



wwPDB EM Validation Summary Report ⓘ

Dec 7, 2022 – 09:46 AM JST

PDB ID : 5H4P
EMDB ID : EMD-9569
Title : Structural snapshot of cytoplasmic pre-60S ribosomal particles bound with Nmd3, Lsg1, Tif6 and Reh1
Authors : Ma, C.; Wu, S.; Li, N.; Chen, Y.; Yan, K.; Li, Z.; Zheng, L.; Lei, J.; Woolford, J.L.; Gao, N.
Deposited on : 2016-11-01
Resolution : 3.07 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:

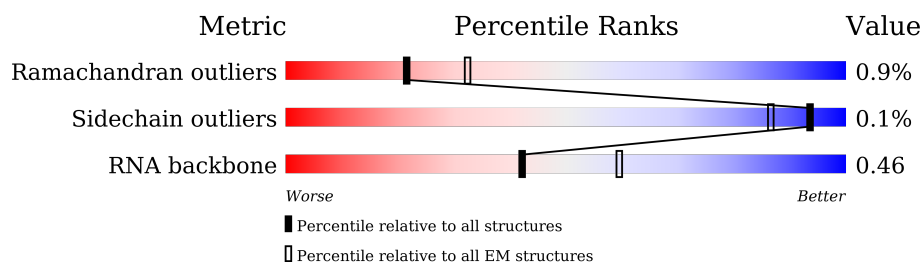
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.07 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 $\leq 5\%$. 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	1	3396	<div> <div>44%</div> <div>68%</div> <div>22%</div> <div>9%</div> </div>
2	3	121	<div> <div>77%</div> <div>83%</div> <div>17%</div> </div>
3	4	158	<div> <div>40%</div> <div>75%</div> <div>25%</div> </div>
4	A	246	<div> <div>59%</div> <div>100%</div> </div>
5	B	387	<div> <div>60%</div> <div>98%</div> </div>
6	C	361	<div> <div>73%</div> <div>99%</div> </div>
7	D	297	<div> <div>93%</div> <div>98%</div> </div>
8	E	176	<div> <div>81%</div> <div>87%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
9	F	244	73% 91% 9%
10	G	256	70% 89% 9%
11	H	191	92% 99% .
12	J	174	96% 94% ..
13	L	199	71% 94% ..
14	M	138	82% 96% ..
15	N	204	65% 99% .
16	O	199	60% 97% ..
17	P	184	66% 99% ..
18	Q	186	83% 99% .
19	R	189	57% 81% 17%
20	S	172	87% 97% .
21	T	160	81% 99% ..
22	U	121	74% 81% 17%
23	V	137	64% 99% .
24	W	155	32% 41% 59%
25	X	142	57% 85% 15%
26	Y	127	73% 98% ..
27	Z	136	82% 97% ...
28	a	149	67% 97% ..
29	b	59	92% 98% .
30	c	105	81% 92% 8%
31	d	113	64% 95% ..
32	e	130	75% 96% ..
33	f	107	61% 99% .

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Mol	Chain	Length	Quality of chain
34	g	121	<div> <div>58%</div> <div>93%</div> <div>7%</div> </div>
35	h	120	<div> <div>68%</div> <div>97%</div> <div>..</div> </div>
36	i	100	<div> <div>93%</div> <div>97%</div> <div>..</div> </div>
37	j	88	<div> <div>60%</div> <div>99%</div> <div>.</div> </div>
38	k	78	<div> <div>91%</div> <div>99%</div> <div>.</div> </div>
39	l	51	<div> <div>75%</div> <div>96%</div> <div>..</div> </div>
40	o	106	<div> <div>69%</div> <div>90%</div> <div>10%</div> </div>
41	p	92	<div> <div>62%</div> <div>99%</div> <div>.</div> </div>
42	w	248	<div> <div>98%</div> <div>96%</div> <div>.</div> </div>
43	y	227	<div> <div>95%</div> <div>99%</div> <div>.</div> </div>
44	z	56	<div> <div>98%</div> <div>96%</div> <div>.</div> </div>

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 122929 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3091	Total	C	N	O	P	0	0
			66124	29535	11927	21571	3091		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	156	Total	C	N	O	S	0	0
			1258	781	265	212			

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	64	Total	C	N	O	S	0	0
			528	340	103	84	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 30 is a protein called 60S ribosomal protein L30.

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

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 40 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	95	Total	C	N	O	S	0	0
			765	481	154	125	5		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	248	Total	C	N	O	S	0	0
			1894	1208	318	361	7		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	227	Total	C	N	O	S	0	0
			1699	1054	296	342	7		

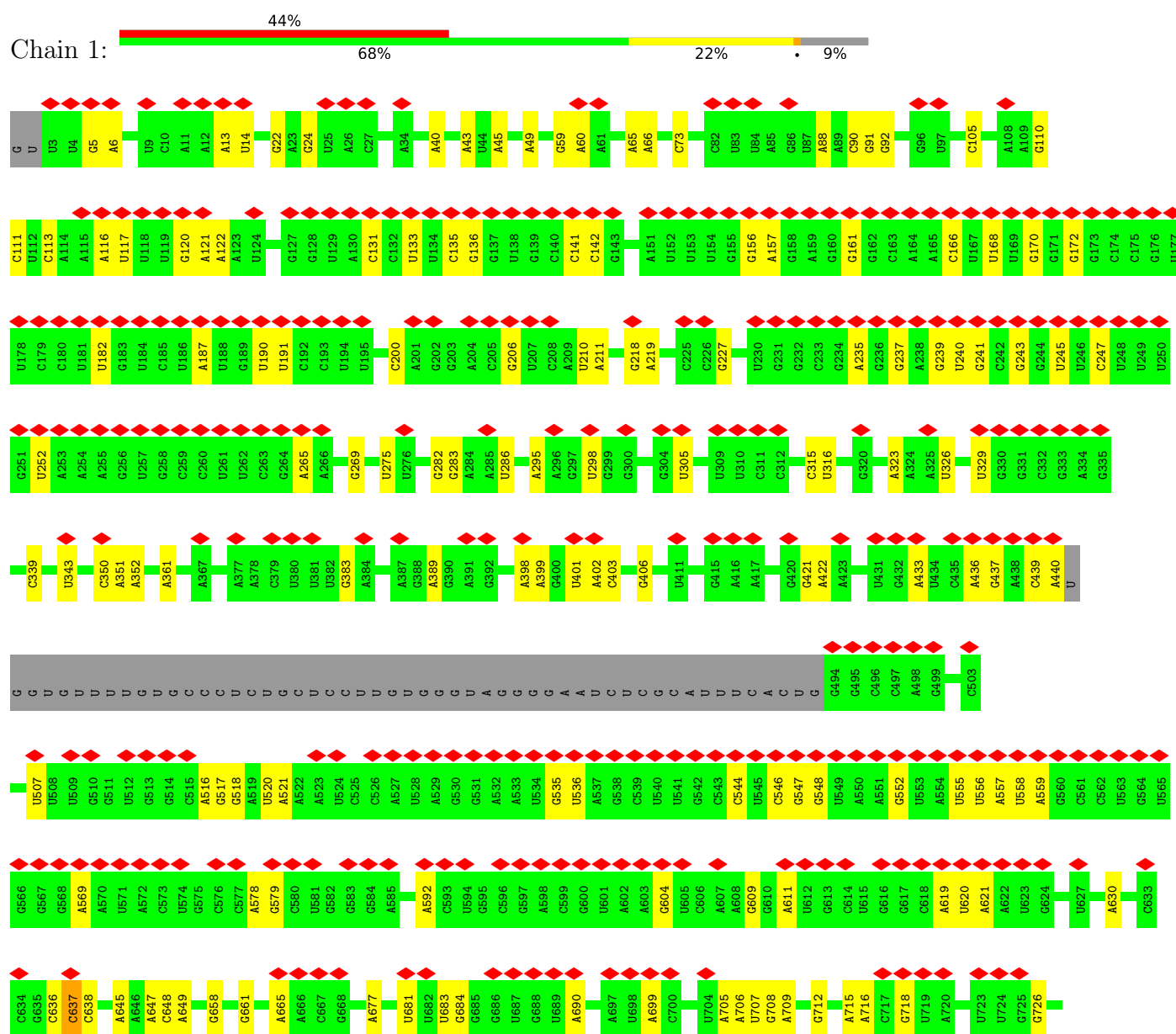
- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

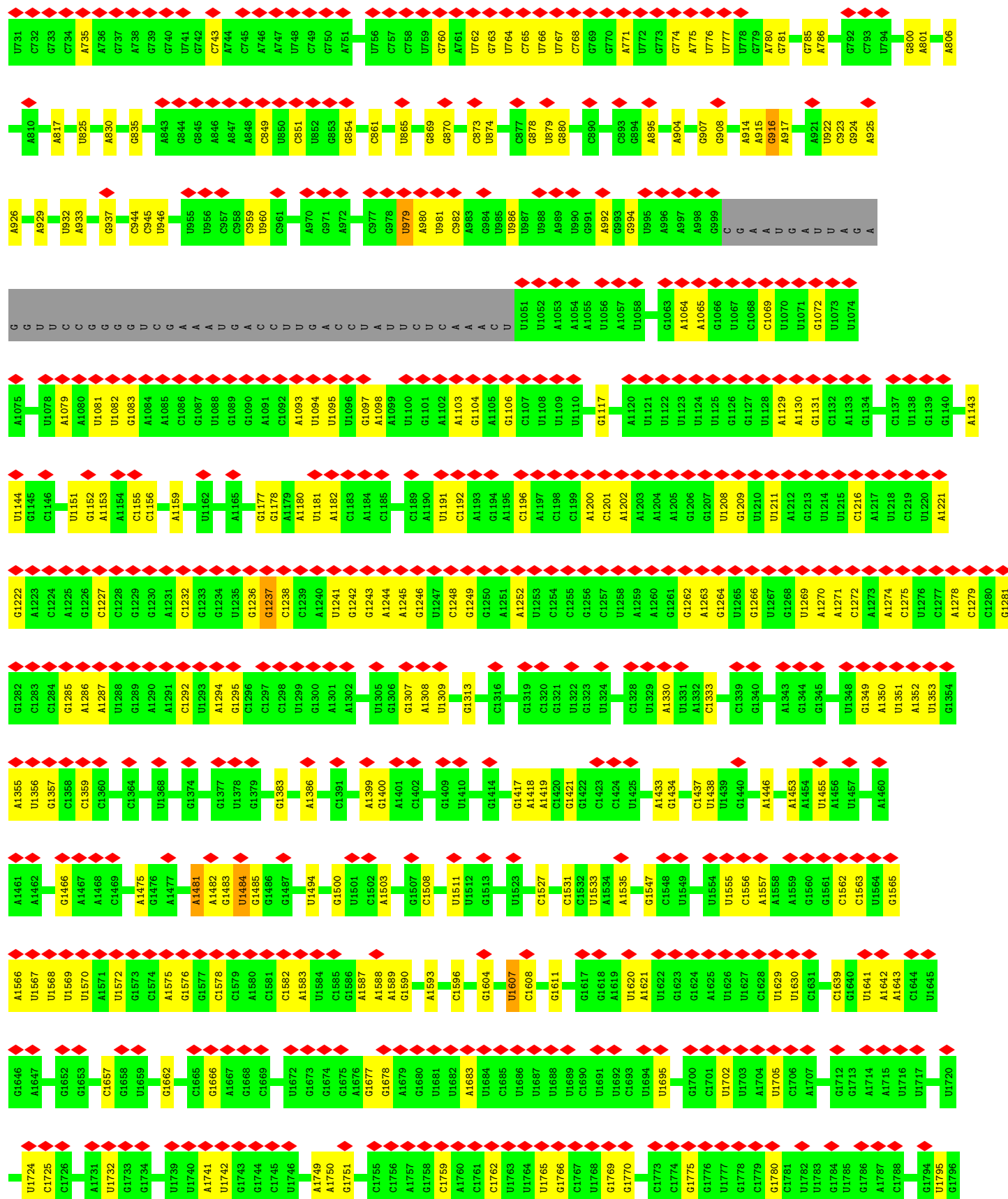
Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	56	Total	C	N	O	S	0	0
			469	289	92	85	3		

3 Residue-property plots

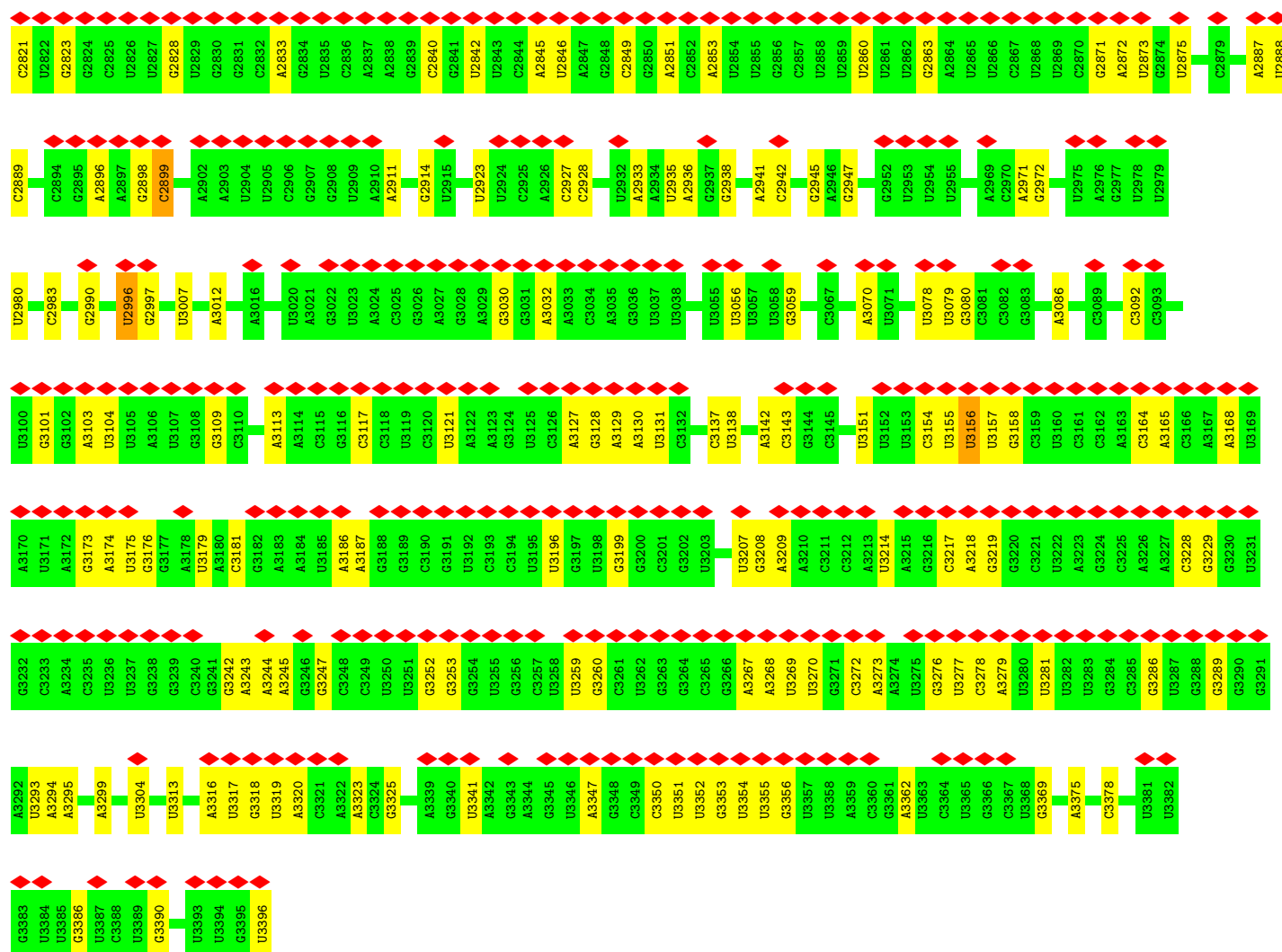
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

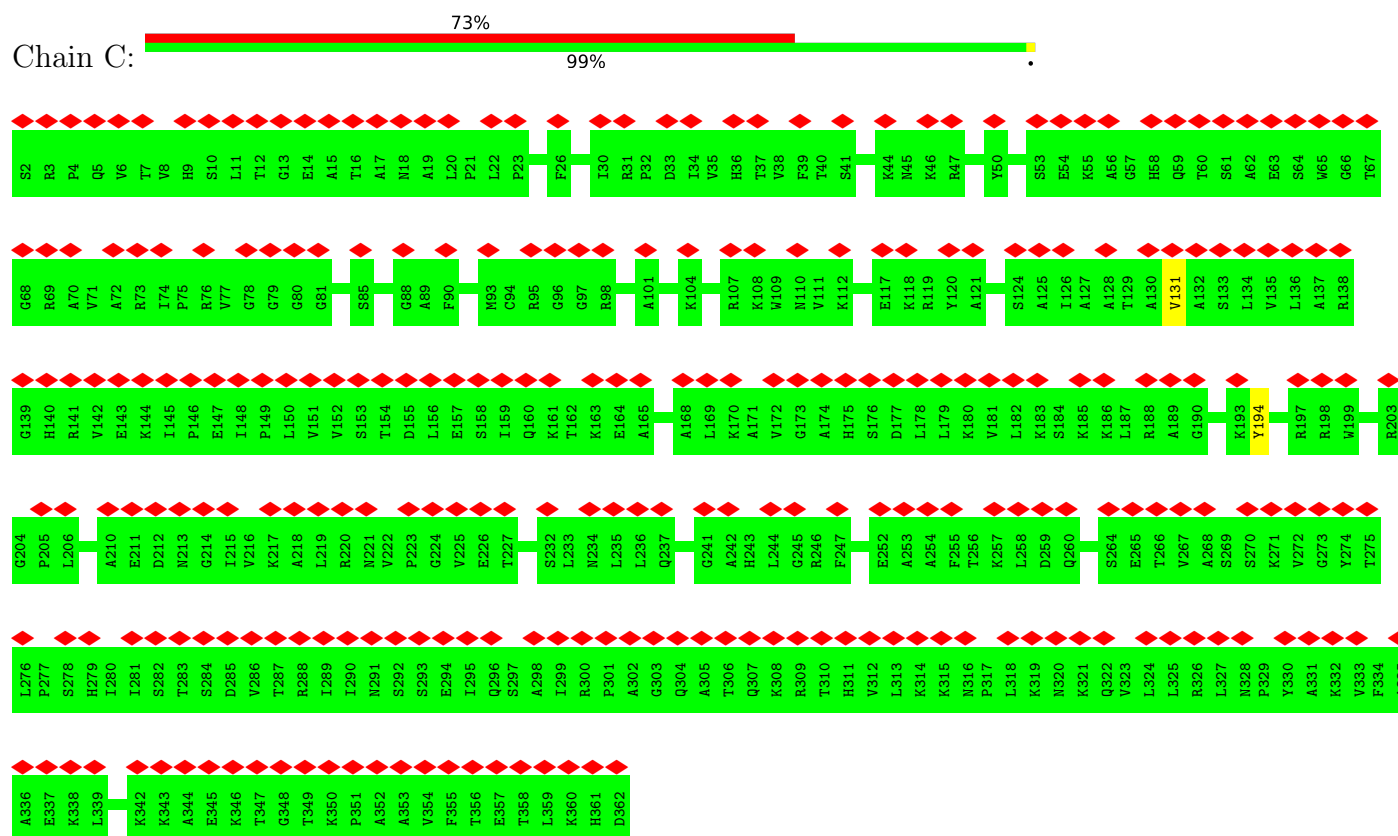
• Molecule 1: 25S ribosomal RNA



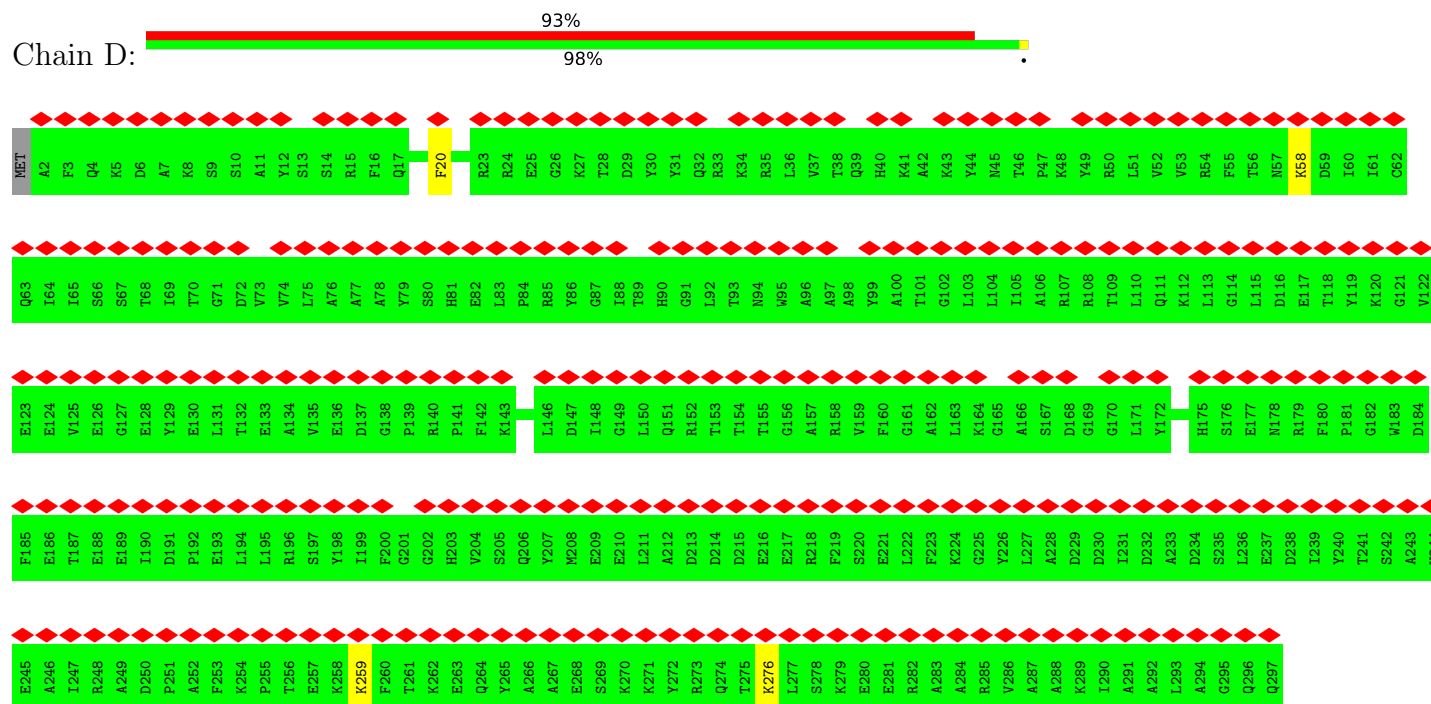




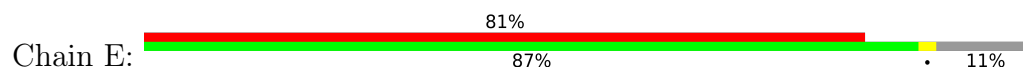


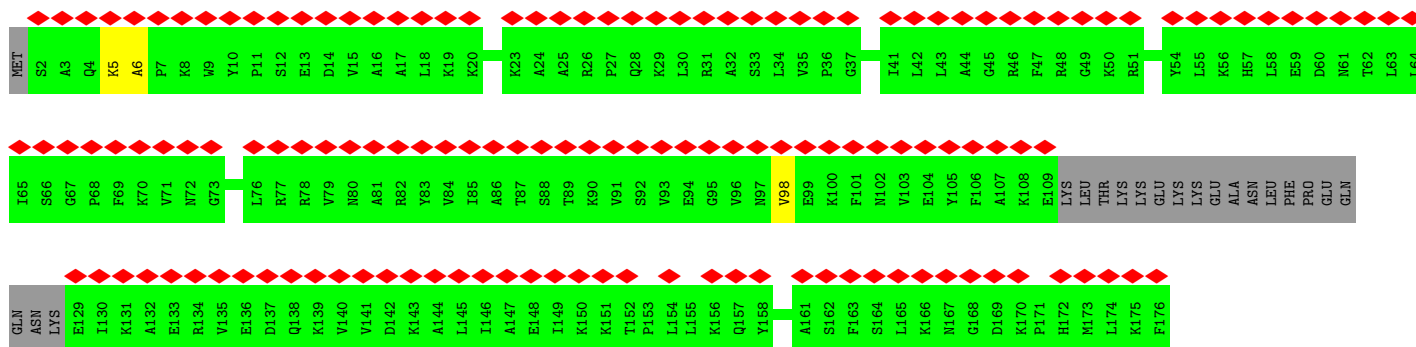


• Molecule 7: 60S ribosomal protein L5

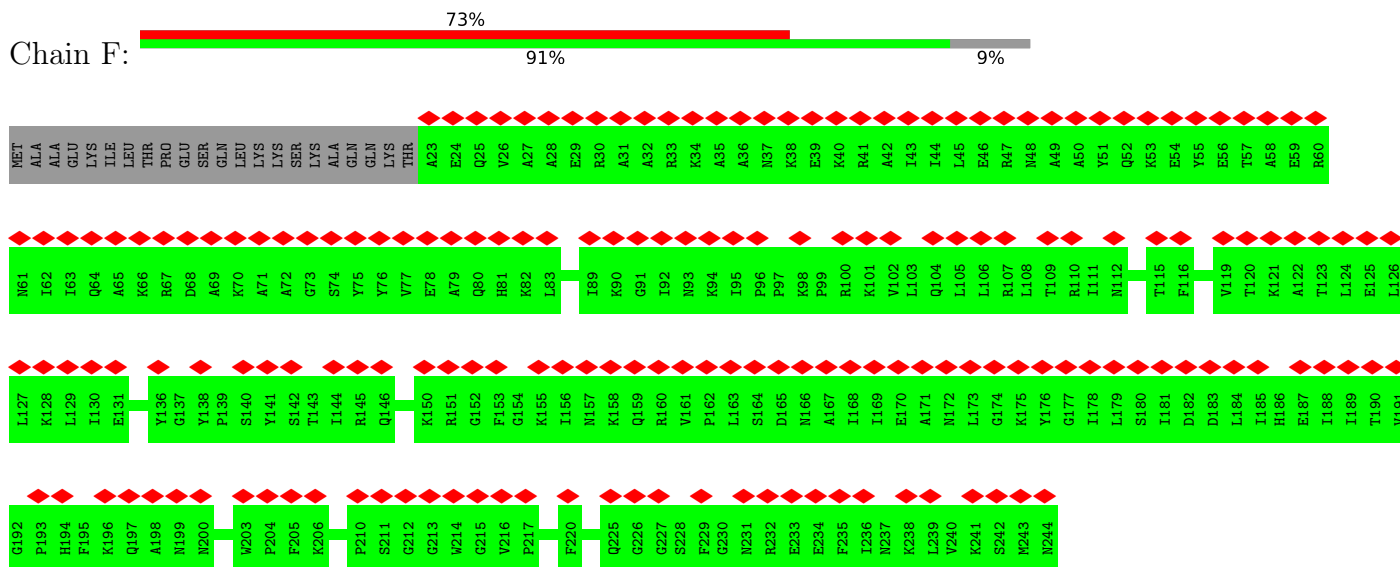


• Molecule 8: 60S ribosomal protein L6-A

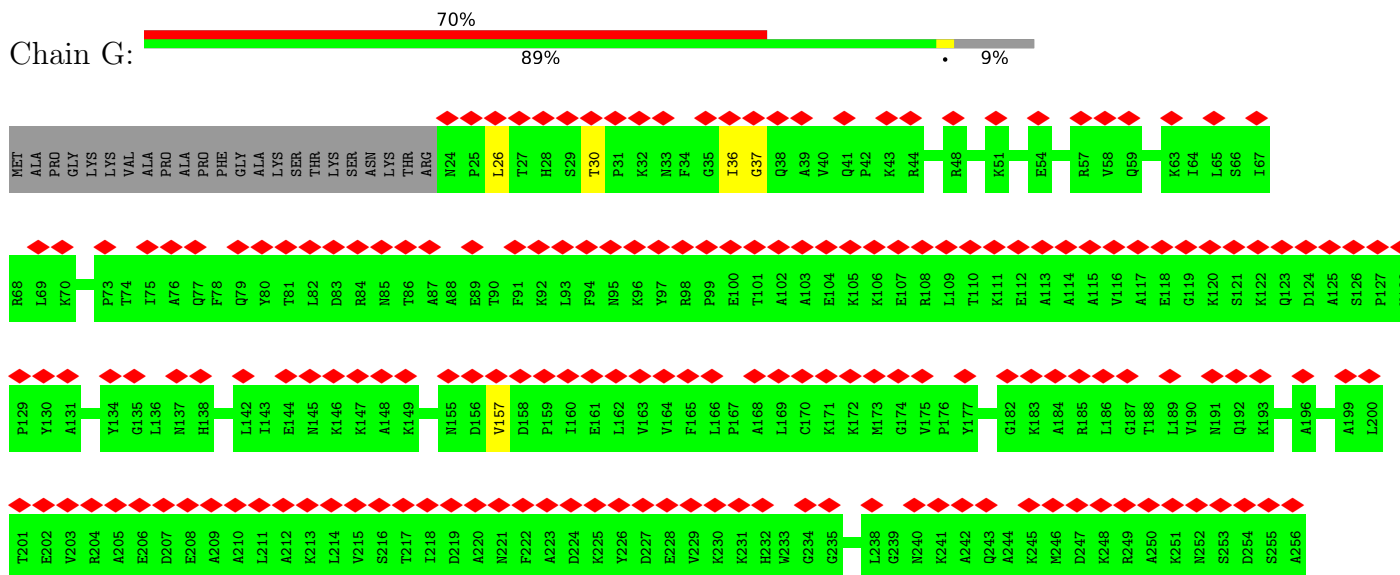




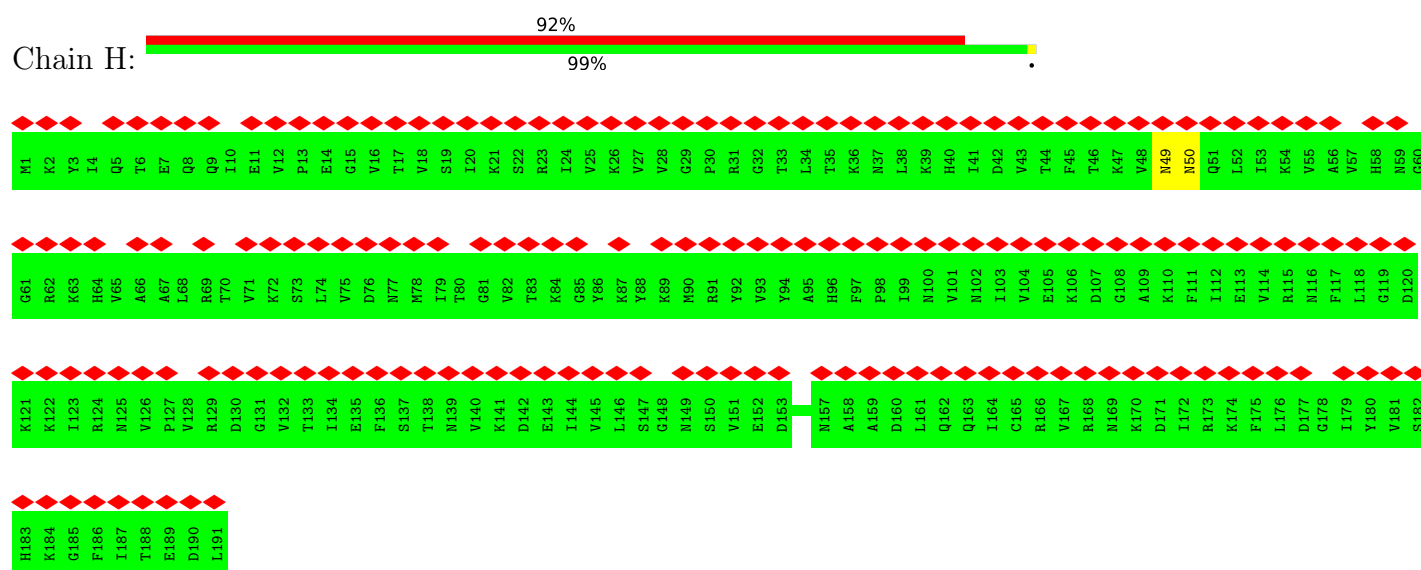
• Molecule 9: 60S ribosomal protein L7-A



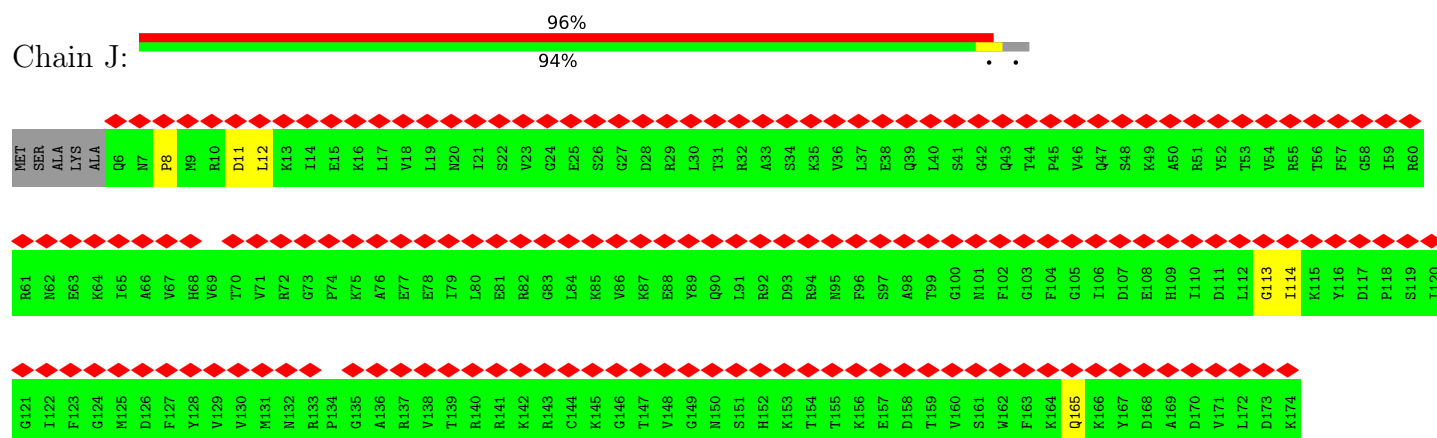
• Molecule 10: 60S ribosomal protein L8-A



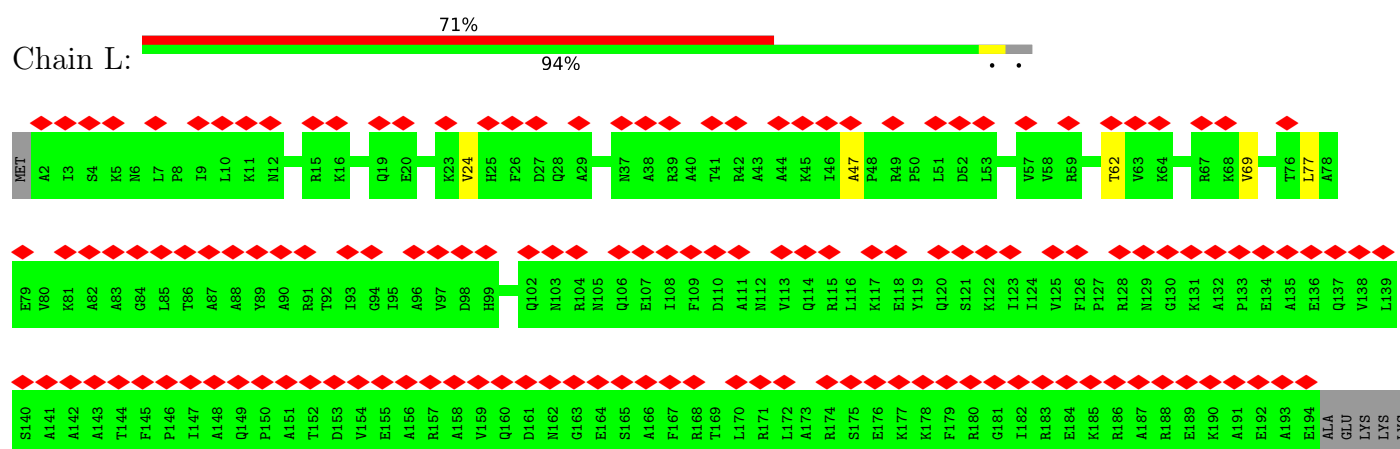
• Molecule 11: 60S ribosomal protein L9-A



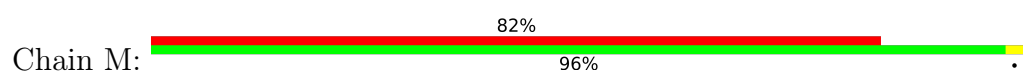
• Molecule 12: 60S ribosomal protein L11-A

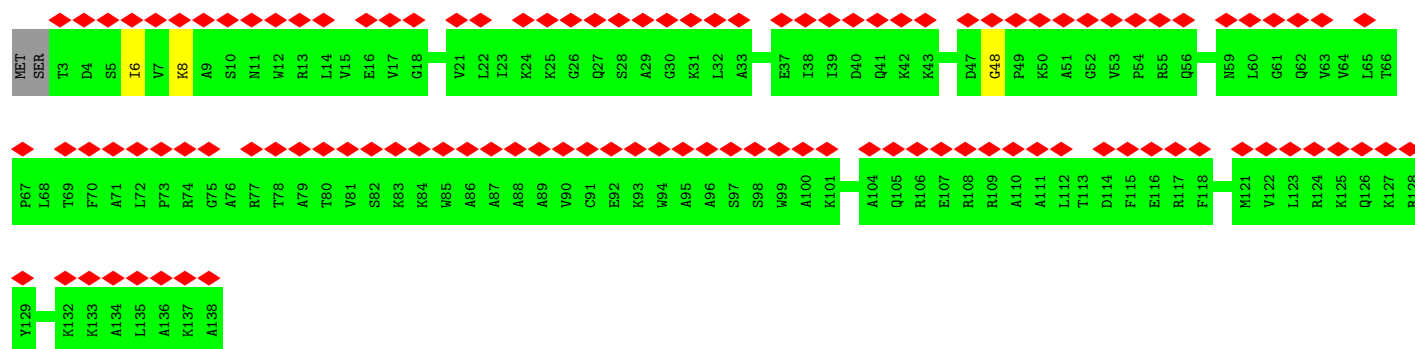


• Molecule 13: 60S ribosomal protein L13-A



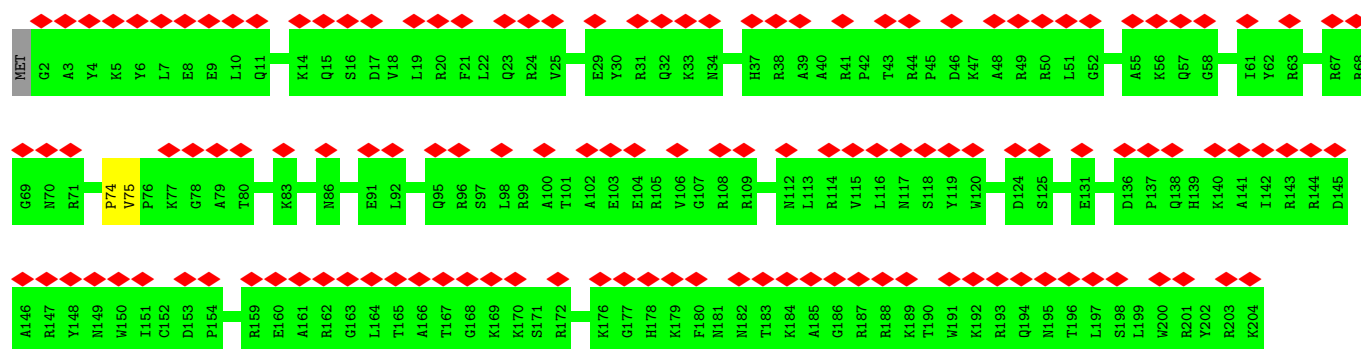
• Molecule 14: 60S ribosomal protein L14-A





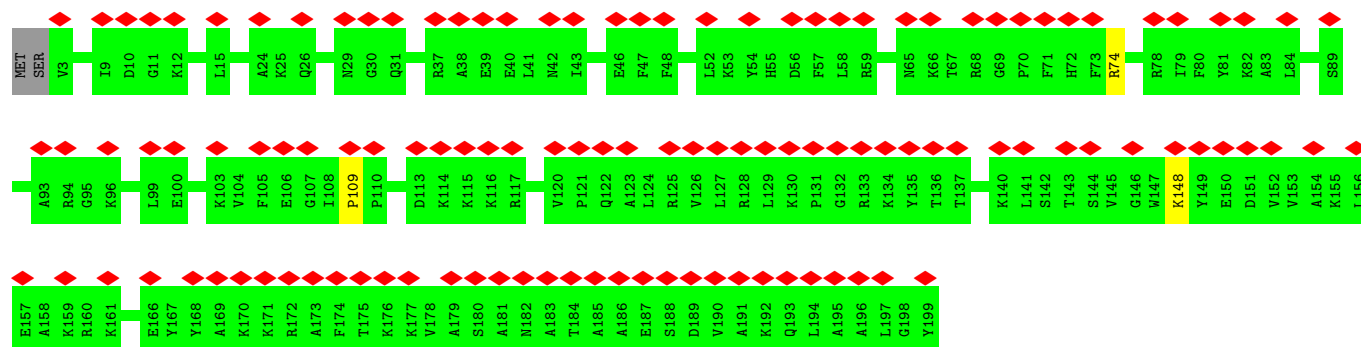
• Molecule 15: 60S ribosomal protein L15-A

Chain N: 65% 99%



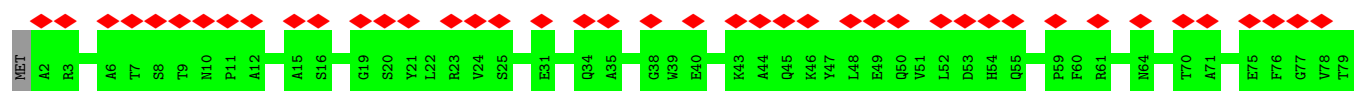
• Molecule 16: 60S ribosomal protein L16-A

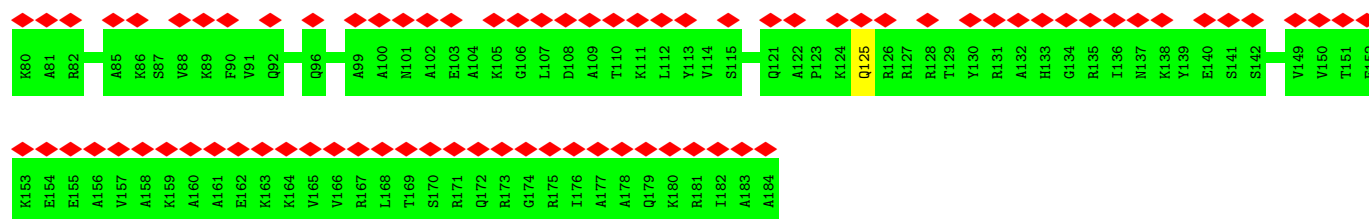
Chain O: 60% 97%



• Molecule 17: 60S ribosomal protein L17-A

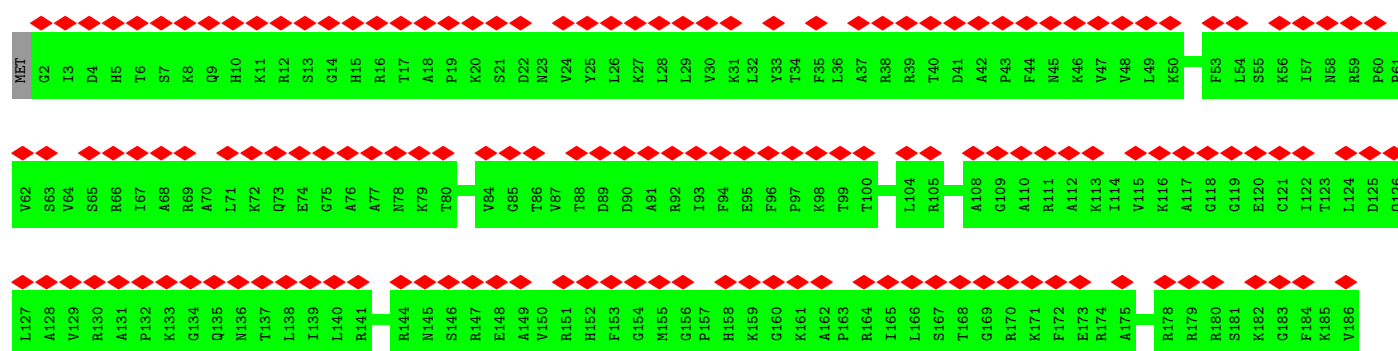
Chain P: 66% 99%





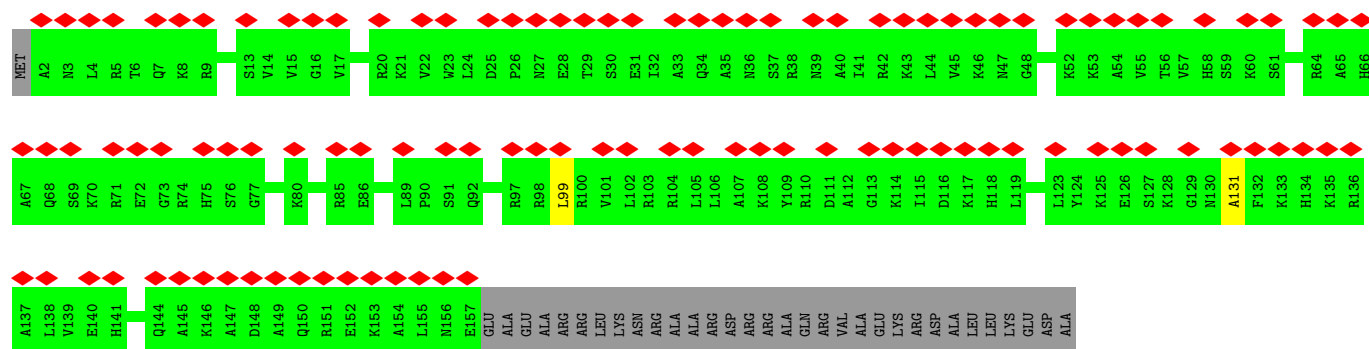
• Molecule 18: 60S ribosomal protein L18-A

Chain Q: .



• Molecule 19: 60S ribosomal protein L19-A

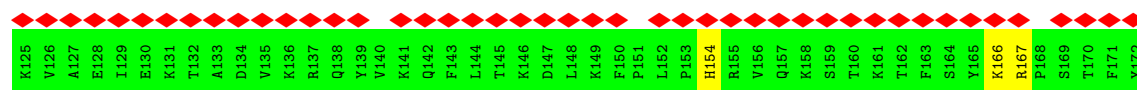
Chain R: .



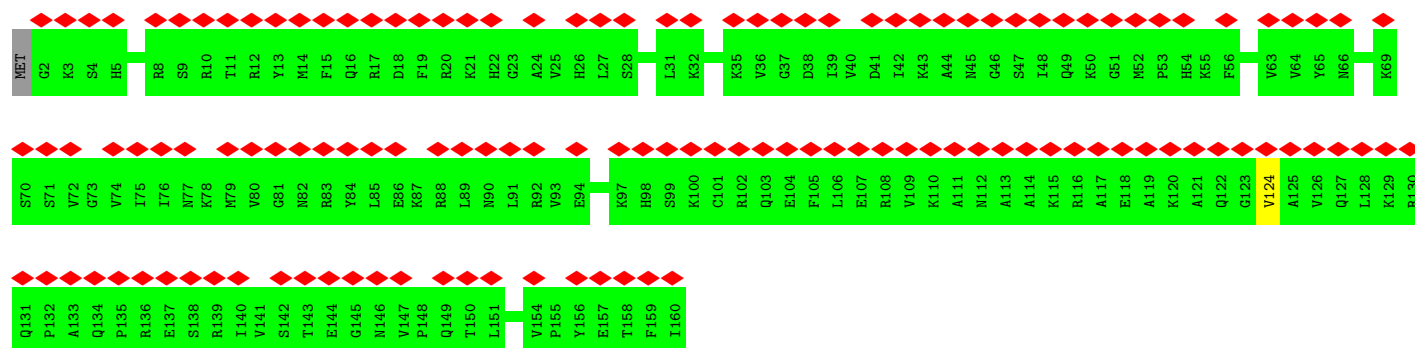
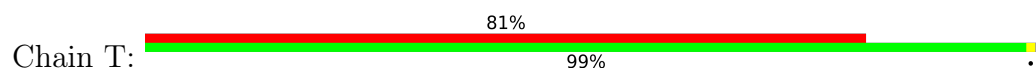
• Molecule 20: 60S ribosomal protein L20-A

Chain S: .

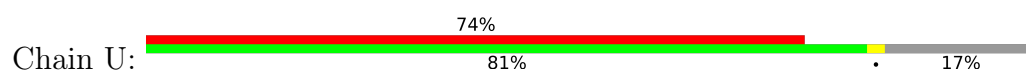




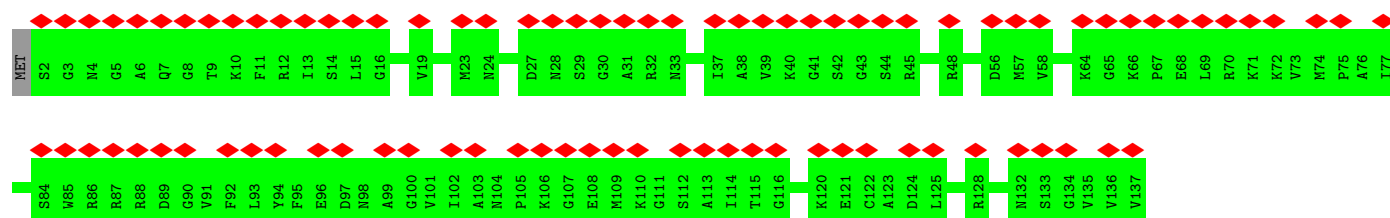
• Molecule 21: 60S ribosomal protein L21-A



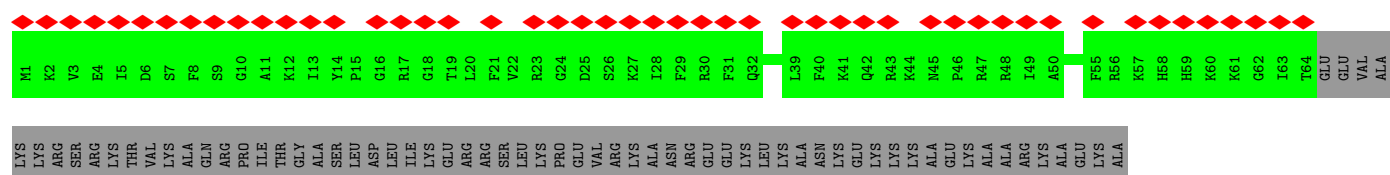
• Molecule 22: 60S ribosomal protein L22-A



• Molecule 23: 60S ribosomal protein L23-A



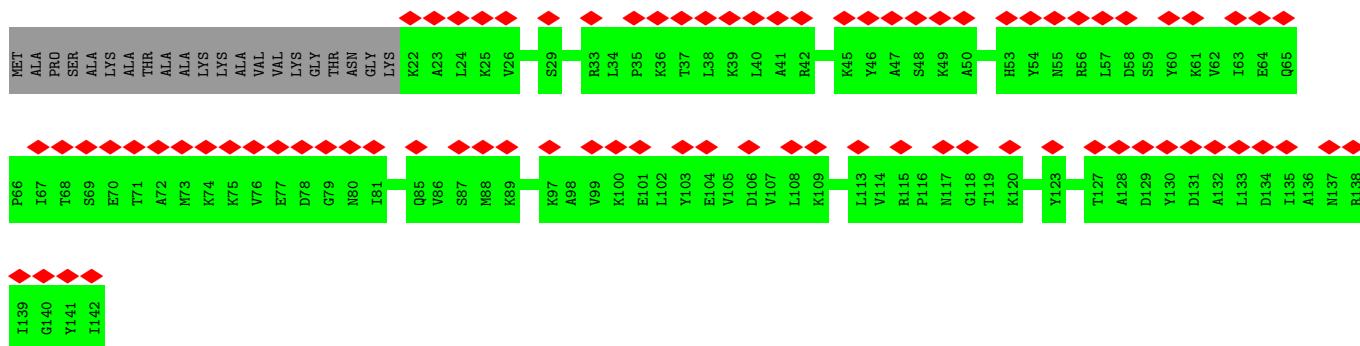
• Molecule 24: 60S ribosomal protein L24-A



LYS
SER
ALA
GLY
THR
GLN
SER
SER
LYS
LYS
PHE
SER
LYS
GLN
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GLN
LYS
VAL
ALA
ALA
THR
SER
SER

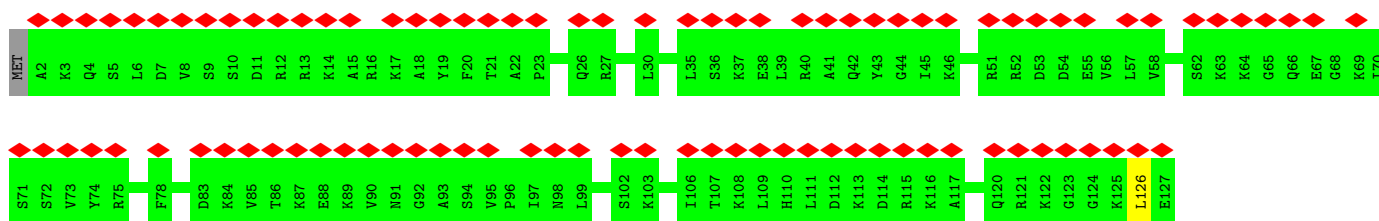
• Molecule 25: 60S ribosomal protein L25

Chain X:



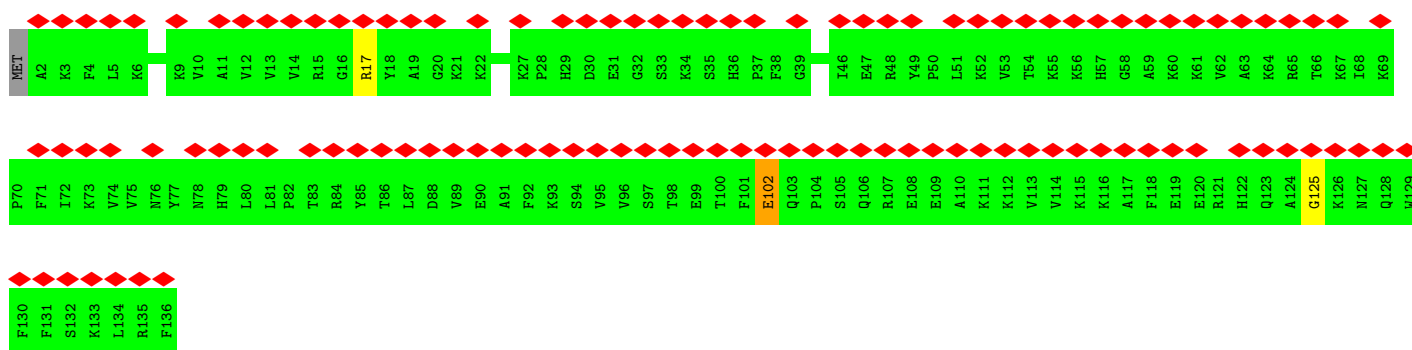
• Molecule 26: 60S ribosomal protein L26-A

Chain Y:



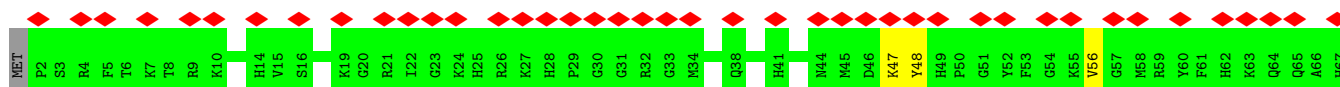
• Molecule 27: 60S ribosomal protein L27-A

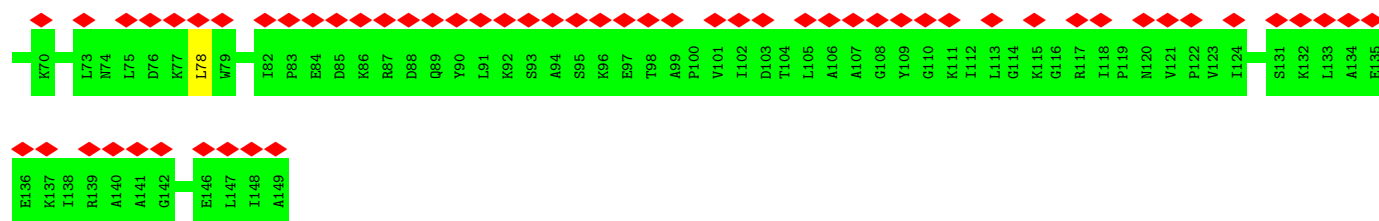
Chain Z:



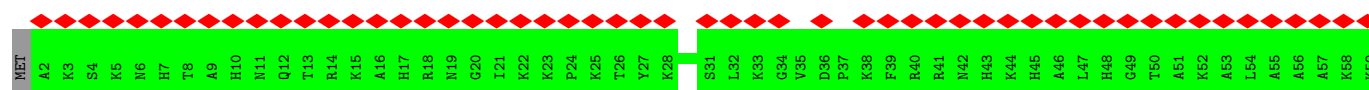
• Molecule 28: 60S ribosomal protein L28

Chain a:

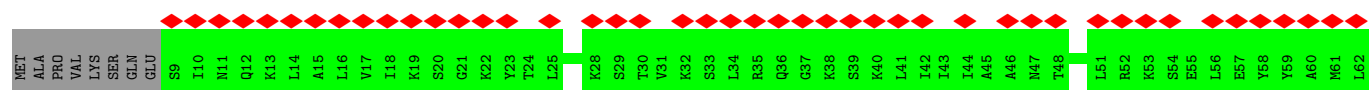




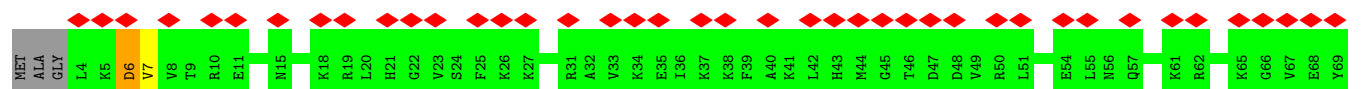
- Molecule 29: 60S ribosomal protein L29



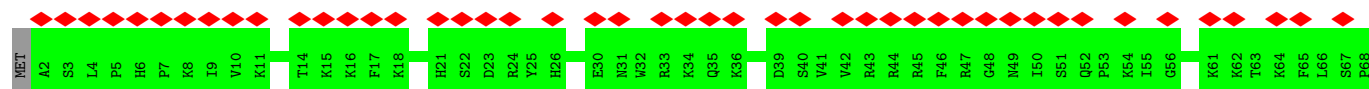
- Molecule 30: 60S ribosomal protein L30



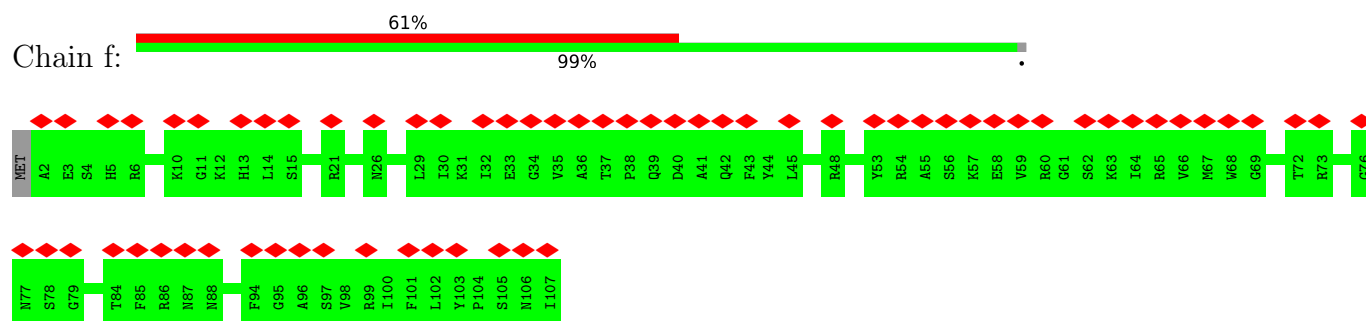
- Molecule 31: 60S ribosomal protein L31-A



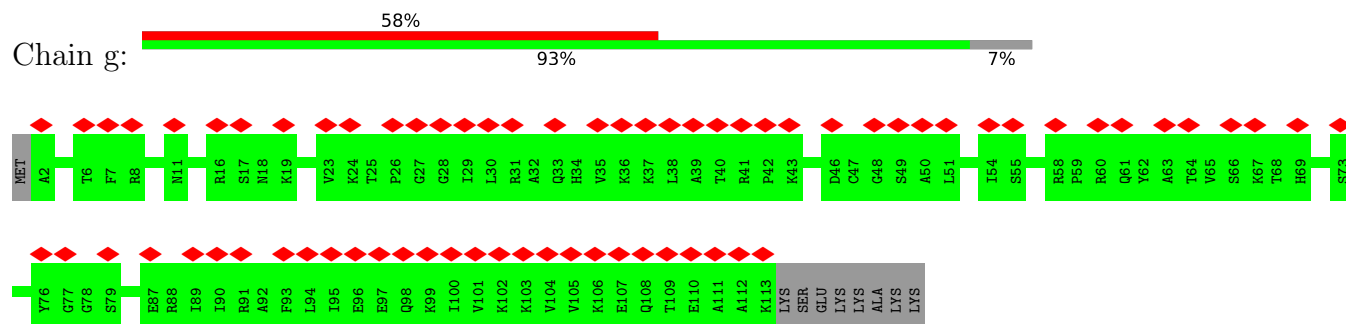
- Molecule 32: 60S ribosomal protein L32



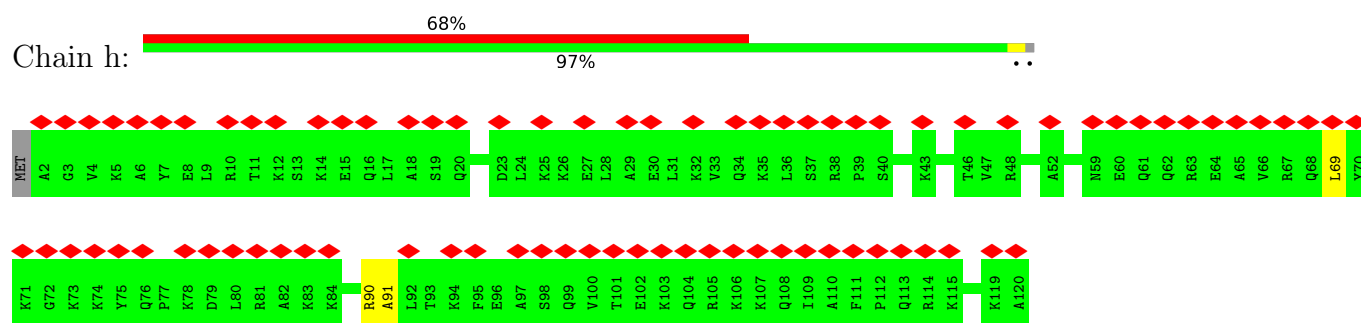
- Molecule 33: 60S ribosomal protein L33-A



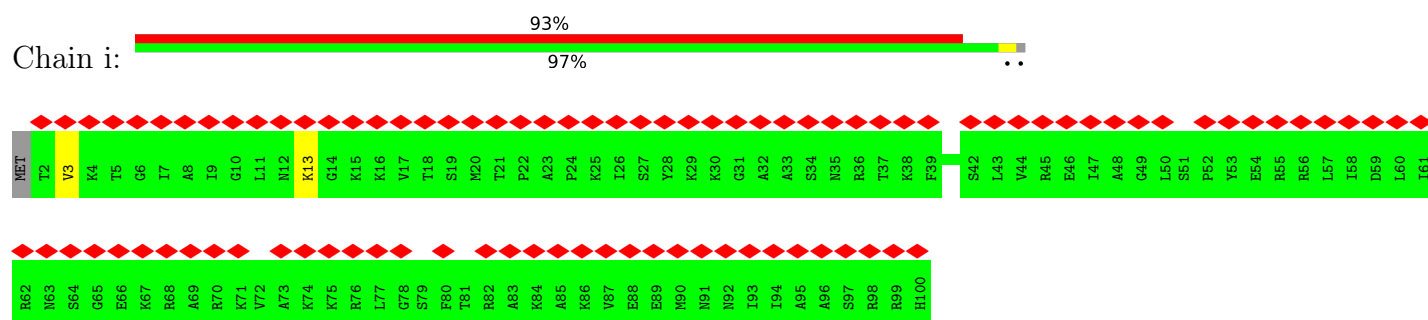
- Molecule 34: 60S ribosomal protein L34-A



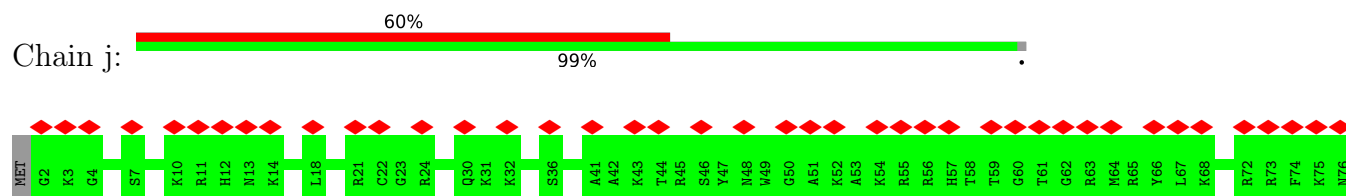
- Molecule 35: 60S ribosomal protein L35-A

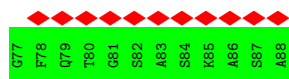


- Molecule 36: 60S ribosomal protein L36-A

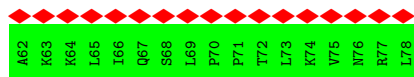
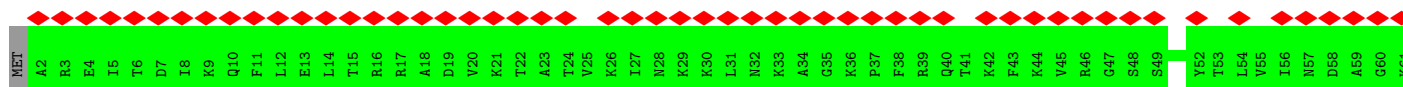
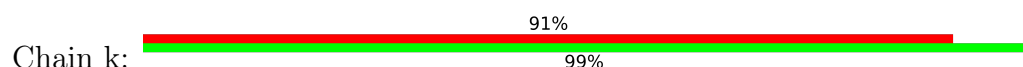


- Molecule 37: 60S ribosomal protein L37-A

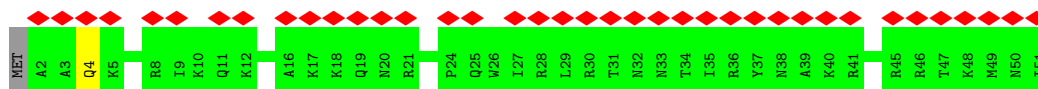
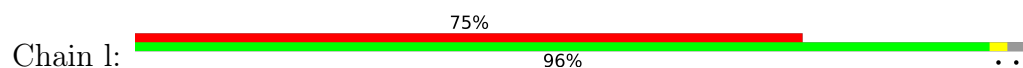




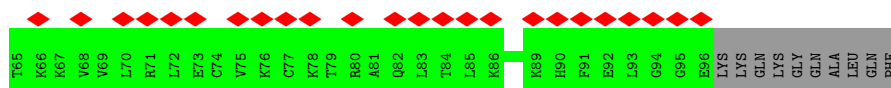
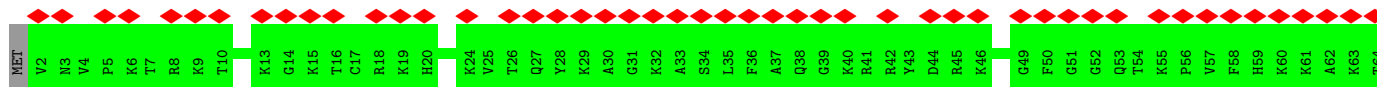
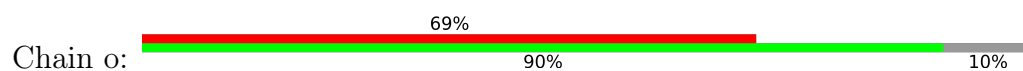
- Molecule 38: 60S ribosomal protein L38



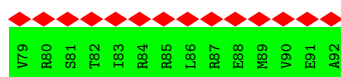
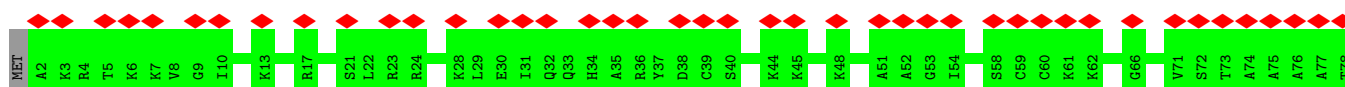
- Molecule 39: 60S ribosomal protein L39



- Molecule 40: 60S ribosomal protein L42-A

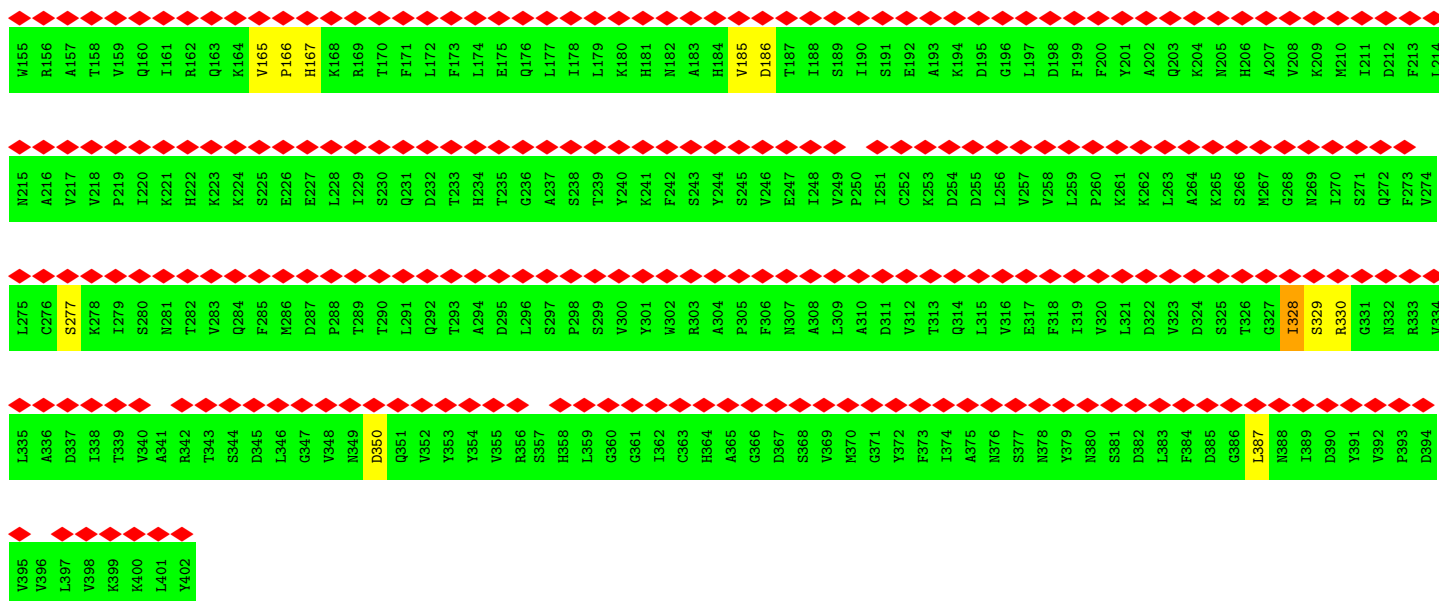


- Molecule 41: 60S ribosomal protein L43-A

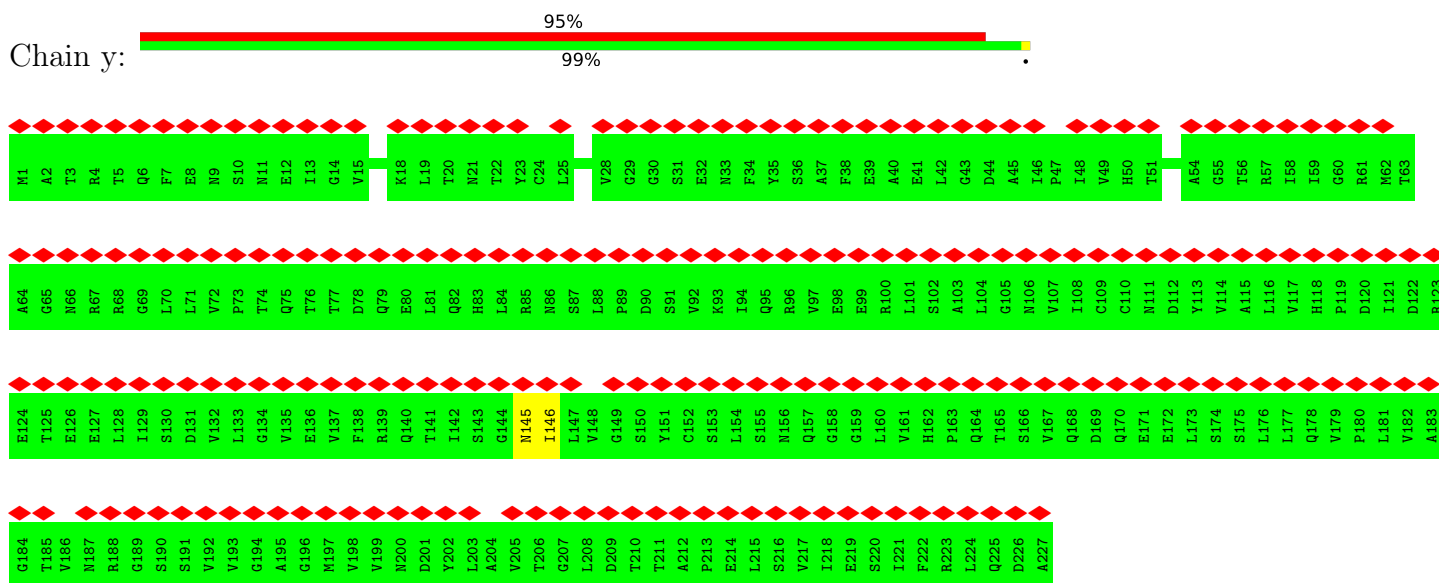


- Molecule 42: 60S ribosomal export protein NMD3

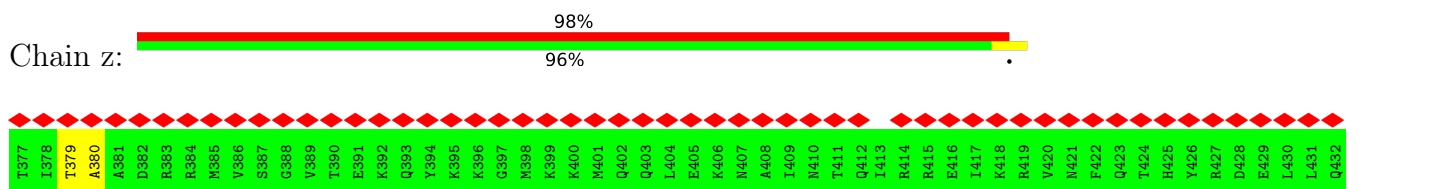




- Molecule 43: Eukaryotic translation initiation factor 6



- Molecule 44: Cytoplasmic 60S subunit biogenesis factor REH1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84240	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 ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.483	Depositor
Minimum map value	-0.325	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.143	Depositor
Map size (\AA)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.88	0/74017	0.89	34/115398 (0.0%)
2	3	0.73	0/2883	0.83	0/4491
3	4	0.94	0/3746	0.86	0/5832
4	A	0.50	0/1908	0.61	0/2564
5	B	0.52	0/3146	0.61	0/4228
6	C	0.46	0/2800	0.61	0/3790
7	D	0.39	0/2425	0.55	0/3271
8	E	0.41	0/1260	0.57	0/1694
9	F	0.46	0/1821	0.57	0/2451
10	G	0.43	0/1836	0.59	0/2481
11	H	0.40	0/1539	0.57	0/2073
12	J	0.34	0/1374	0.55	0/1842
13	L	0.44	0/1568	0.63	0/2106
14	M	0.43	0/1068	0.55	0/1438
15	N	0.52	0/1757	0.63	0/2354
16	O	0.51	1/1585 (0.1%)	0.58	0/2128
17	P	0.48	0/1465	0.61	0/1968
18	Q	0.44	0/1465	0.62	0/1965
19	R	0.42	0/1275	0.57	1/1702 (0.1%)
20	S	0.48	0/1481	0.57	0/1990
21	T	0.44	0/1300	0.56	0/1743
22	U	0.40	0/812	0.58	0/1099
23	V	0.46	0/1018	0.64	0/1369
24	W	0.44	0/540	0.56	0/717
25	X	0.46	0/979	0.61	0/1321
26	Y	0.42	0/1004	0.62	1/1341 (0.1%)
27	Z	0.46	0/1118	0.60	0/1497
28	a	0.46	0/1204	0.63	0/1612
29	b	0.35	0/473	0.50	0/629
30	c	0.46	0/751	0.53	0/1008
31	d	0.47	0/890	0.55	0/1196
32	e	0.45	0/1041	0.58	0/1394
33	f	0.52	0/868	0.56	0/1168
34	g	0.48	0/890	0.57	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.40	0/978	0.55	1/1301 (0.1%)
36	i	0.40	0/778	0.61	0/1034
37	j	0.48	0/696	0.62	0/923
38	k	0.38	0/618	0.58	0/826
39	l	0.47	0/443	0.58	0/588
40	o	0.46	0/777	0.61	0/1028
41	p	0.53	0/701	0.58	0/934
42	w	0.51	2/1931 (0.1%)	0.64	2/2629 (0.1%)
43	y	0.38	0/1720	0.56	0/2341
44	z	0.37	0/472	0.56	0/626
All	All	0.74	3/132421 (0.0%)	0.79	39/195279 (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
5	B	0	2
7	D	0	1
10	G	0	1
11	H	0	1
12	J	0	1
13	L	0	1
14	M	0	1
16	O	0	2
17	P	0	1
20	S	0	2
22	U	0	1
27	Z	0	1
31	d	0	1
32	e	0	1
35	h	0	1
39	l	0	1
42	w	0	1
43	y	0	1
All	All	0	21

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	186	ASP	C-N	11.11	1.59	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	165	VAL	C-N	7.19	1.48	1.34
16	O	74	ARG	C-N	-5.12	1.22	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2572	C	N1-C2-O2	8.73	124.14	118.90
42	w	165	VAL	O-C-N	8.29	136.85	121.10
1	1	2572	C	C2-N1-C1'	7.83	127.42	118.80
1	1	1269	U	C2-N1-C1'	7.74	126.99	117.70
26	Y	126	LEU	CA-CB-CG	6.84	131.03	115.30

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	385	LYS	Peptide
5	B	81	THR	Peptide
7	D	58	LYS	Peptide
10	G	30	THR	Peptide
11	H	49	ASN	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [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	
4	A	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
5	B	384/387 (99%)	357 (93%)	25 (6%)	2 (0%)	29	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	359/361 (99%)	329 (92%)	29 (8%)	1 (0%)	41	71
7	D	294/297 (99%)	267 (91%)	24 (8%)	3 (1%)	15	47
8	E	152/176 (86%)	143 (94%)	6 (4%)	3 (2%)	7	29
9	F	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
10	G	231/256 (90%)	208 (90%)	20 (9%)	3 (1%)	12	40
11	H	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	29	61
12	J	167/174 (96%)	144 (86%)	18 (11%)	5 (3%)	4	21
13	L	191/199 (96%)	172 (90%)	16 (8%)	3 (2%)	9	35
14	M	134/138 (97%)	123 (92%)	9 (7%)	2 (2%)	10	37
15	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	15	47
16	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
17	P	181/184 (98%)	178 (98%)	3 (2%)	0	100	100
18	Q	183/186 (98%)	172 (94%)	11 (6%)	0	100	100
19	R	154/189 (82%)	147 (96%)	6 (4%)	1 (1%)	25	57
20	S	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	8	32
21	T	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	25	57
22	U	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	15	47
23	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
24	W	62/155 (40%)	60 (97%)	2 (3%)	0	100	100
25	X	119/142 (84%)	113 (95%)	6 (5%)	0	100	100
26	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
27	Z	133/136 (98%)	124 (93%)	6 (4%)	3 (2%)	6	26
28	a	146/149 (98%)	131 (90%)	11 (8%)	4 (3%)	5	23
29	b	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
30	c	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
31	d	107/113 (95%)	101 (94%)	4 (4%)	2 (2%)	8	31
32	e	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	19	52
33	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
34	g	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
35	h	117/120 (98%)	110 (94%)	6 (5%)	1 (1%)	17	49
36	i	97/100 (97%)	82 (84%)	13 (13%)	2 (2%)	7	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
38	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
39	l	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
40	o	93/106 (88%)	84 (90%)	9 (10%)	0	100	100
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	w	246/248 (99%)	220 (89%)	19 (8%)	7 (3%)	5	23
43	y	225/227 (99%)	220 (98%)	4 (2%)	1 (0%)	34	66
44	z	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	3	17
All	All	6348/6731 (94%)	5900 (93%)	394 (6%)	54 (1%)	21	49

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
10	G	36	ILE
28	a	78	LEU
32	e	123	LYS
42	w	328	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	189/189 (100%)	189 (100%)	0	100	100
5	B	318/323 (98%)	317 (100%)	1 (0%)	92	96
6	C	288/288 (100%)	287 (100%)	1 (0%)	92	96
7	D	244/245 (100%)	244 (100%)	0	100	100
8	E	134/153 (88%)	134 (100%)	0	100	100
9	F	186/205 (91%)	186 (100%)	0	100	100
10	G	187/208 (90%)	186 (100%)	1 (0%)	88	94
11	H	171/171 (100%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	J	147/150 (98%)	147 (100%)	0	100	100
13	L	154/159 (97%)	153 (99%)	1 (1%)	86	93
14	M	107/109 (98%)	107 (100%)	0	100	100
15	N	175/176 (99%)	175 (100%)	0	100	100
16	O	160/162 (99%)	160 (100%)	0	100	100
17	P	145/146 (99%)	145 (100%)	0	100	100
18	Q	150/151 (99%)	150 (100%)	0	100	100
19	R	129/154 (84%)	129 (100%)	0	100	100
20	S	156/156 (100%)	156 (100%)	0	100	100
21	T	136/137 (99%)	136 (100%)	0	100	100
22	U	87/107 (81%)	87 (100%)	0	100	100
23	V	104/105 (99%)	104 (100%)	0	100	100
24	W	56/129 (43%)	56 (100%)	0	100	100
25	X	104/118 (88%)	104 (100%)	0	100	100
26	Y	109/110 (99%)	109 (100%)	0	100	100
27	Z	115/116 (99%)	115 (100%)	0	100	100
28	a	118/119 (99%)	118 (100%)	0	100	100
29	b	46/47 (98%)	46 (100%)	0	100	100
30	c	81/88 (92%)	81 (100%)	0	100	100
31	d	92/97 (95%)	92 (100%)	0	100	100
32	e	109/111 (98%)	109 (100%)	0	100	100
33	f	90/91 (99%)	90 (100%)	0	100	100
34	g	95/103 (92%)	95 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	81/82 (99%)	81 (100%)	0	100	100
37	j	70/71 (99%)	70 (100%)	0	100	100
38	k	68/69 (99%)	68 (100%)	0	100	100
39	l	45/46 (98%)	45 (100%)	0	100	100
40	o	82/91 (90%)	82 (100%)	0	100	100
41	p	71/72 (99%)	71 (100%)	0	100	100
42	w	205/221 (93%)	203 (99%)	2 (1%)	76	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	y	189/194 (97%)	189 (100%)	0	100	100
44	z	51/51 (100%)	51 (100%)	0	100	100
All	All	5348/5625 (95%)	5342 (100%)	6 (0%)	93	97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	24	VAL
42	w	328	ILE
42	w	330	ARG
6	C	194	TYR
5	B	85	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
41	p	34	HIS
42	w	332	ASN
17	P	133	HIS
16	O	90	HIS
43	y	86	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3086/3396 (90%)	747 (24%)	47 (1%)
2	3	120/121 (99%)	20 (16%)	1 (0%)
3	4	157/158 (99%)	39 (24%)	2 (1%)
All	All	3363/3675 (91%)	806 (23%)	50 (1%)

5 of 806 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	14	U
1	1	22	G
1	1	24	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2227	C
1	1	2771	U
3	4	85	G
1	1	2372	A
1	1	2537	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

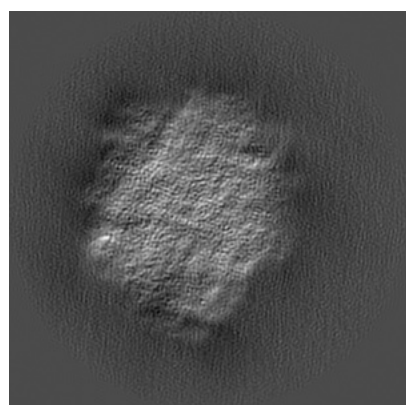
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9569. These allow visual inspection of the internal detail of the map and identification of artifacts.

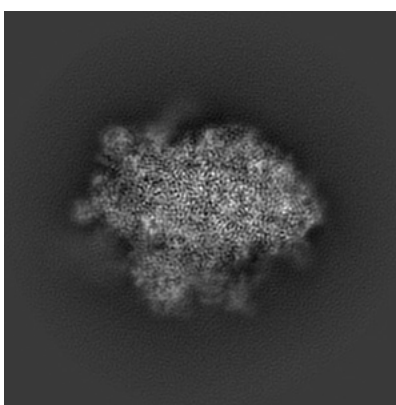
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

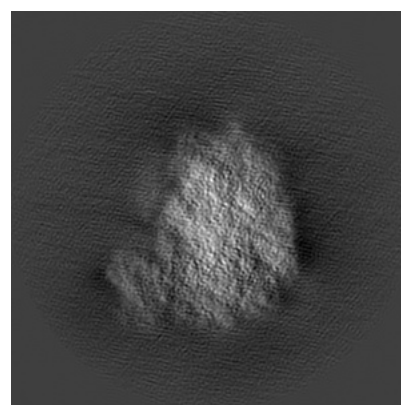
6.1.1 Primary map



X



Y

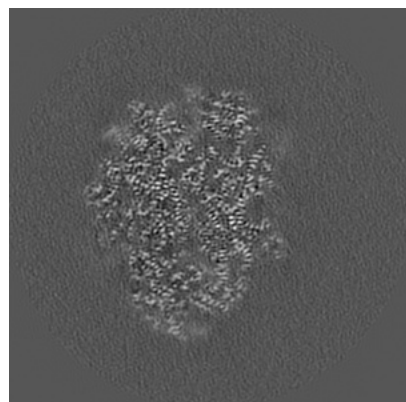


Z

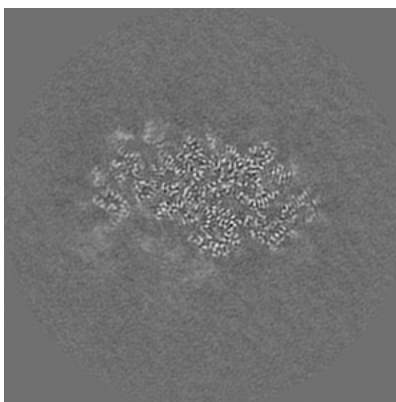
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

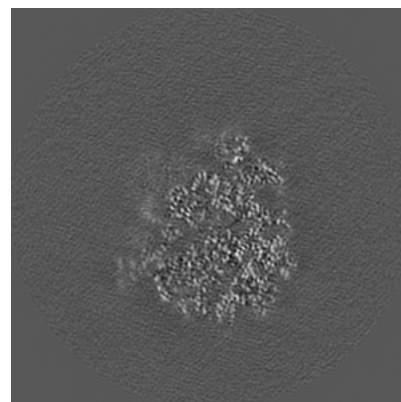
6.2.1 Primary map



X Index: 180



Y Index: 180

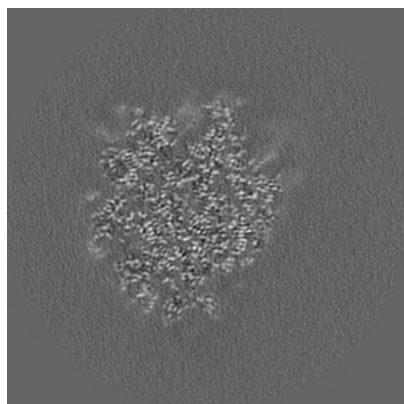


Z Index: 180

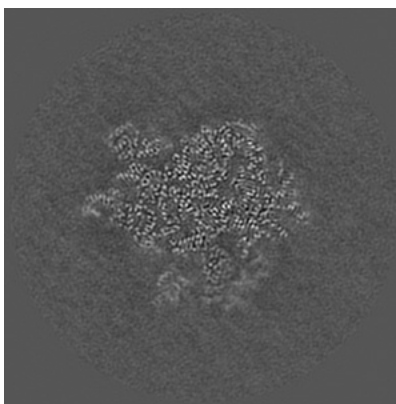
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

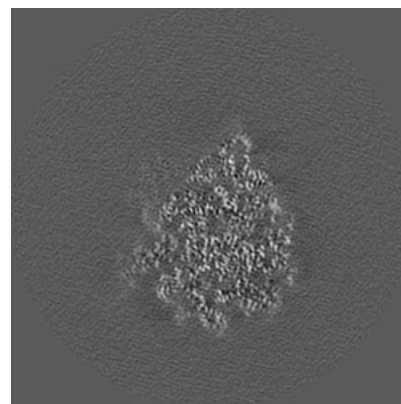
6.3.1 Primary map



X Index: 193



Y Index: 133



Z Index: 188

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

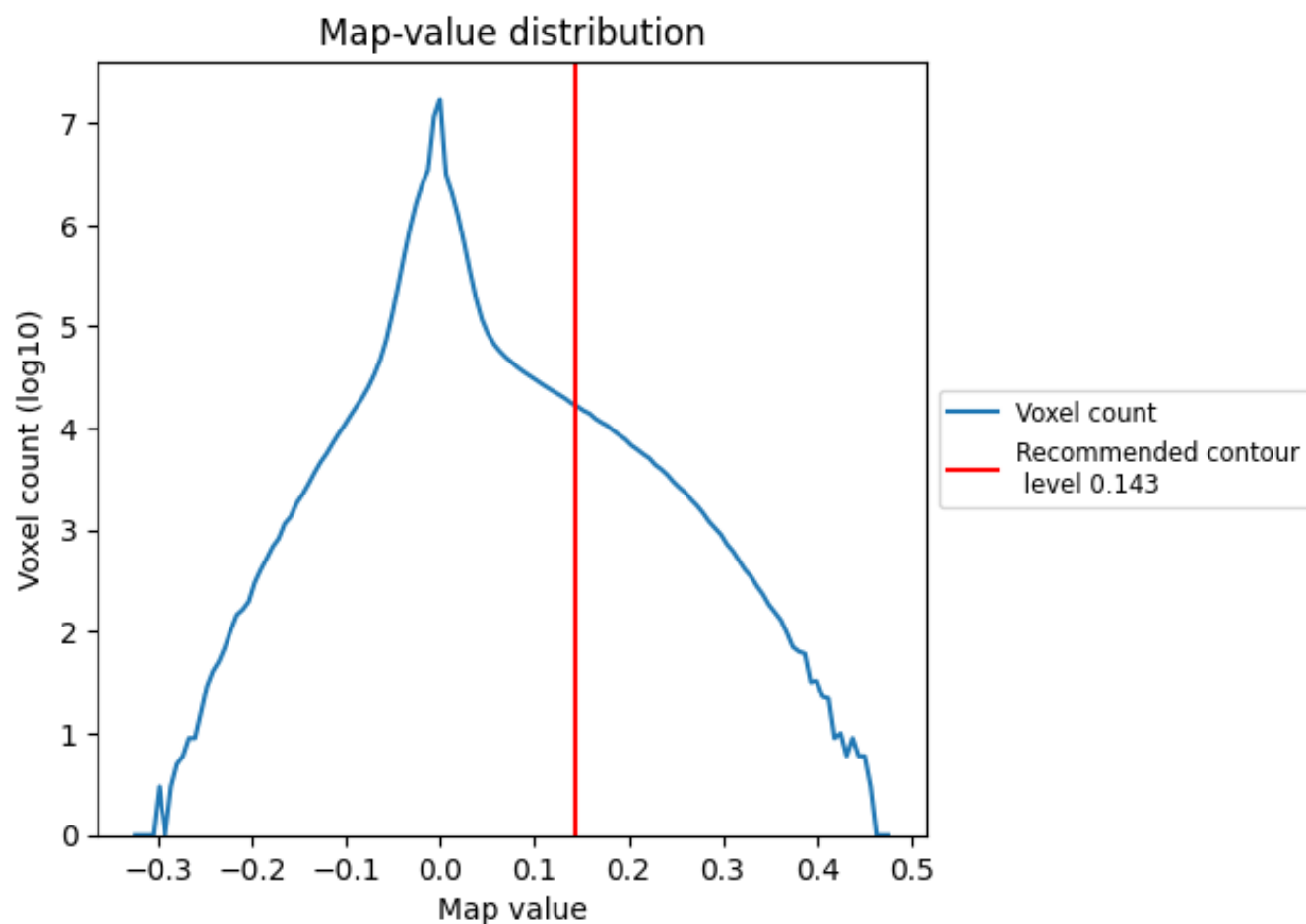
6.5 Mask visualisation

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

7 Map analysis [i](#)

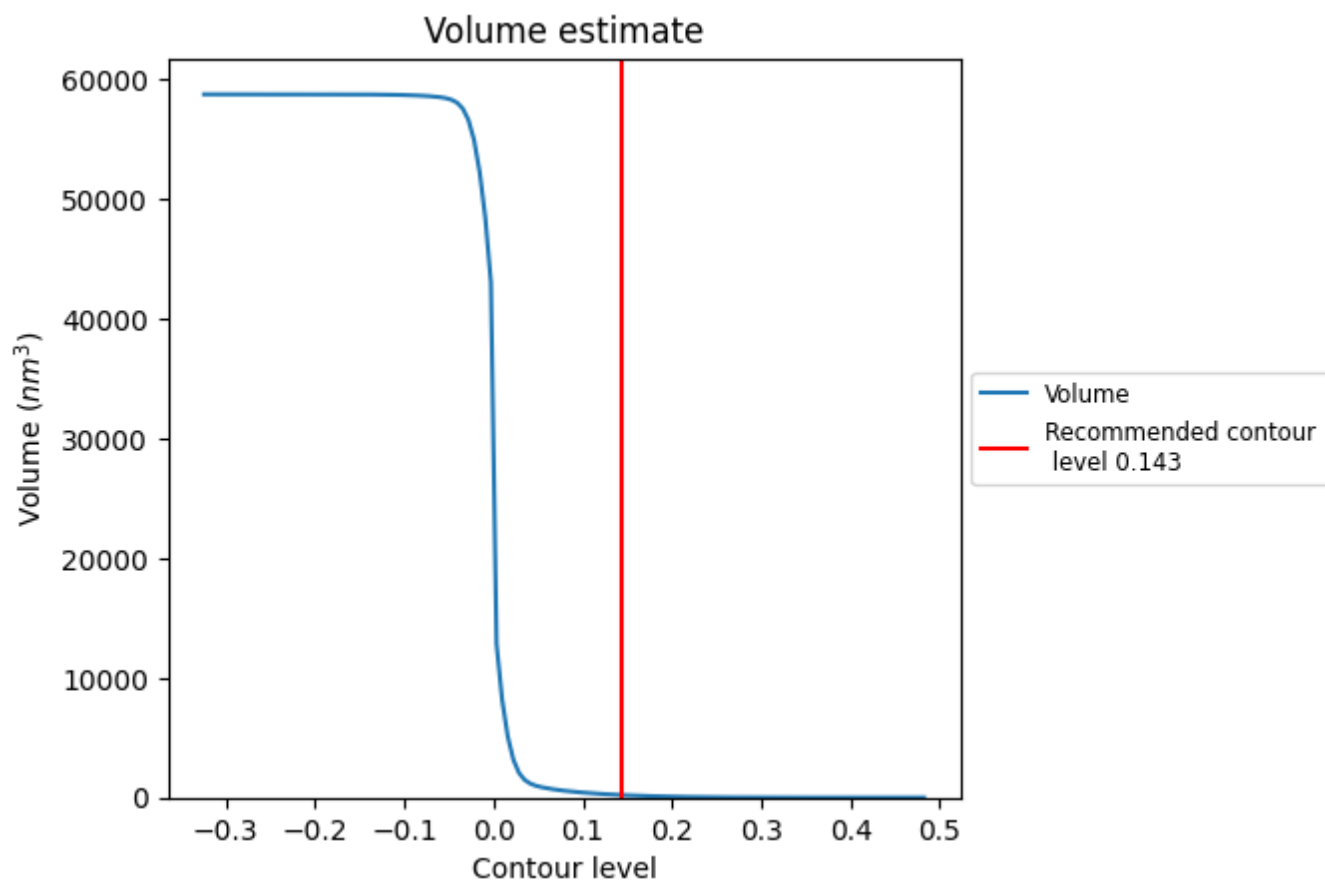
This section contains the results of statistical analysis of the map.

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.

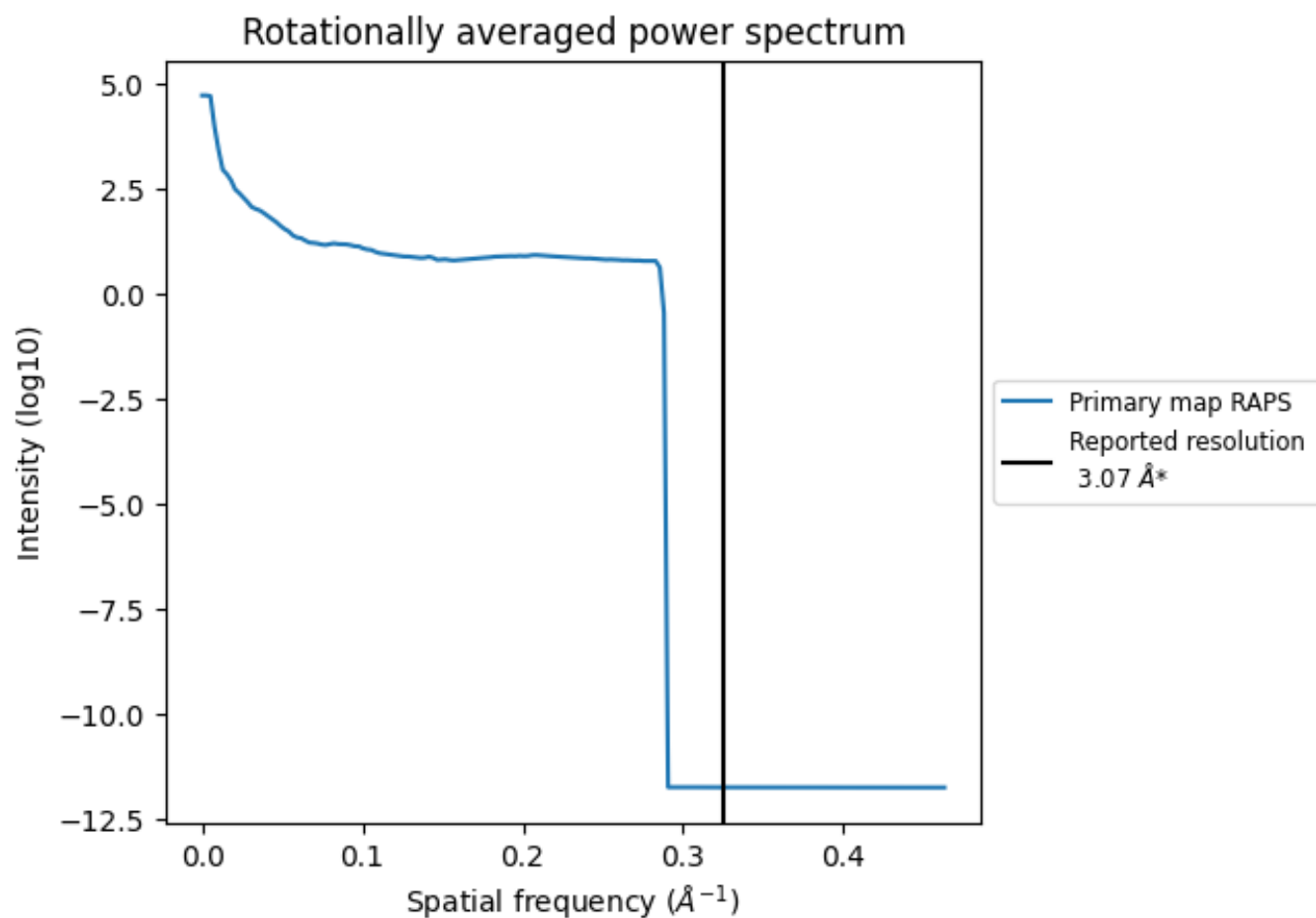
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 212 nm³; this corresponds to an approximate mass of 192 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 0.326 Å⁻¹

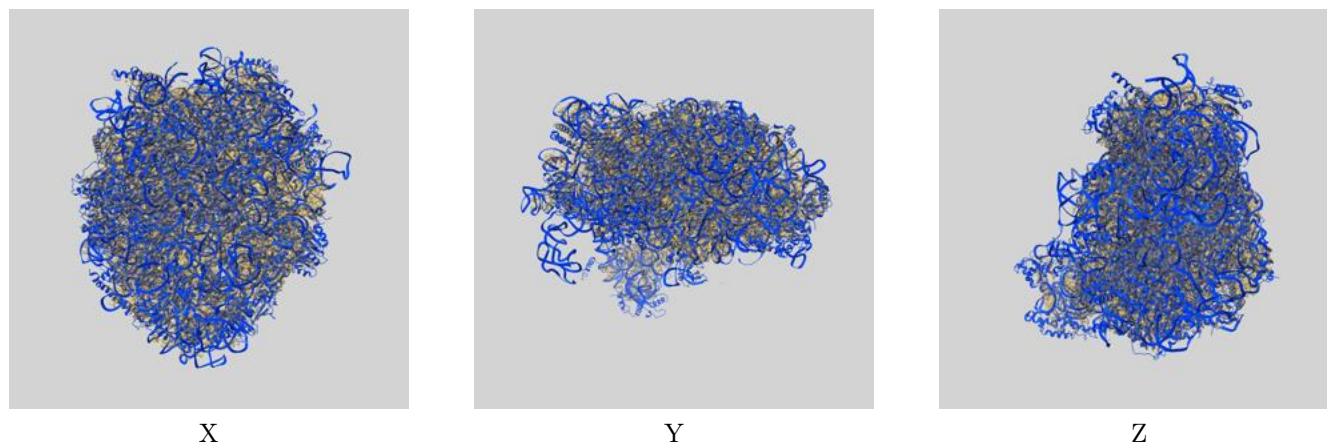
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

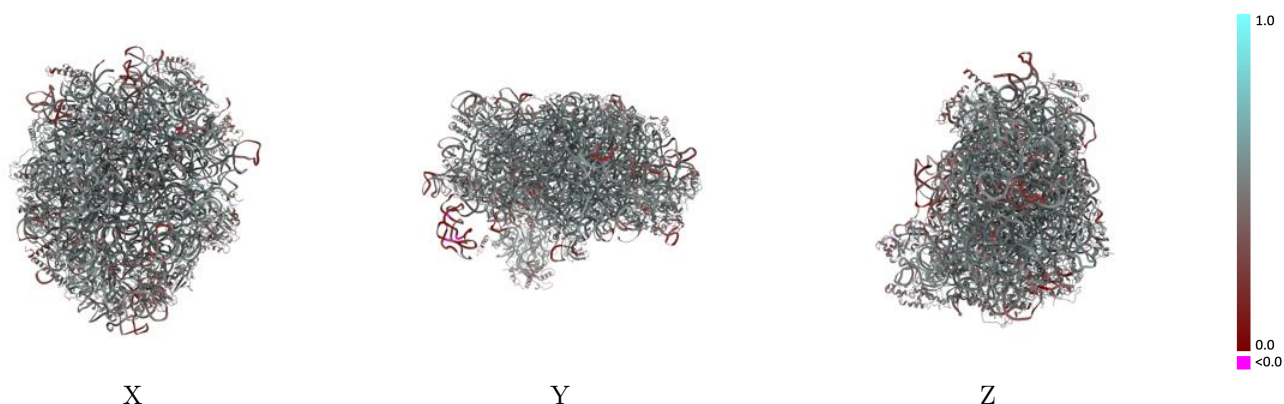
This section contains information regarding the fit between EMDB map EMD-9569 and PDB model 5H4P. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



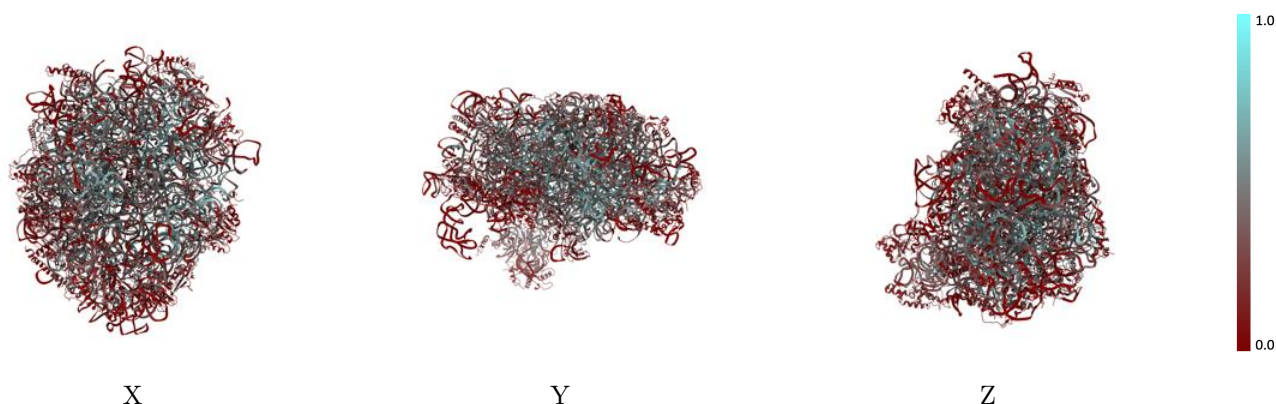
The images above show the 3D surface view of the map at the recommended contour level 0.143 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



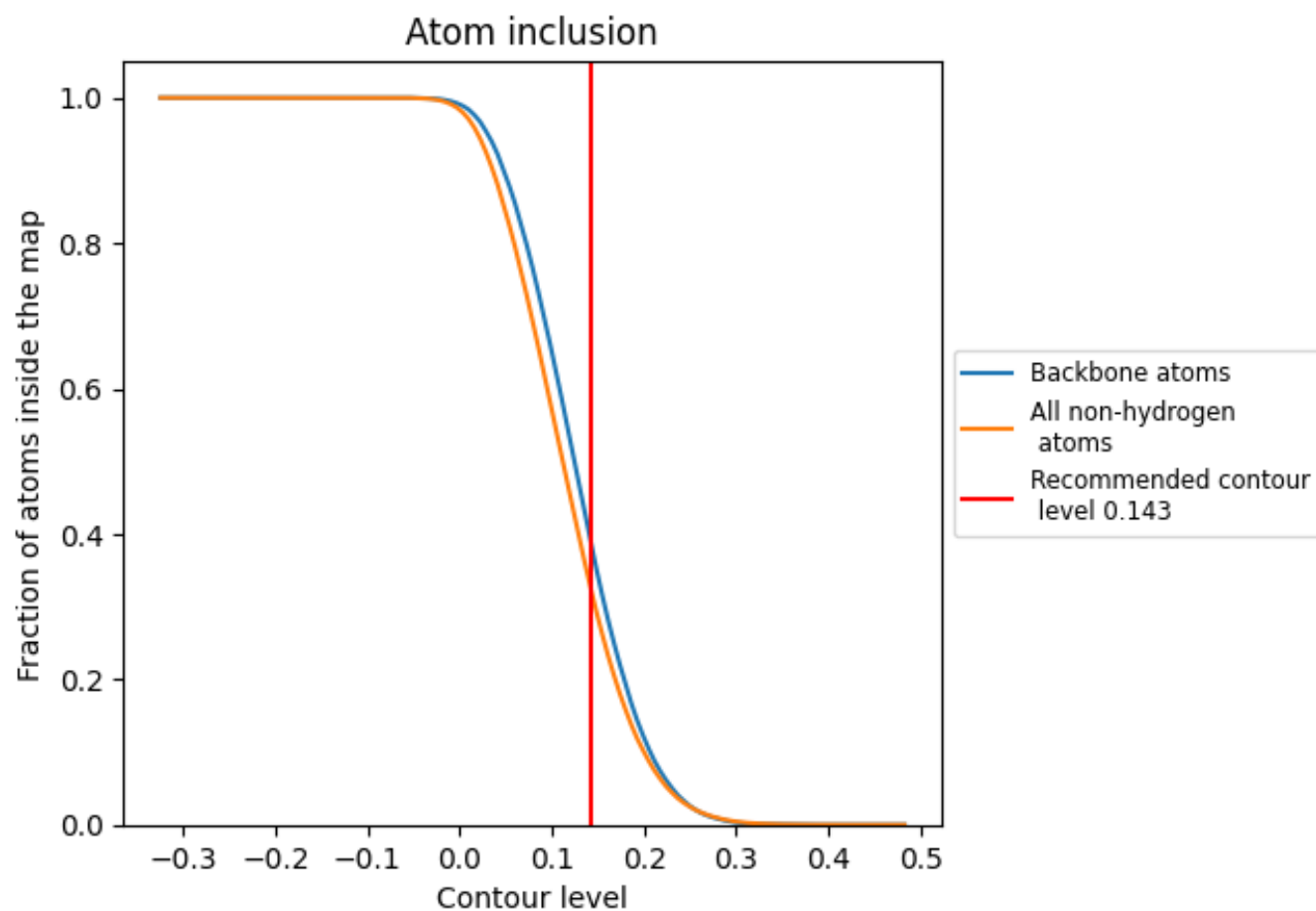
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.143).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 32% 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 (0.143) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3204	 0.4830
1	 0.3758	 0.4820
3	 0.2737	 0.4830
4	 0.4378	 0.5040
A	 0.3589	 0.5090
B	 0.3575	 0.5000
C	 0.2725	 0.4980
D	 0.1029	 0.4330
E	 0.1385	 0.4730
F	 0.2698	 0.5000
G	 0.2376	 0.4730
H	 0.1362	 0.4590
J	 0.0593	 0.4070
L	 0.2542	 0.4830
M	 0.2222	 0.4870
N	 0.3561	 0.5130
O	 0.3362	 0.5110
P	 0.3080	 0.4810
Q	 0.2251	 0.4990
R	 0.3045	 0.4830
S	 0.2068	 0.4840
T	 0.1992	 0.4760
U	 0.1394	 0.4490
V	 0.3064	 0.5020
W	 0.2383	 0.4910
X	 0.3142	 0.4980
Y	 0.2609	 0.4990
Z	 0.2101	 0.4720
a	 0.3012	 0.5060
b	 0.1239	 0.4470
c	 0.1751	 0.4550
d	 0.3071	 0.4890
e	 0.2757	 0.5100
f	 0.3459	 0.5150
g	 0.3349	 0.4920



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Chain	Atom inclusion	Q-score
h	 0.2853	 0.4870
i	 0.1436	 0.4550
j	 0.3771	 0.5170
k	 0.1202	 0.4530
l	 0.3277	 0.5160
o	 0.2775	 0.4800
p	 0.3169	 0.4830
w	 0.0840	 0.4590
y	 0.1048	 0.4390
z	 0.0615	 0.4690