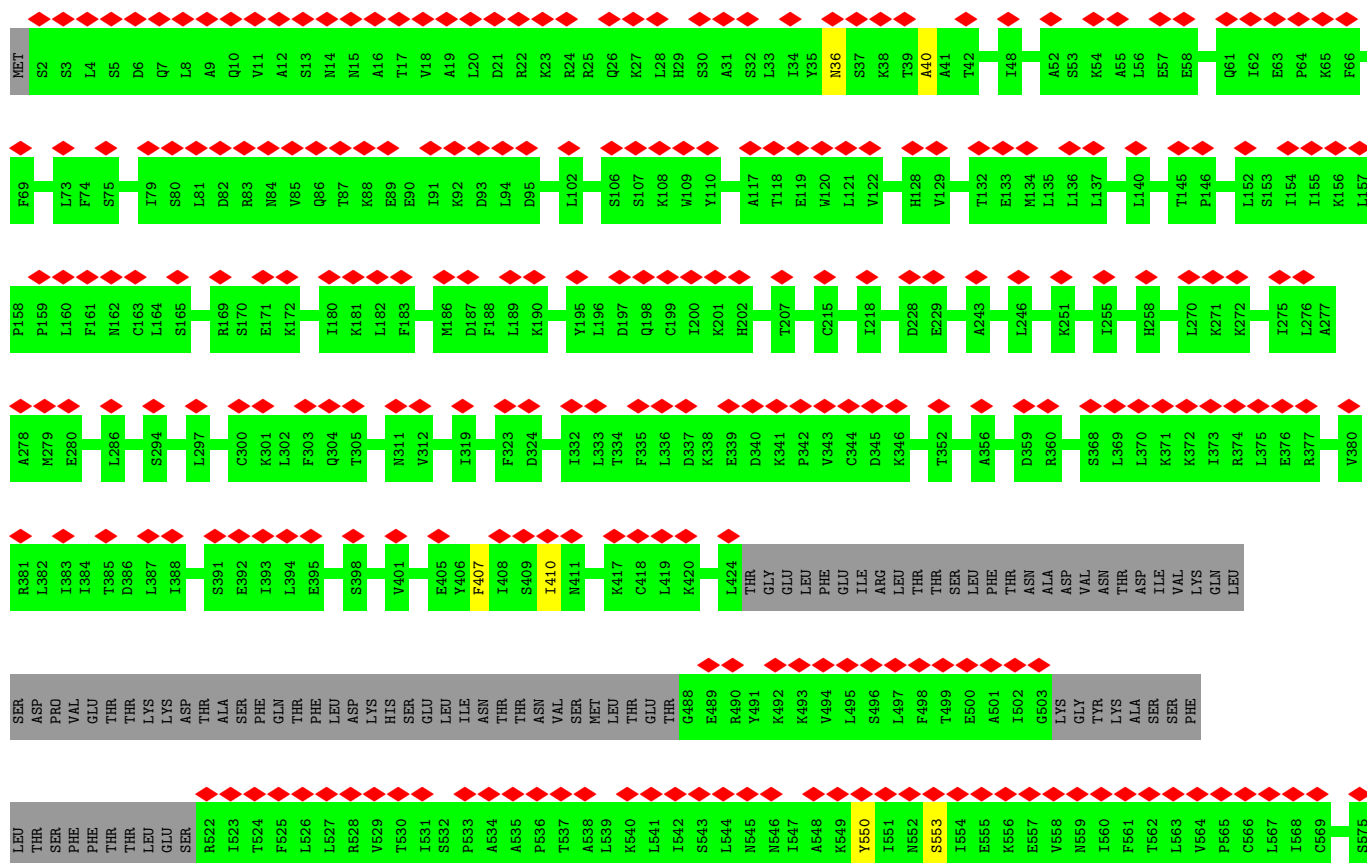


• Molecule 7: U3 small nucleolar RNA-associated protein 5

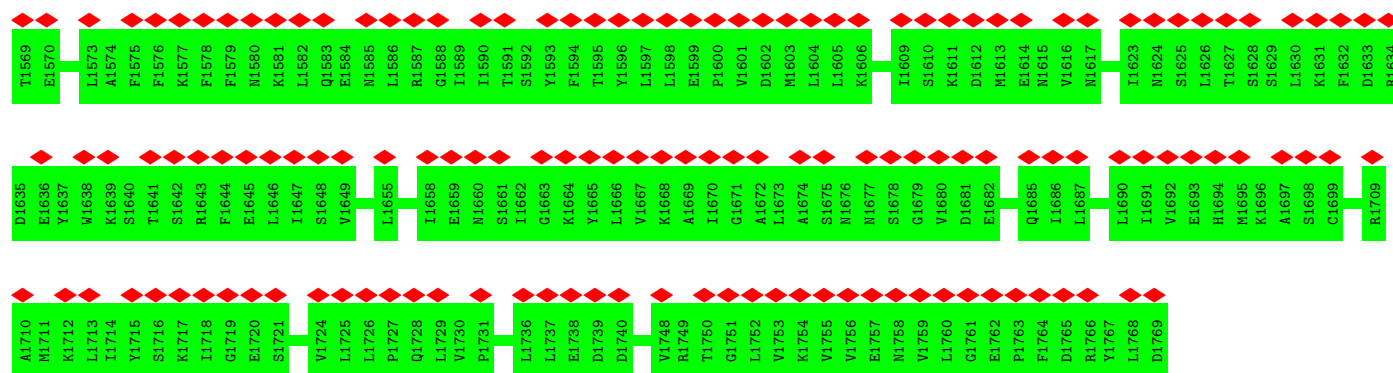




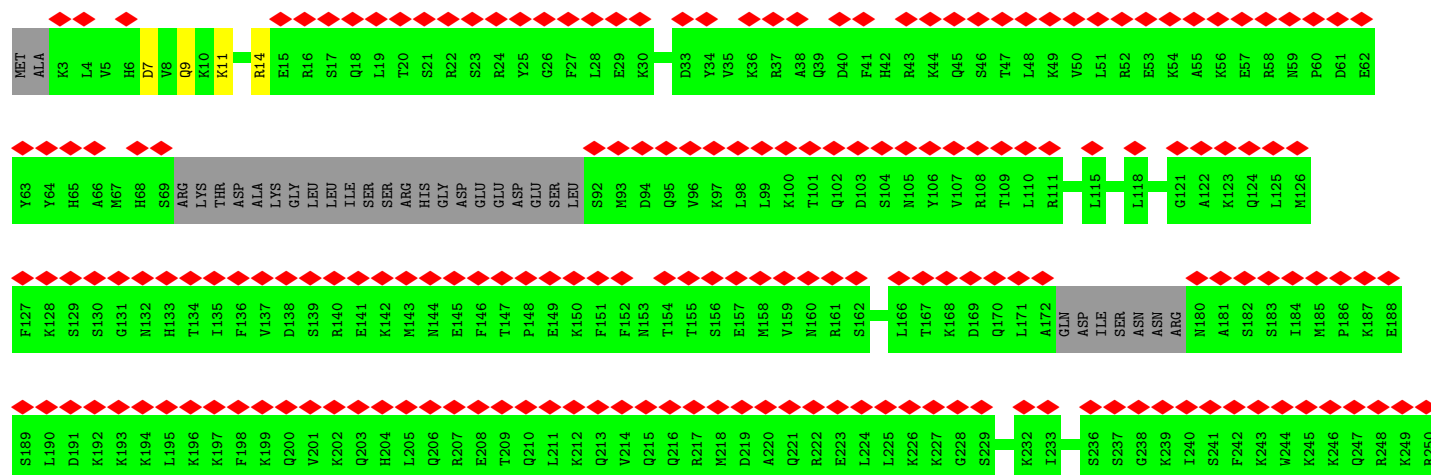
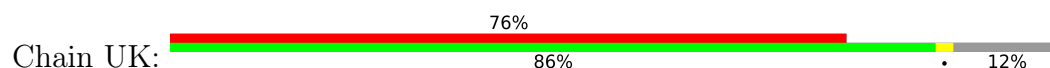
• Molecule 8: U3 small nucleolar RNA-associated protein 10



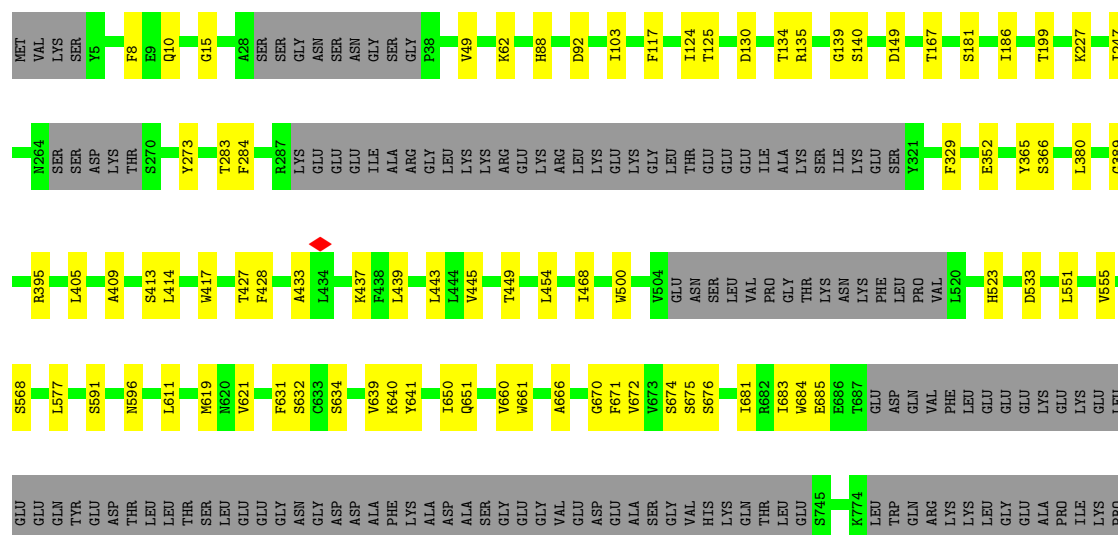
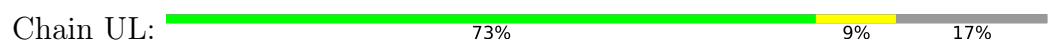


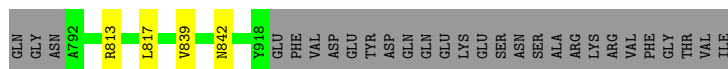


• Molecule 9: U3 small nucleolar RNA-associated protein 11



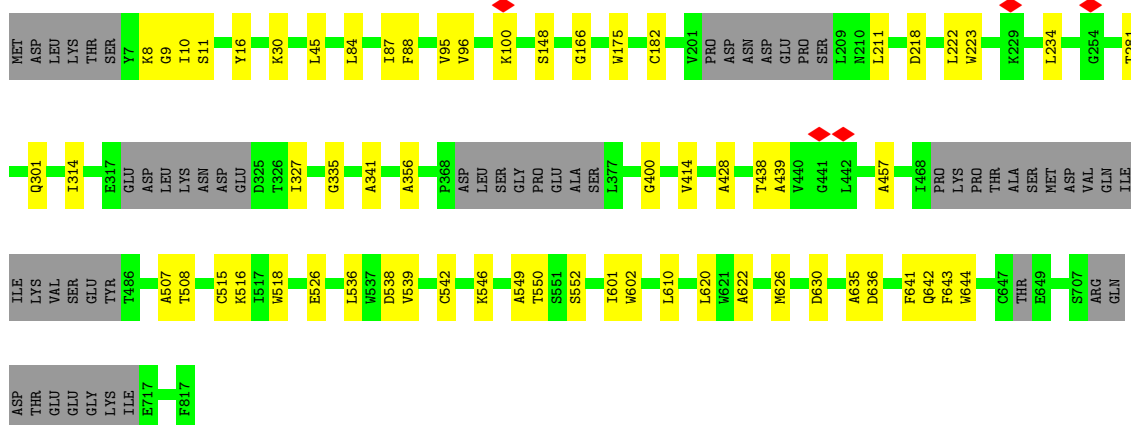
• Molecule 10: U3 small nucleolar RNA-associated protein 12





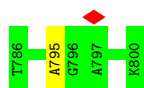
- Molecule 11: U3 small nucleolar RNA-associated protein 13

Chain UM: 86% 8% 7%



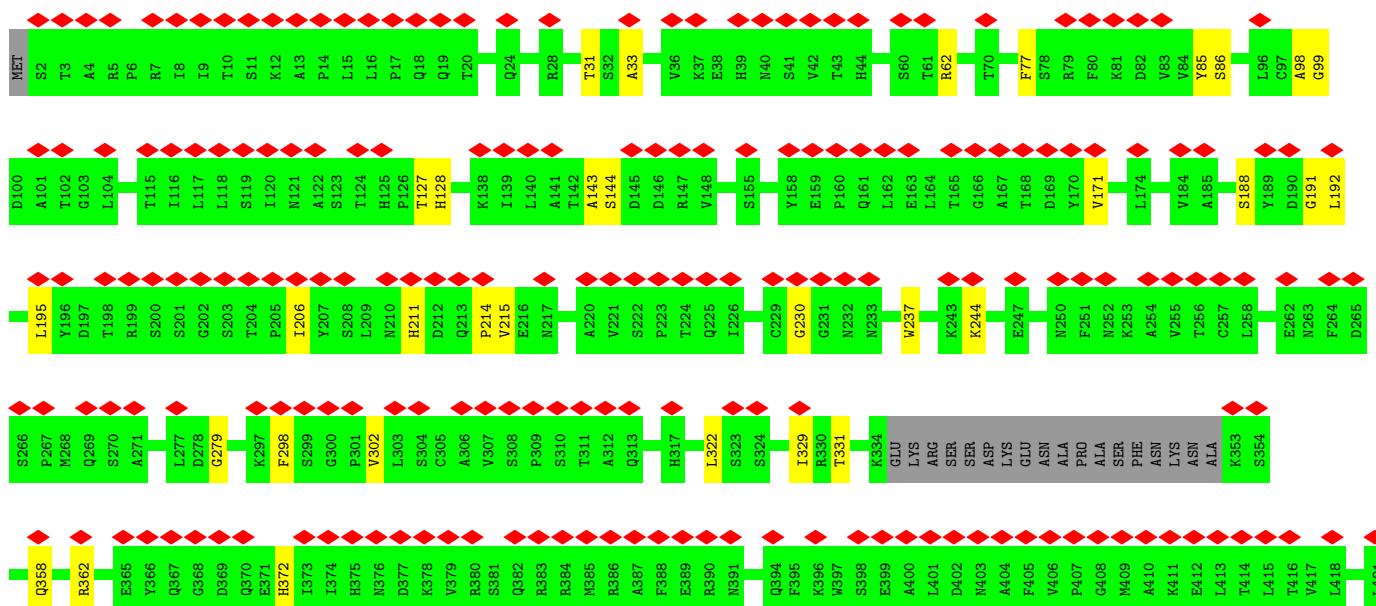
- Molecule 12: U3 small nucleolar RNA-associated protein 14

Chain UN: 7% 93% 7%

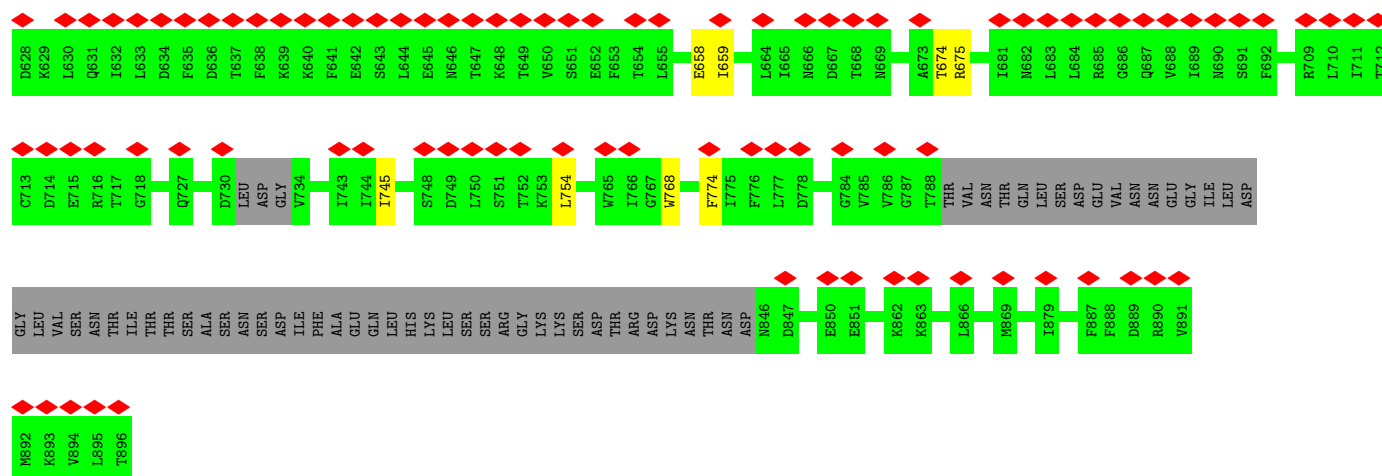


- Molecule 13: U3 small nucleolar RNA-associated protein 15

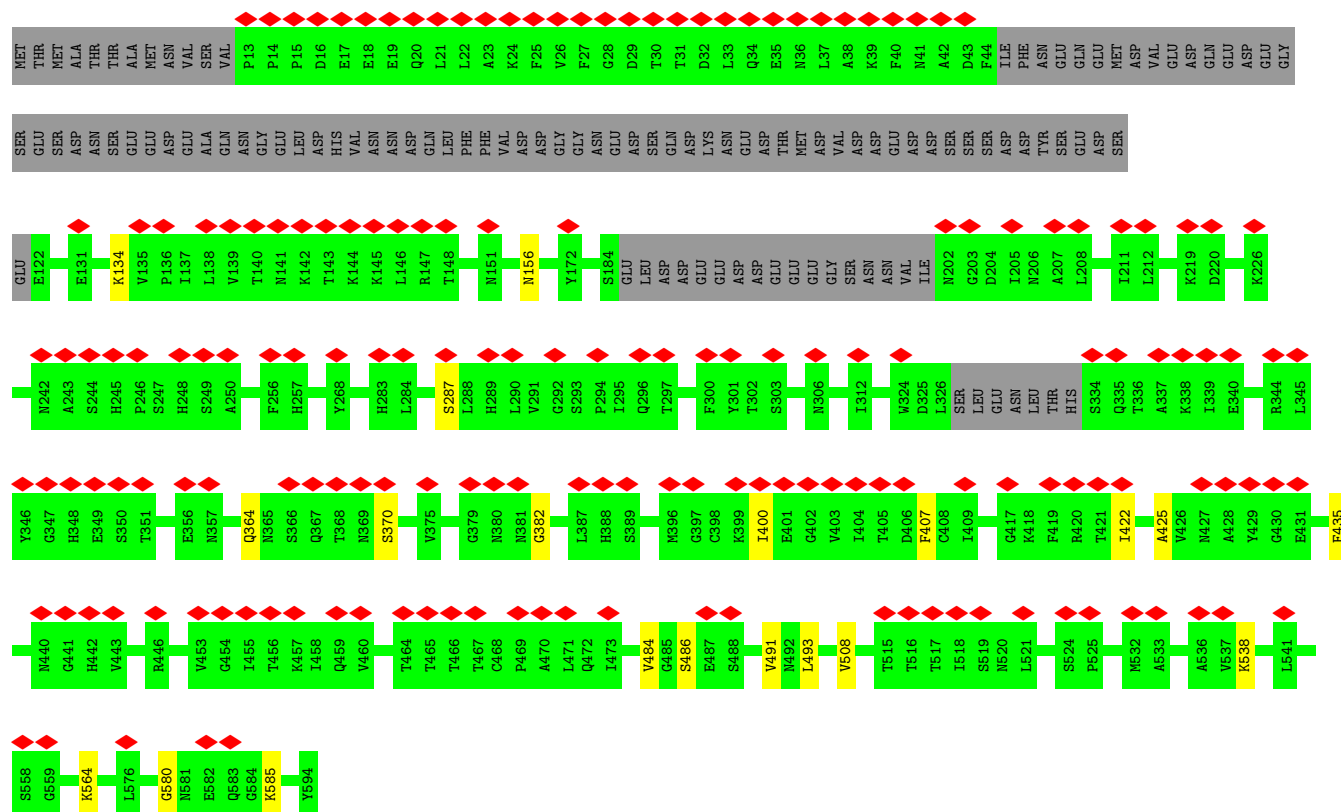
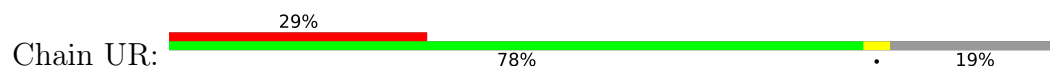
Chain UO: 52% 89% 7%



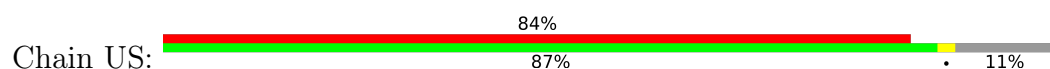




- Molecule 16: U3 small nucleolar RNA-associated protein 18



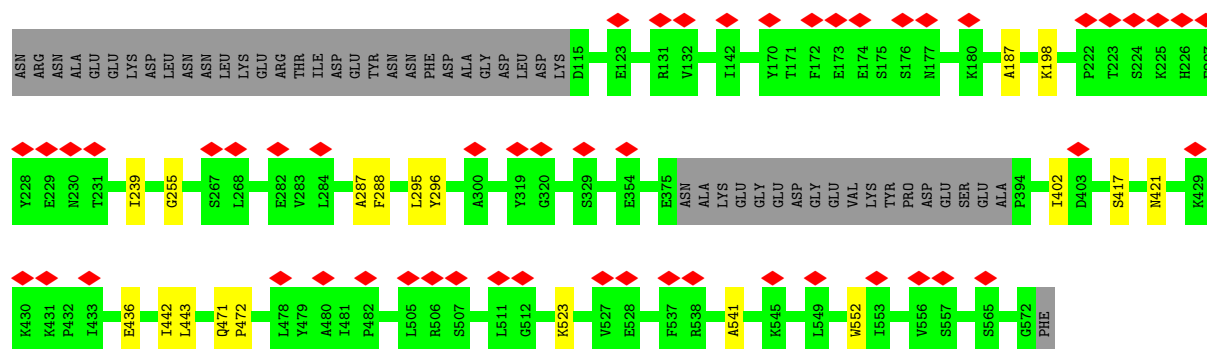
- Molecule 17: Nucleolar complex protein 4





- Molecule 19: U3 small nucleolar RNA-associated protein 21

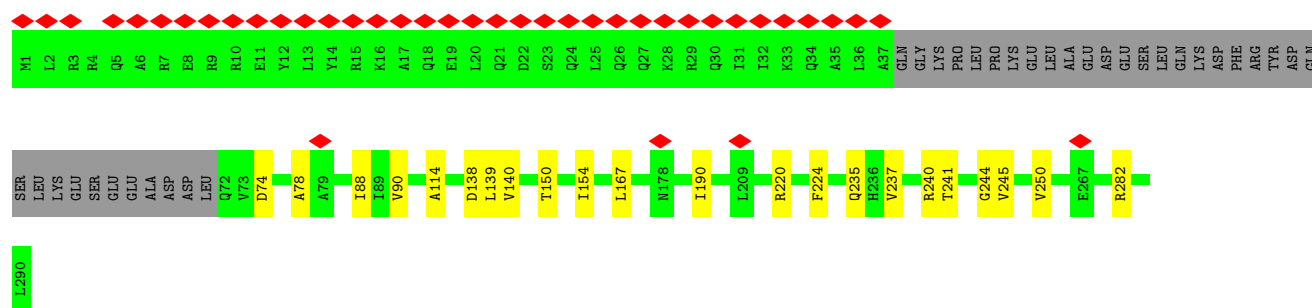
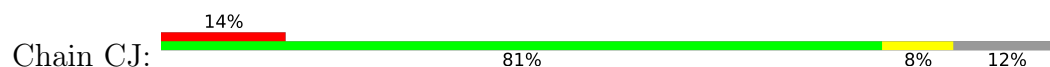




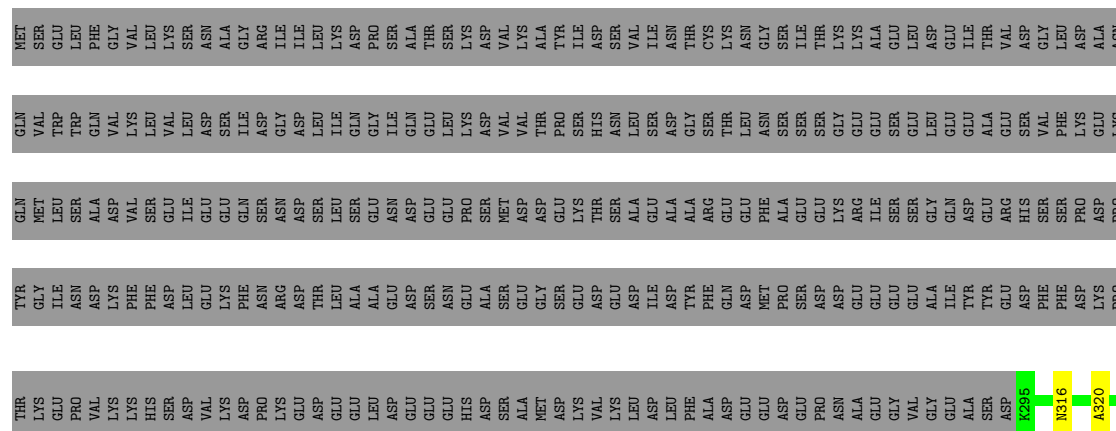
• Molecule 27: U3 small nucleolar ribonucleoprotein protein IMP3



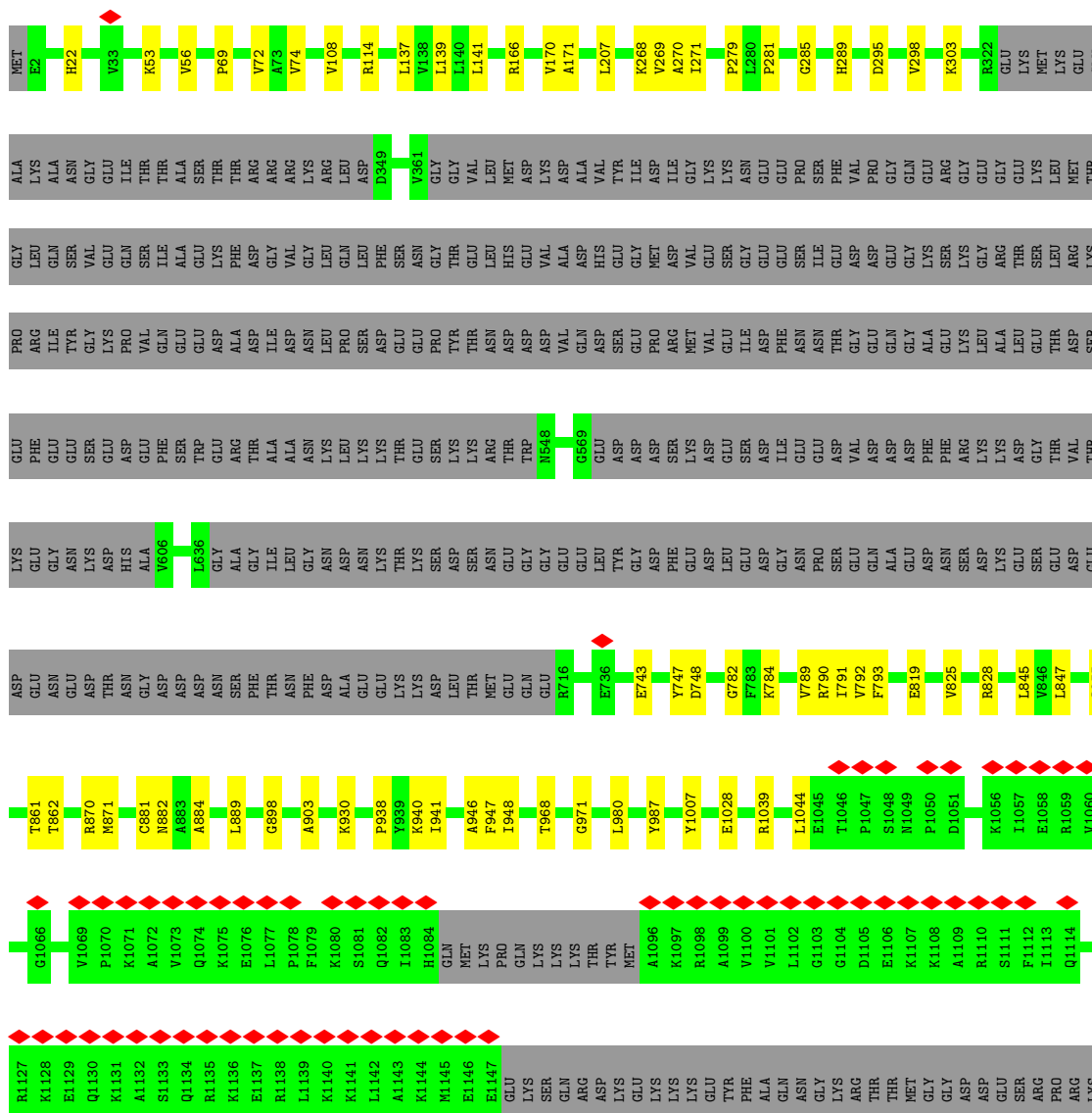
• Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP4



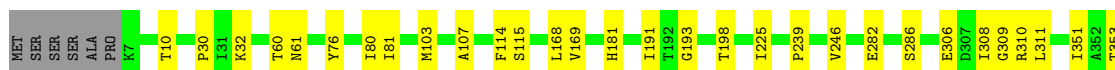
• Molecule 29: U3 small nucleolar RNA-associated protein MPP10

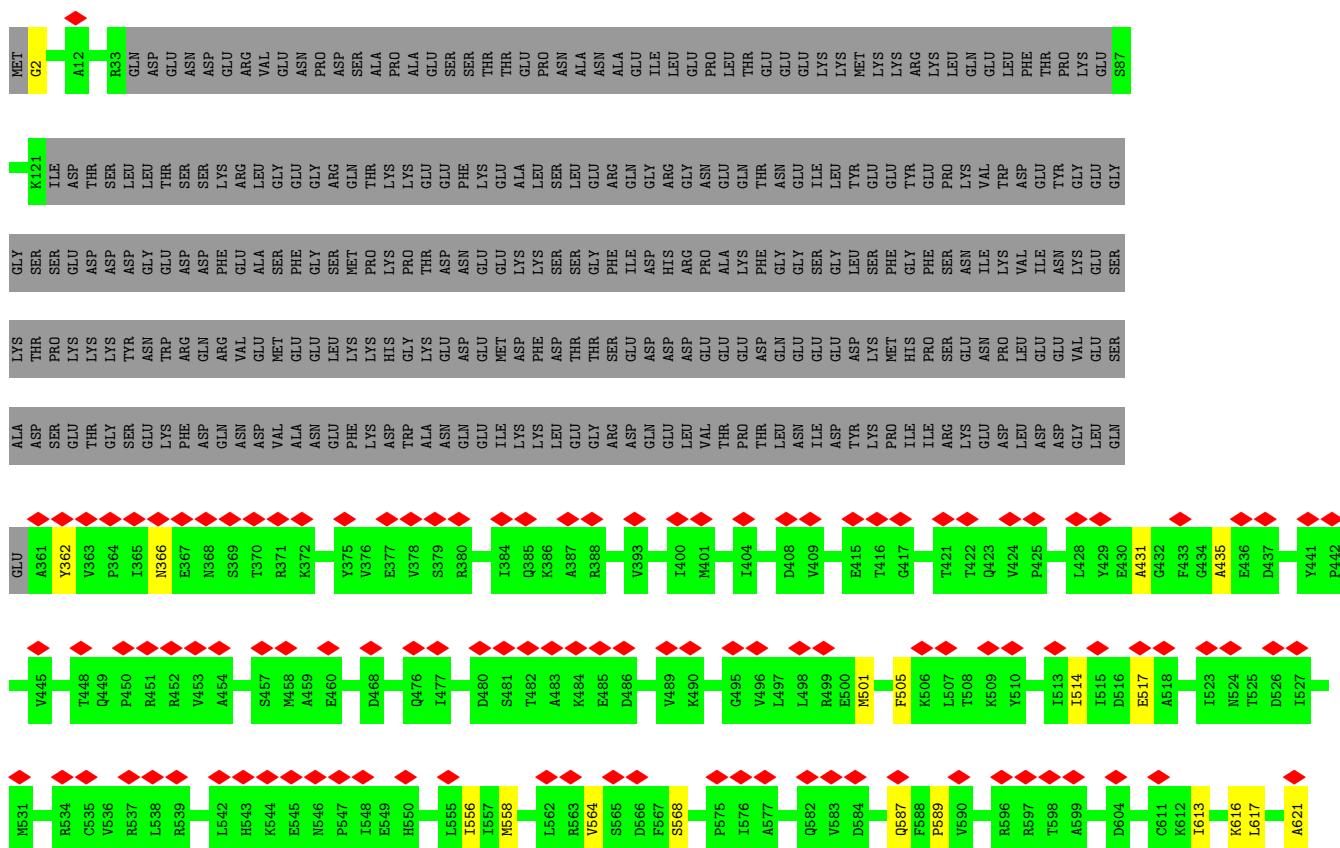


- Molecule 30: Ribosome biogenesis protein BMS1



- Molecule 31: RNA 3'-terminal phosphate cyclase-like protein

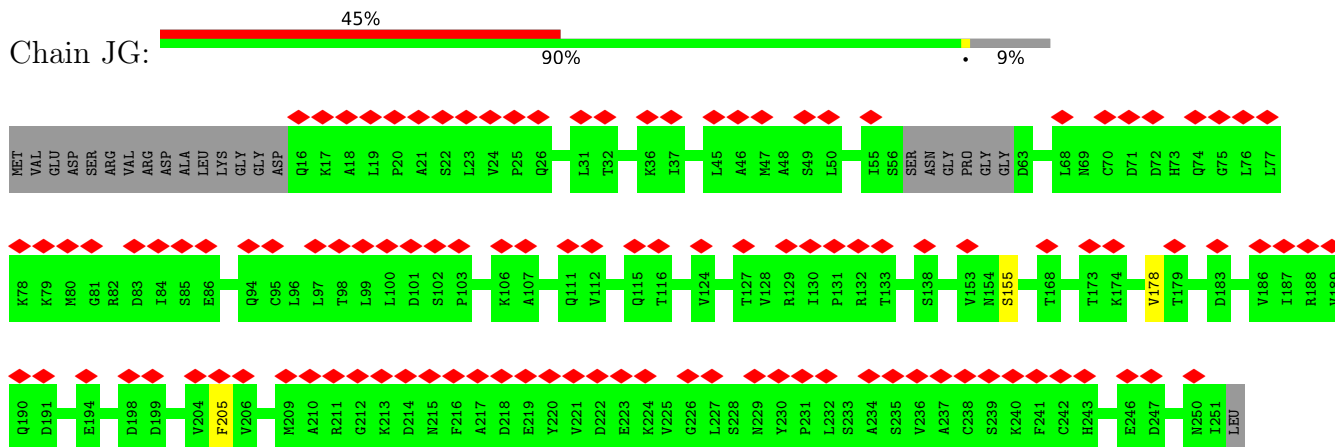






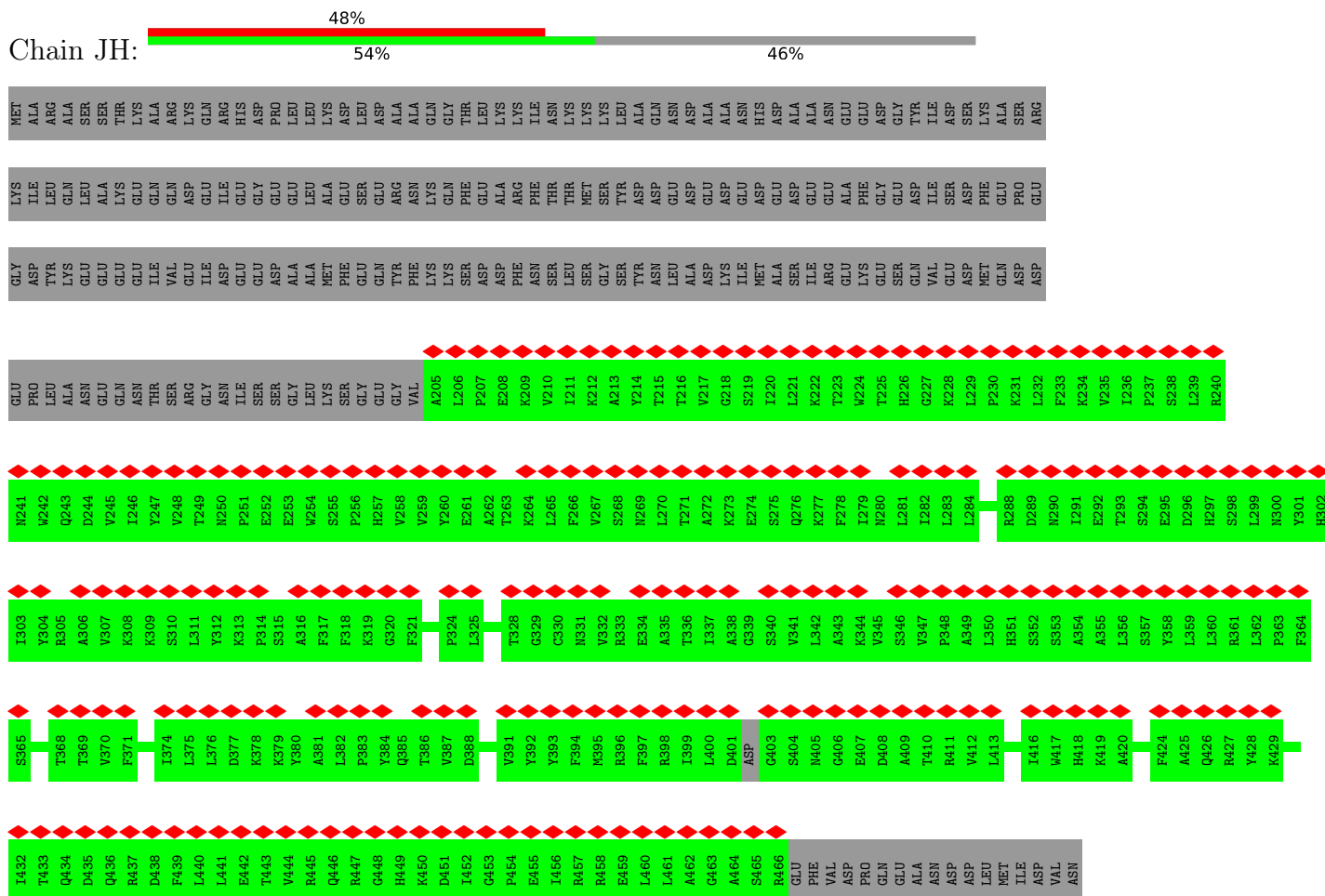
- Molecule 34: Ribosomal RNA small subunit methyltransferase NEP1

Chain JG:



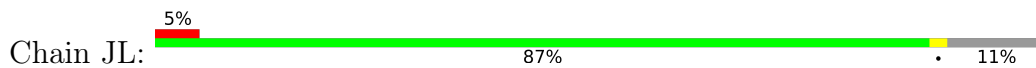
- Molecule 35: Essential nuclear protein 1

Chain JH:

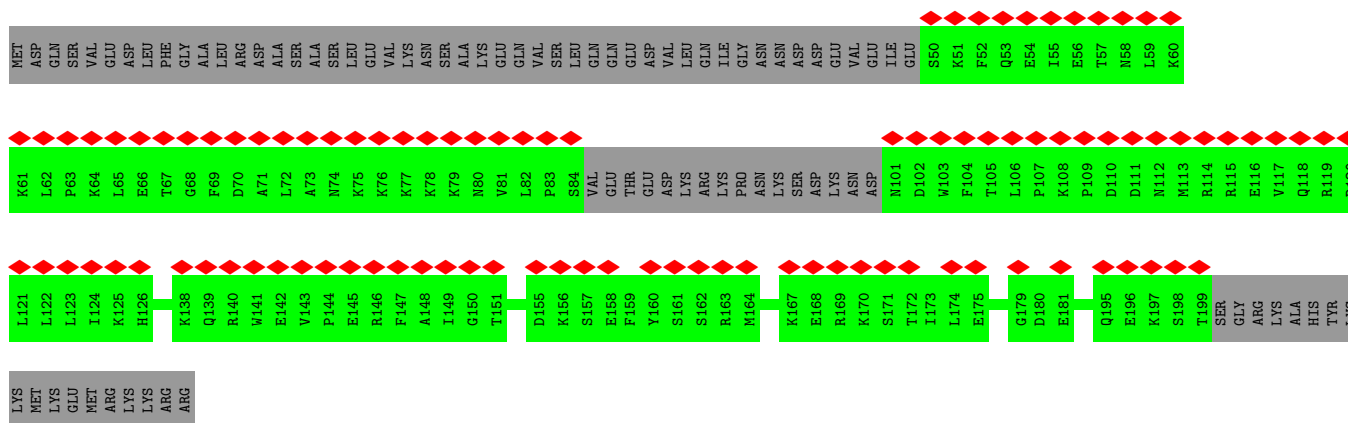


- Molecule 36: Dimethyladenosine transferase

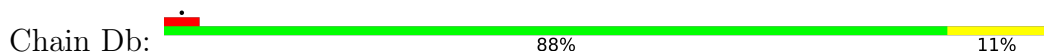
Chain JL:



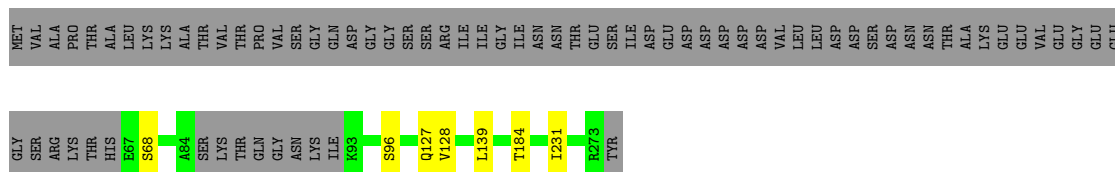
- Molecule 37: rRNA-processing protein FCF2



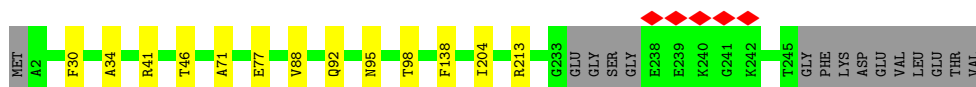
- Molecule 38: 40S ribosomal protein S27-A



- Molecule 39: Pre-rRNA-processing protein PNO1

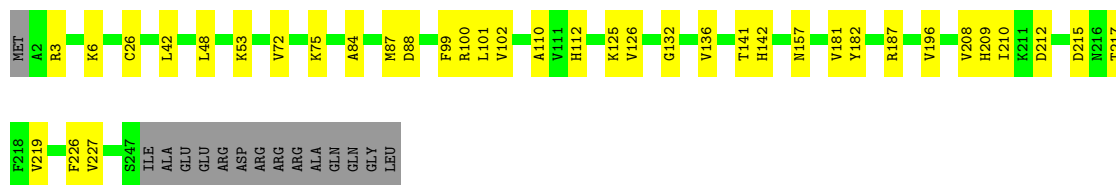


- Molecule 40: 40S ribosomal protein S1-A



- Molecule 41: 40S ribosomal protein S4-A

Chain DE:  80% 14% 6%



- Molecule 42: 40S ribosomal protein S5

Chain DF:  92% 5%



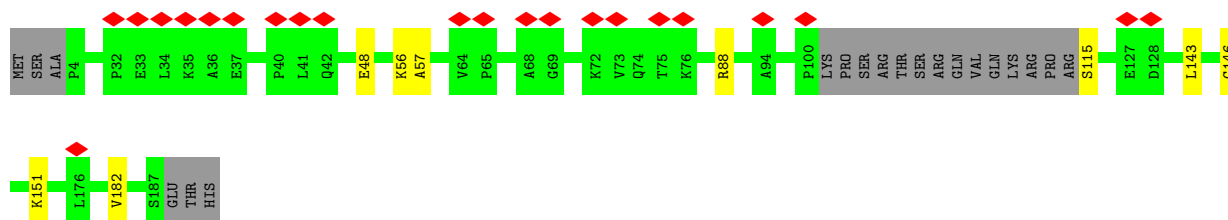
- Molecule 43: 40S ribosomal protein S6-A

Chain DG:  83% 9% 8%



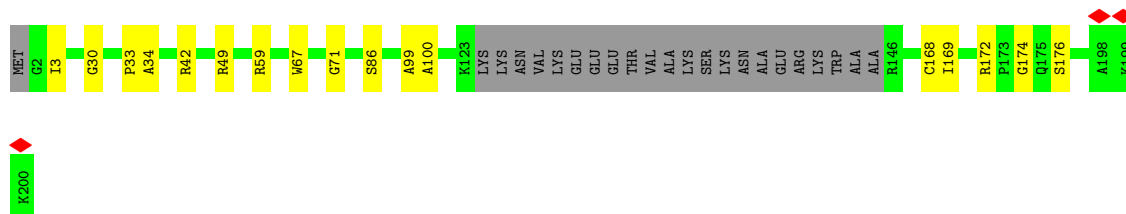
- Molecule 44: 40S ribosomal protein S7-A

Chain DH:  12% 85% 5% 11%



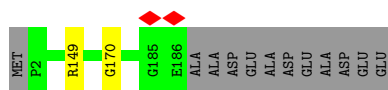
- Molecule 45: 40S ribosomal protein S8-A

Chain DI:  80% 8% 12%

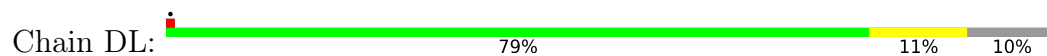


- Molecule 46: 40S ribosomal protein S9-A

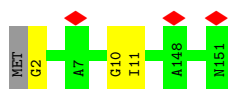
Chain DJ:  93% 6%



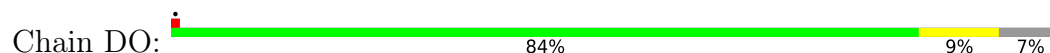
- Molecule 47: 40S ribosomal protein S11-A



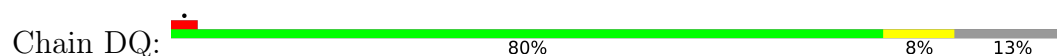
- Molecule 48: 40S ribosomal protein S13



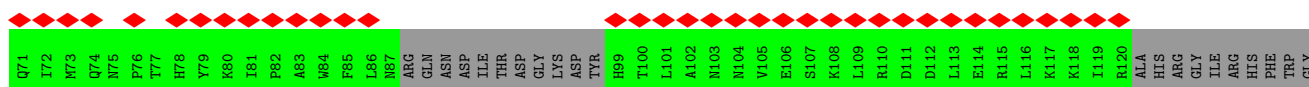
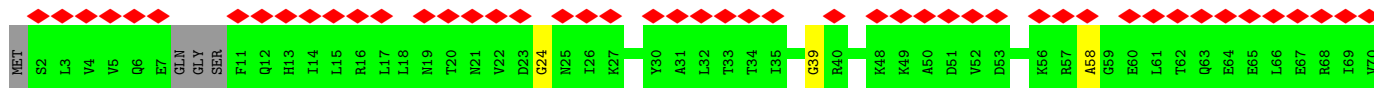
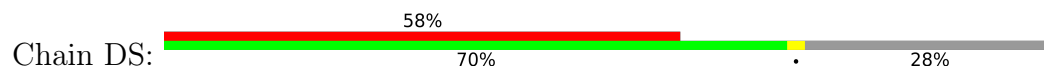
- Molecule 49: 40S ribosomal protein S14-A



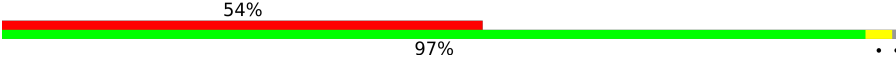
- Molecule 50: 40S ribosomal protein S16-A

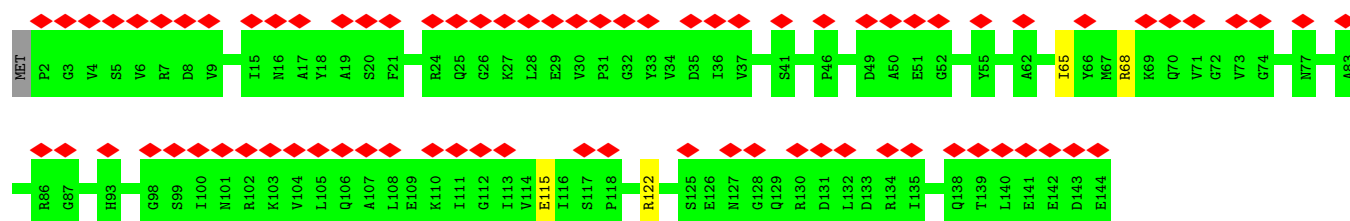


- Molecule 51: 40S ribosomal protein S18-A

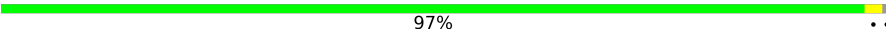


- Molecule 52: 40S ribosomal protein S19-A

Chain DT: 

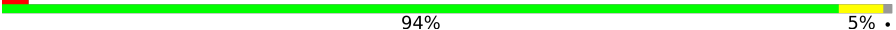


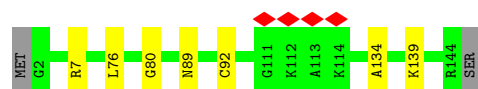
- Molecule 53: 40S ribosomal protein S22-A

Chain DW: 



- Molecule 54: 40S ribosomal protein S23-A

Chain DX: 



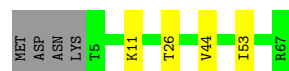
- Molecule 55: 40S ribosomal protein S24-A

Chain DY: 



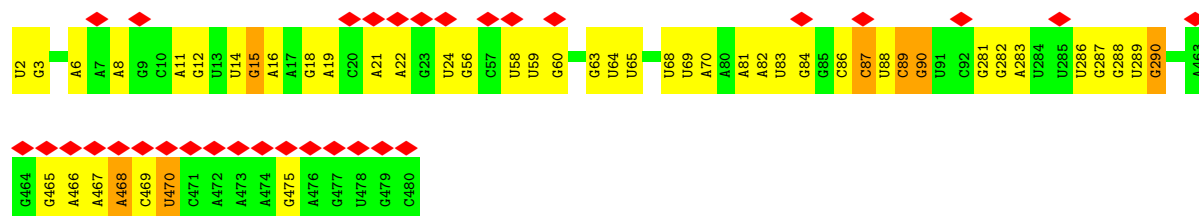
- Molecule 56: 40S ribosomal protein S28-A

Chain Dc: 



- Molecule 57: 5ETS RNA

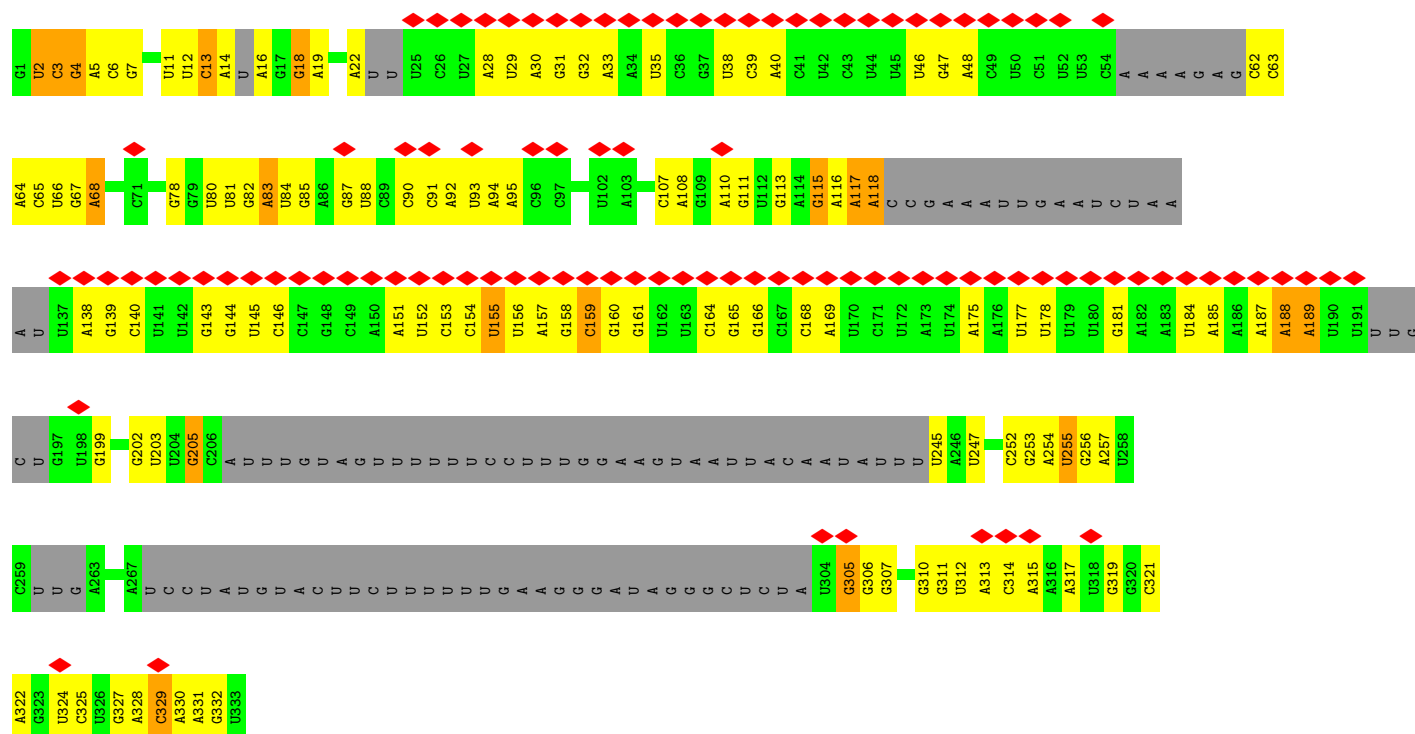
Chain D2: 



- Molecule 58: 18S rRNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11312	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.036	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	508.32, 508.32, 508.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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	UA	0.31	0/3913	0.67	0/5447
2	UB	0.28	0/2745	0.71	4/3822 (0.1%)
3	UC	0.25	0/419	0.56	0/578
4	UD	0.24	0/3275	0.64	0/4556
5	UE	0.27	0/436	0.51	0/607
6	UH	0.30	0/2358	0.89	13/3265 (0.4%)
7	UI	0.24	0/2348	0.62	0/3266
8	UJ	0.25	0/5555	0.59	0/7747
9	UK	0.29	0/1087	0.63	0/1514
10	UL	0.30	0/3839	0.66	0/5337
11	UM	0.27	0/3757	0.65	0/5222
12	UN	0.18	0/70	0.59	0/94
13	UO	0.24	0/2439	0.62	1/3397 (0.0%)
14	UP	0.25	0/297	0.48	0/413
15	UQ	0.22	0/4057	0.58	0/5649
16	UR	0.22	0/2368	0.61	2/3289 (0.1%)
17	US	0.33	0/2459	0.72	5/3433 (0.1%)
18	UT	0.26	0/5415	0.60	0/7559
19	UU	0.26	0/4324	0.66	4/6010 (0.1%)
20	UV	0.23	0/5436	0.58	2/7572 (0.0%)
21	UX	0.28	0/825	0.64	0/1147
22	CA	0.26	0/1188	0.65	0/1648
22	CB	0.24	0/1120	0.56	1/1554 (0.1%)
23	CD	0.20	0/1878	0.51	0/2614
24	CE	0.23	0/2153	0.57	0/2999
25	CF	0.32	0/600	0.70	0/836
25	CG	0.32	0/600	0.71	0/836
26	CH	0.25	0/2299	0.63	0/3194
27	CI	0.27	0/869	0.61	0/1211
28	CJ	0.29	0/1266	0.67	0/1762
29	CK	0.25	0/1102	0.56	0/1534
30	CL	0.31	0/3989	0.66	0/5549

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	CM	0.32	0/1766	0.62	0/2451
32	CN	0.21	0/1046	0.54	0/1456
33	JD	0.26	0/4001	0.66	0/5563
34	JF	0.22	0/1069	0.59	2/1488 (0.1%)
34	JG	0.21	0/1139	0.53	0/1586
35	JH	0.24	0/1293	0.57	0/1801
36	JL	0.24	0/1400	0.56	0/1950
37	JM	0.26	0/665	0.63	0/926
38	Db	0.30	0/399	0.60	0/554
39	JJ	0.28	0/980	0.60	0/1361
40	DA	0.29	0/1185	0.61	0/1648
41	DE	0.35	0/1206	0.71	1/1673 (0.1%)
42	DF	0.28	0/1054	0.61	0/1468
43	DG	0.30	0/1072	0.56	0/1489
44	DH	0.30	0/841	0.65	0/1170
45	DI	0.30	0/867	0.59	0/1201
46	DJ	0.30	0/914	0.61	0/1272
47	DL	0.32	0/691	0.67	0/961
48	DN	0.28	0/741	0.52	0/1031
49	DO	0.28	0/619	0.63	0/856
50	DQ	0.30	0/615	0.67	0/854
51	DS	0.20	0/518	0.58	0/718
52	DT	0.21	0/699	0.54	0/968
53	DW	0.29	0/633	0.64	0/878
54	DX	0.32	0/698	0.69	0/966
55	DY	0.33	0/660	0.58	0/917
56	Dc	0.28	0/309	0.58	0/428
57	D2	0.19	0/1946	0.41	0/3024
58	D3	0.32	0/34494	0.48	4/53725 (0.0%)
59	D4	0.20	0/5267	0.40	0/8178
All	All	0.28	0/143273	0.58	39/206222 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	UD	0	1
11	UM	0	2
15	UQ	0	1
18	UT	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
21	UX	0	1
23	CD	0	1
25	CF	0	1
25	CG	0	1
33	JD	0	2
45	DI	0	1
All	All	0	13

There are no bond length outliers.

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	UU	246	ILE	CA-C-N	12.24	135.14	119.84
19	UU	246	ILE	C-N-CA	12.24	135.14	119.84
2	UB	400	PRO	N-CA-CB	8.13	111.32	103.51
58	D3	1706	C	C4'-C3'-O3'	7.92	124.88	113.00
17	US	110	PRO	N-CA-CB	7.92	110.70	103.34

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	UD	353	GLU	Peptide
11	UM	218	ASP	Peptide
11	UM	400	GLY	Peptide
15	UQ	146	HIS	Peptide
18	UT	706	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	UA	3916	0	1763	42	0
2	UB	2754	0	1194	3	0
3	UC	421	0	187	1	0
4	UD	3280	0	1410	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	UE	437	0	181	0	0
6	UH	2372	0	989	7	0
7	UI	2353	0	1028	7	0
8	UJ	5567	0	2408	10	0
9	UK	1090	0	458	5	0
10	UL	3846	0	1712	47	0
11	UM	3763	0	1687	36	0
12	UN	71	0	38	1	0
13	UO	2441	0	1083	22	0
14	UP	298	0	122	0	0
15	UQ	4062	0	1723	14	0
16	UR	2372	0	1043	11	0
17	US	2462	0	1051	5	0
18	UT	5419	0	2305	14	0
19	UU	4328	0	1933	26	0
20	UV	5442	0	2336	13	0
21	UX	827	0	364	2	0
22	CA	1190	0	547	4	0
22	CB	1122	0	514	4	0
23	CD	1880	0	871	1	0
24	CE	2155	0	1051	5	0
25	CF	601	0	289	0	0
25	CG	601	0	289	2	0
26	CH	2302	0	1031	10	0
27	CI	871	0	364	4	0
28	CJ	1268	0	566	14	0
29	CK	1106	0	487	2	0
30	CL	3995	0	1769	40	0
31	CM	1767	0	795	15	0
32	CN	1049	0	457	3	0
33	JD	4010	0	1748	22	0
34	JF	1071	0	467	5	0
34	JG	1141	0	500	2	0
35	JH	1295	0	570	0	0
36	JL	1401	0	604	3	0
37	JM	667	0	281	0	0
38	Db	400	0	179	5	0
39	JJ	982	0	435	5	0
40	DA	1187	0	531	7	0
41	DE	1207	0	541	21	0
42	DF	1055	0	496	4	0
43	DG	1073	0	488	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	DH	843	0	373	5	0
45	DI	869	0	421	10	0
46	DJ	915	0	422	2	0
47	DL	692	0	300	11	0
48	DN	742	0	345	3	0
49	DO	620	0	311	6	0
50	DQ	616	0	285	6	0
51	DS	521	0	224	2	0
52	DT	700	0	334	3	0
53	DW	634	0	289	3	0
54	DX	699	0	322	4	0
55	DY	661	0	312	5	0
56	Dc	310	0	134	2	0
57	D2	1741	0	876	37	0
58	D3	30846	0	15532	896	0
59	D4	4723	0	2398	101	0
60	Db	1	0	0	0	0
60	UX	1	0	0	0	0
All	All	139051	0	63763	1507	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1507 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:UR:382:GLY:HA3	16:UR:400:ILE:O	1.25	1.32
11:UM:30:LYS:HA	11:UM:45:LEU:O	1.28	1.29
13:UO:191:GLY:HA3	13:UO:211:HIS:O	1.20	1.28
28:CJ:150:THR:HA	28:CJ:167:LEU:O	1.34	1.24
1:UA:77:GLY:HA3	1:UA:95:PHE:O	1.08	1.22

There are no symmetry-related clashes.

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	UA	786/923 (85%)	728 (93%)	58 (7%)	0	100	100
2	UB	535/810 (66%)	505 (94%)	28 (5%)	2 (0%)	30	67
3	UC	82/610 (13%)	76 (93%)	6 (7%)	0	100	100
4	UD	653/776 (84%)	609 (93%)	44 (7%)	0	100	100
5	UE	86/575 (15%)	85 (99%)	1 (1%)	0	100	100
6	UH	451/713 (63%)	376 (83%)	51 (11%)	24 (5%)	1	15
7	UI	465/643 (72%)	439 (94%)	26 (6%)	0	100	100
8	UJ	1093/1769 (62%)	1038 (95%)	55 (5%)	0	100	100
9	UK	213/250 (85%)	201 (94%)	12 (6%)	0	100	100
10	UL	764/943 (81%)	712 (93%)	52 (7%)	0	100	100
11	UM	750/817 (92%)	682 (91%)	68 (9%)	0	100	100
12	UN	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
13	UO	489/513 (95%)	458 (94%)	31 (6%)	0	100	100
14	UP	58/214 (27%)	56 (97%)	2 (3%)	0	100	100
15	UQ	810/896 (90%)	749 (92%)	61 (8%)	0	100	100
16	UR	473/594 (80%)	446 (94%)	27 (6%)	0	100	100
17	US	488/552 (88%)	453 (93%)	33 (7%)	2 (0%)	30	67
18	UT	1081/2493 (43%)	1006 (93%)	74 (7%)	1 (0%)	48	83
19	UU	870/939 (93%)	806 (93%)	62 (7%)	2 (0%)	43	78
20	UV	1086/1237 (88%)	1054 (97%)	32 (3%)	0	100	100
21	UX	163/189 (86%)	152 (93%)	11 (7%)	0	100	100
22	CA	238/327 (73%)	224 (94%)	14 (6%)	0	100	100
22	CB	224/327 (68%)	214 (96%)	10 (4%)	0	100	100
23	CD	376/504 (75%)	364 (97%)	11 (3%)	1 (0%)	36	72
24	CE	431/511 (84%)	409 (95%)	22 (5%)	0	100	100
25	CF	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	CG	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
26	CH	461/573 (80%)	421 (91%)	40 (9%)	0	100	100
27	CI	171/183 (93%)	160 (94%)	11 (6%)	0	100	100
28	CJ	252/290 (87%)	228 (90%)	24 (10%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	CK	214/593 (36%)	207 (97%)	7 (3%)	0	100	100
30	CL	796/1183 (67%)	748 (94%)	48 (6%)	0	100	100
31	CM	358/367 (98%)	347 (97%)	10 (3%)	1 (0%)	36	72
32	CN	205/297 (69%)	195 (95%)	10 (5%)	0	100	100
33	JD	792/1267 (62%)	720 (91%)	69 (9%)	3 (0%)	30	67
34	JF	212/252 (84%)	206 (97%)	6 (3%)	0	100	100
34	JG	226/252 (90%)	215 (95%)	11 (5%)	0	100	100
35	JH	257/483 (53%)	248 (96%)	9 (4%)	0	100	100
36	JL	281/318 (88%)	270 (96%)	11 (4%)	0	100	100
37	JM	130/217 (60%)	124 (95%)	6 (5%)	0	100	100
38	Db	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
39	JJ	195/274 (71%)	190 (97%)	5 (3%)	0	100	100
40	DA	236/255 (92%)	215 (91%)	21 (9%)	0	100	100
41	DE	244/261 (94%)	224 (92%)	20 (8%)	0	100	100
42	DF	211/225 (94%)	193 (92%)	18 (8%)	0	100	100
43	DG	216/236 (92%)	208 (96%)	8 (4%)	0	100	100
44	DH	166/190 (87%)	158 (95%)	8 (5%)	0	100	100
45	DI	173/200 (86%)	169 (98%)	4 (2%)	0	100	100
46	DJ	183/197 (93%)	171 (93%)	12 (7%)	0	100	100
47	DL	138/156 (88%)	133 (96%)	5 (4%)	0	100	100
48	DN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
49	DO	125/137 (91%)	117 (94%)	8 (6%)	0	100	100
50	DQ	123/143 (86%)	115 (94%)	8 (6%)	0	100	100
51	DS	99/146 (68%)	94 (95%)	5 (5%)	0	100	100
52	DT	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
53	DW	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
54	DX	141/145 (97%)	129 (92%)	12 (8%)	0	100	100
55	DY	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
56	Dc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
All	All	20209/27941 (72%)	18926 (94%)	1247 (6%)	36 (0%)	44	78

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	UH	59	PRO
6	UH	61	PRO
6	UH	68	PRO
6	UH	127	TYR
6	UH	235	PRO

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
57	D2	76/81 (93%)	25 (32%)	0
58	D3	1434/1802 (79%)	488 (34%)	29 (2%)
59	D4	214/333 (64%)	57 (26%)	3 (1%)
All	All	1724/2216 (77%)	570 (33%)	32 (1%)

5 of 570 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
57	D2	6	A
57	D2	8	A
57	D2	11	A
57	D2	12	G
57	D2	14	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	D3	1781	A
59	D4	143	G
58	D3	721	U
58	D3	720	G
59	D4	156	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 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 [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
57	D2	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D2	92:C	O3'	281:G	P	62.93
1	D2	292:A	O3'	463:A	P	44.88
1	D2	70:A	O3'	80:A	P	19.25
1	D2	24:U	O3'	56:G	P	15.48

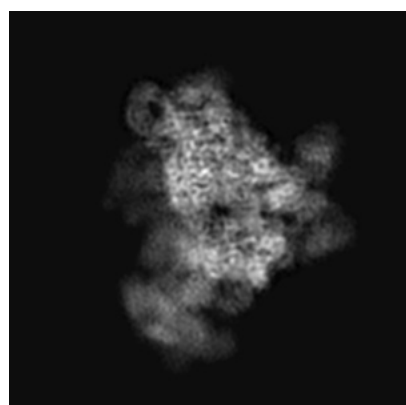
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11361. These allow visual inspection of the internal detail of the map and identification of artifacts.

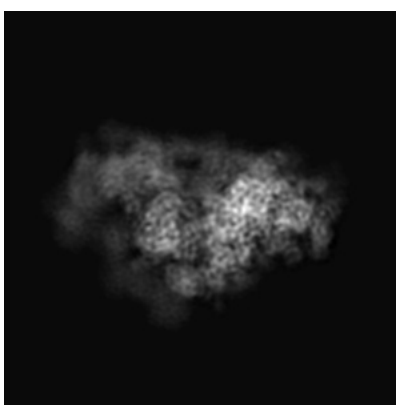
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

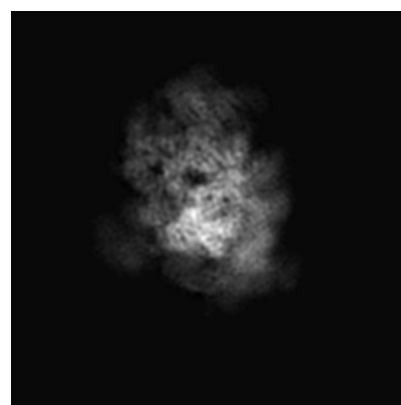
6.1.1 Primary map



X



Y

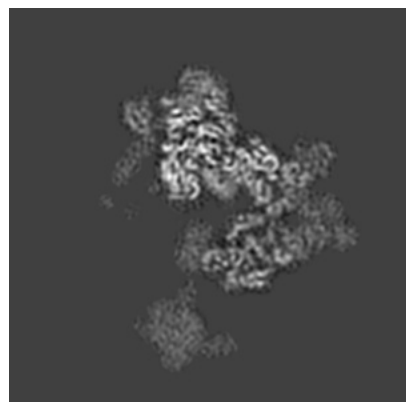


Z

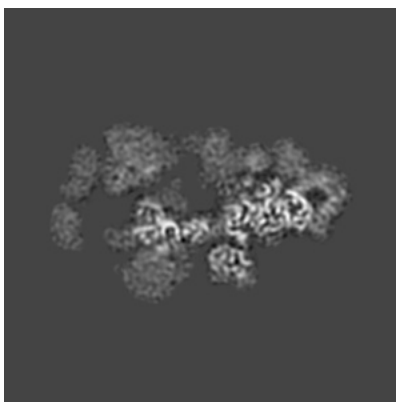
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

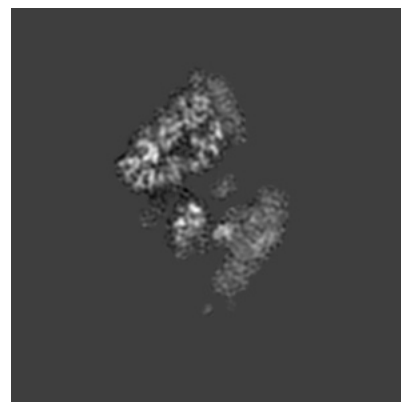
6.2.1 Primary map



X Index: 240



Y Index: 240

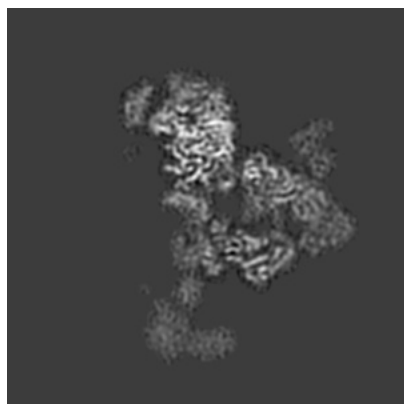


Z Index: 240

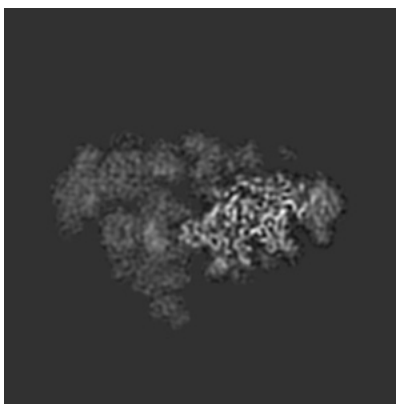
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

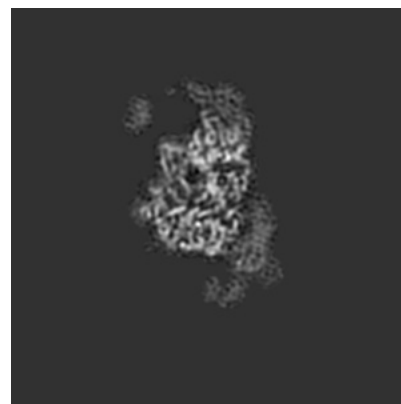
6.3.1 Primary map



X Index: 226



Y Index: 222

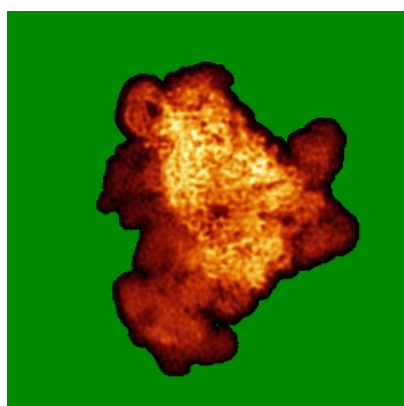


Z Index: 287

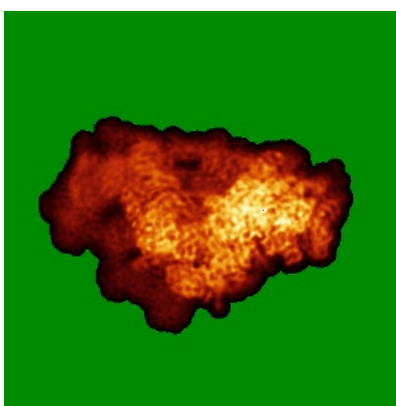
The images above show the largest variance slices of the map in three orthogonal directions.

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

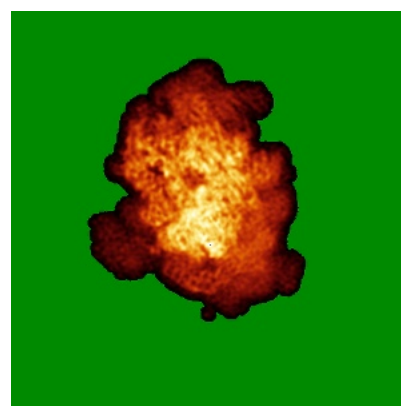
6.4.1 Primary map



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 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

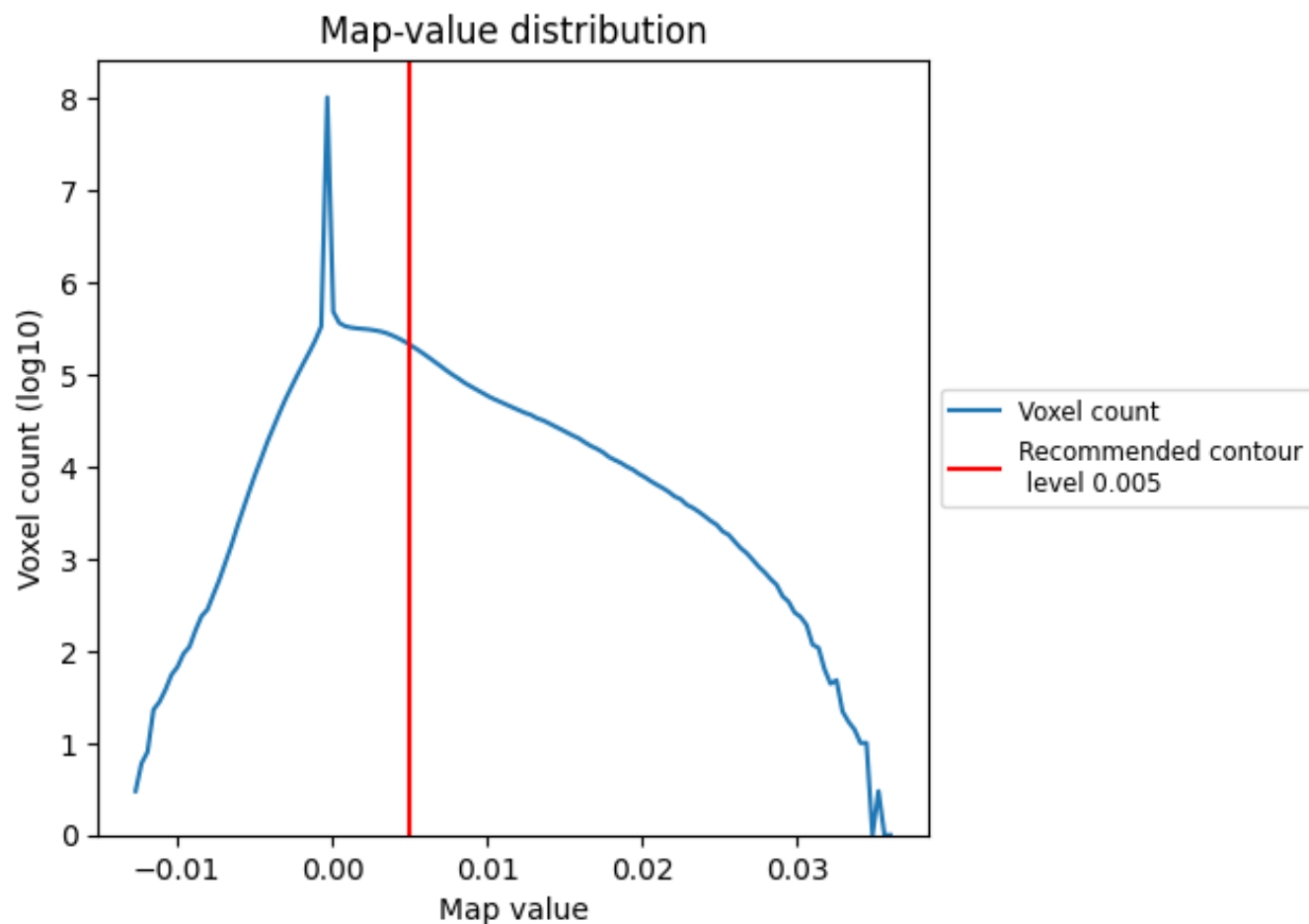
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

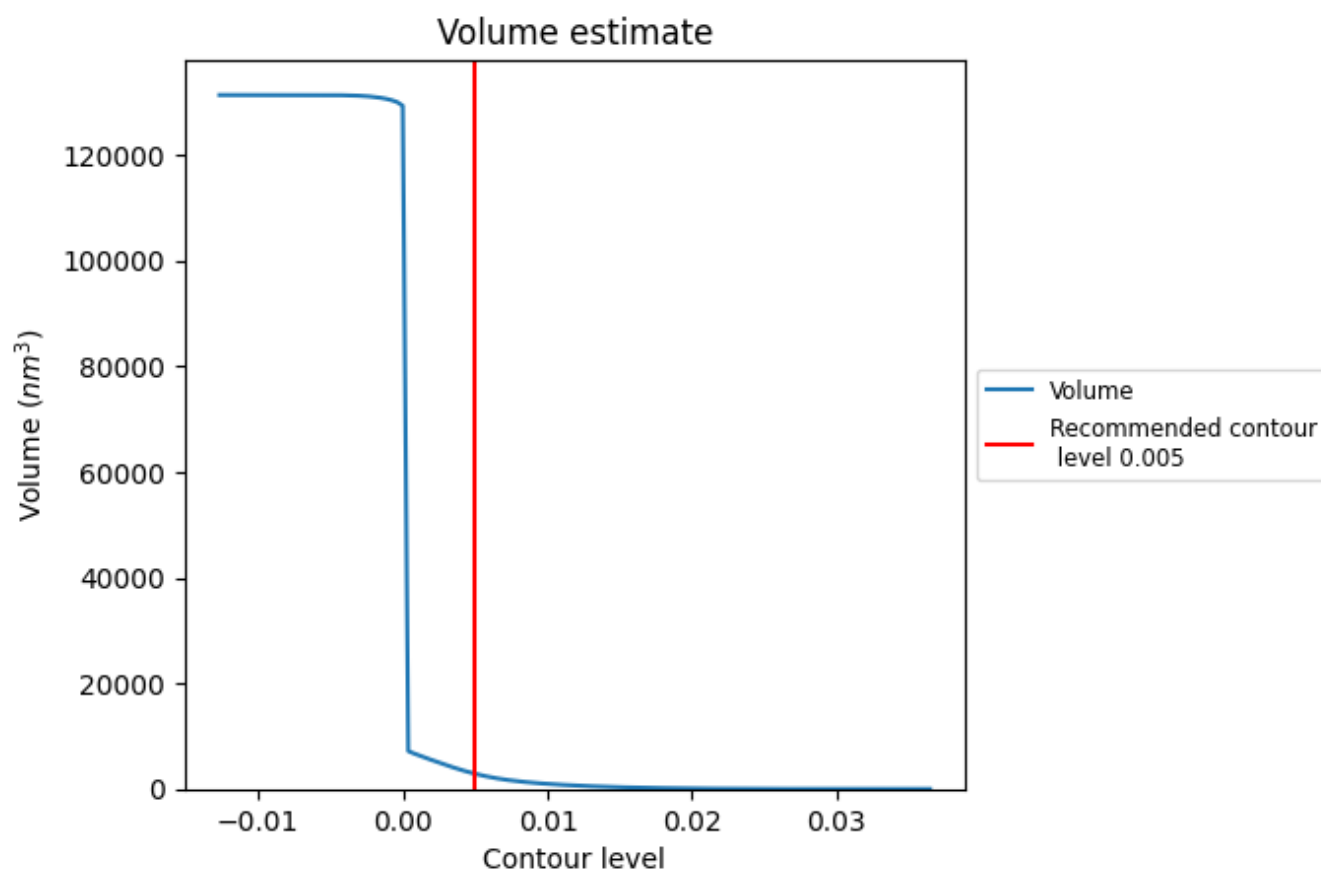
This section contains the results of statistical analysis of the map.

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.

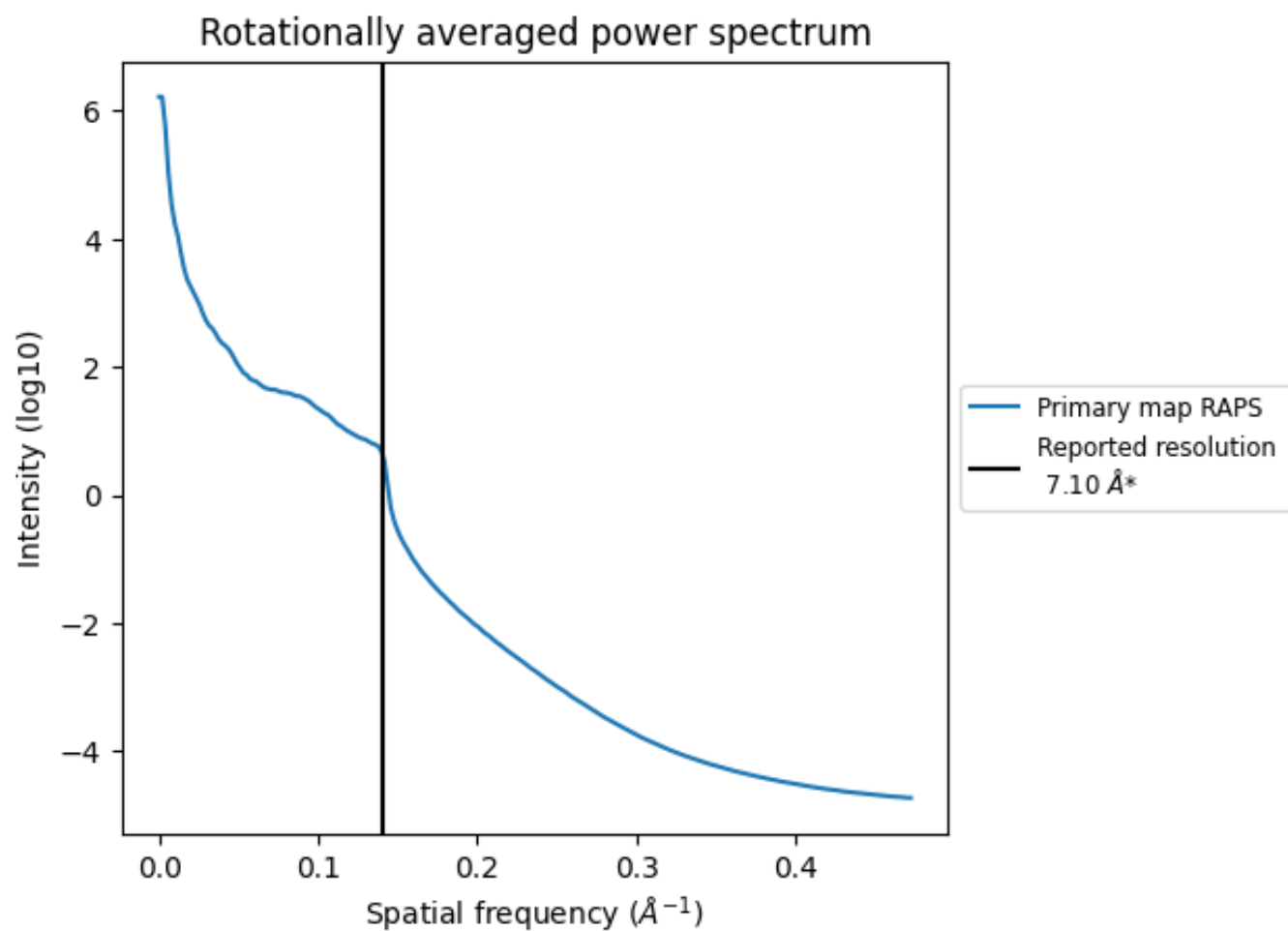
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2869 nm³; this corresponds to an approximate mass of 2592 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 ⓘ

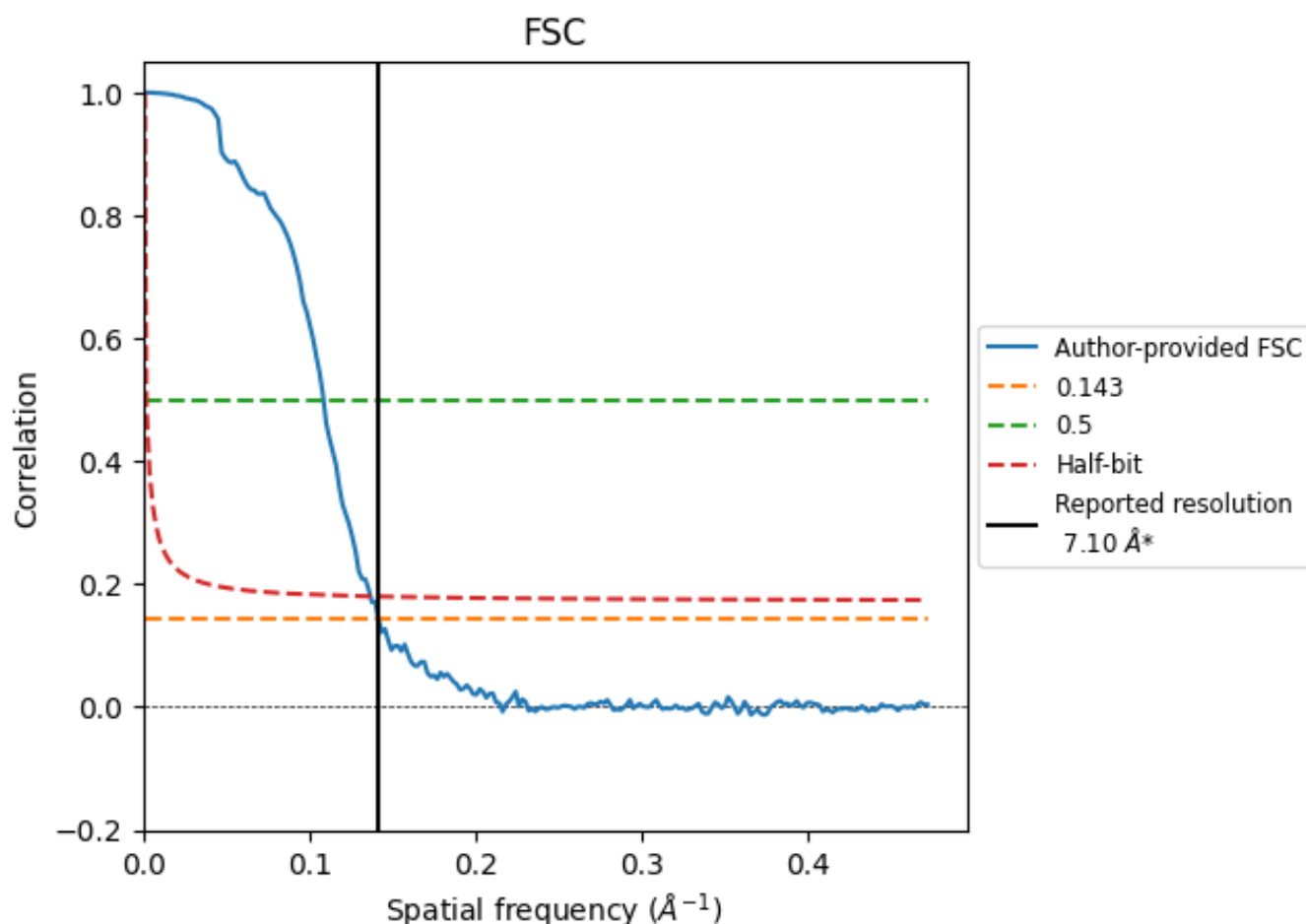


*Reported resolution corresponds to spatial frequency of 0.141 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.141 Å⁻¹

8.2 Resolution estimates [i](#)

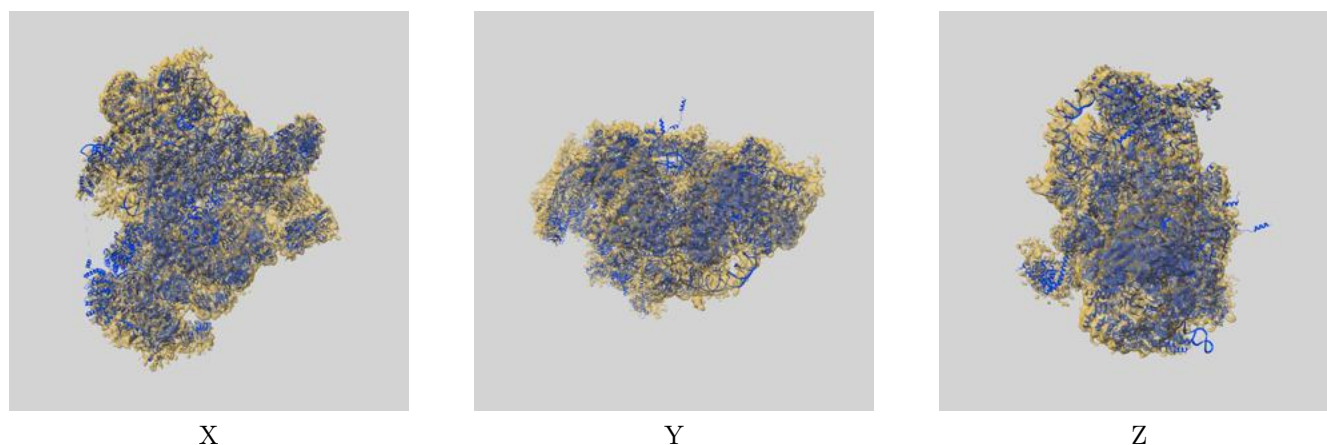
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.10	-	-
Author-provided FSC curve	7.06	9.21	7.31
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11361 and PDB model 6ZQE. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



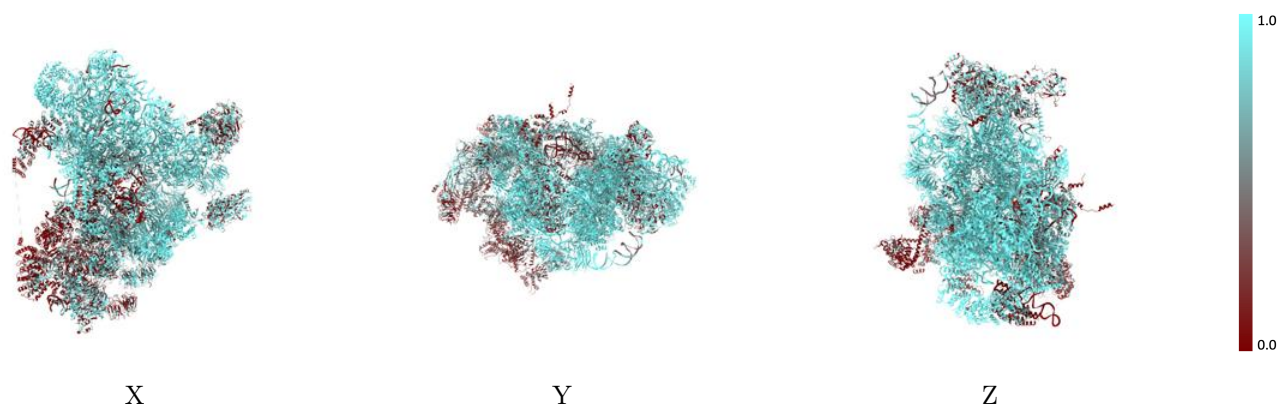
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



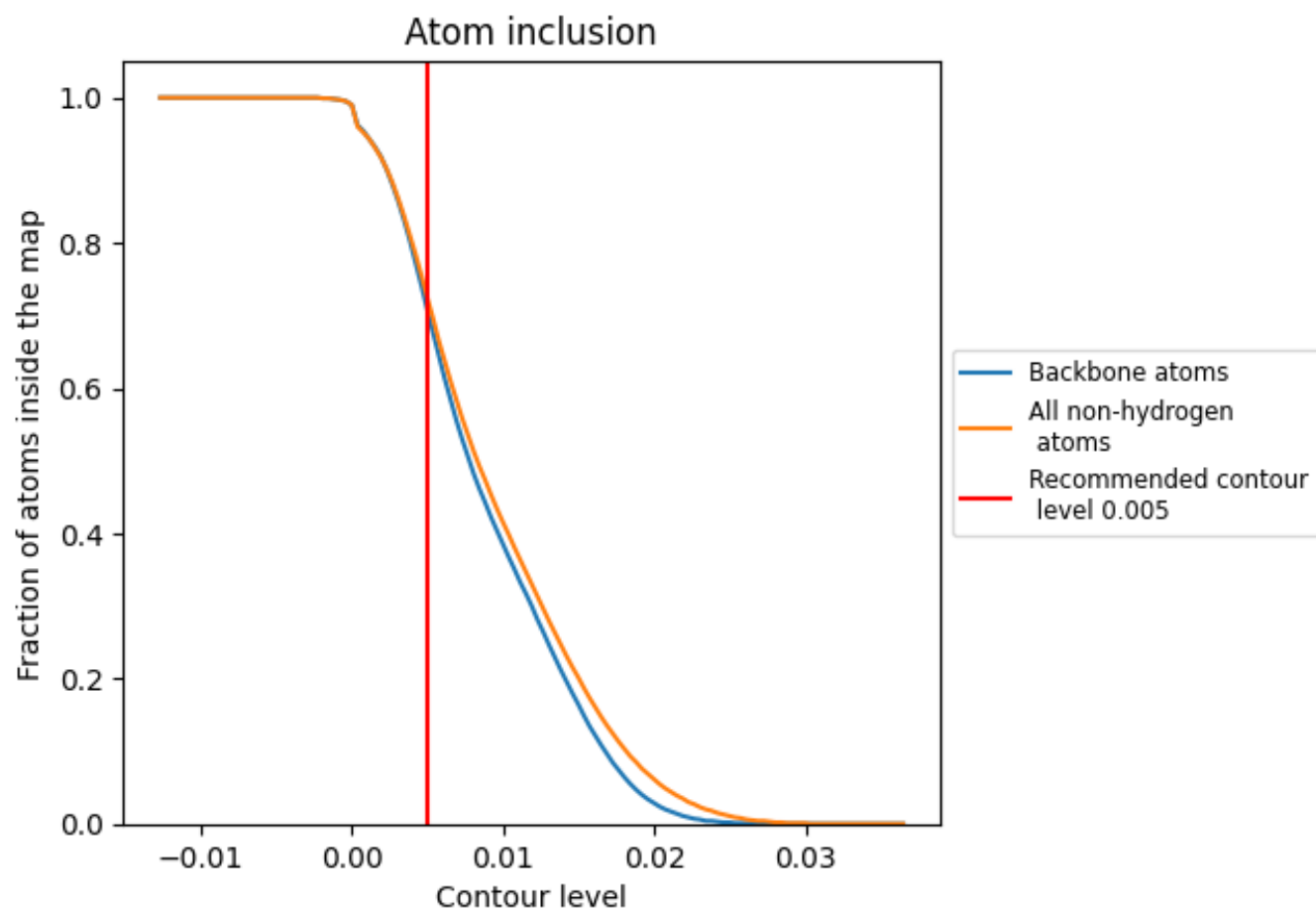
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion ⓘ



At the recommended contour level, 71% of all backbone atoms, 72% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.1560
CA	 0.5220	 0.1380
CB	 0.2380	 0.0330
CD	 0.7640	 0.1470
CE	 0.5320	 0.0740
CF	 0.5460	 0.1030
CG	 0.7600	 0.1950
CH	 0.8460	 0.1680
CI	 0.8140	 0.1660
CJ	 0.8320	 0.2000
CK	 0.9710	 0.2540
CL	 0.8890	 0.2370
CM	 0.9900	 0.2520
CN	 0.5320	 0.1560
D2	 0.4810	 0.0410
D3	 0.9290	 0.2040
D4	 0.4880	 0.0760
DA	 0.9740	 0.2680
DE	 0.9900	 0.2810
DF	 0.9600	 0.2430
DG	 0.9940	 0.2460
DH	 0.8490	 0.1400
DI	 0.9780	 0.2410
DJ	 0.9800	 0.2600
DL	 0.9810	 0.2610
DN	 0.9780	 0.2600
DO	 0.9900	 0.2380
DQ	 0.9450	 0.2030
DS	 0.2070	 0.0630
DT	 0.4540	 0.0750
DW	 0.9870	 0.2470
DX	 0.9510	 0.2510
DY	 0.9860	 0.2710
Db	 0.9650	 0.2250
Dc	 0.9970	 0.2860



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
JD	 0.6420	 0.1390
JF	 0.1760	 0.0400
JG	 0.4970	 0.0620
JH	 0.1200	 0.0050
JJ	 0.9910	 0.2550
JL	 0.9210	 0.1980
JM	 0.2670	 0.0590
UA	 0.9550	 0.2120
UB	 0.1660	 0.0250
UC	 0.6220	 0.2200
UD	 0.5070	 0.0520
UE	 0.3870	 -0.0000
UH	 0.2430	 0.0310
UI	 0.5290	 0.0700
UJ	 0.3290	 0.0840
UK	 0.1450	 0.0480
UL	 0.9910	 0.2380
UM	 0.9810	 0.2160
UN	 0.9010	 0.0490
UO	 0.4550	 0.0720
UP	 0.0000	 -0.0320
UQ	 0.5870	 0.0210
UR	 0.6290	 0.0600
US	 0.0800	 0.0080
UT	 0.9610	 0.2330
UU	 0.9100	 0.1650
UV	 0.5520	 0.1750
UX	 0.4600	 0.1600