



wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 02:30 am BST

PDB ID : 6EM1 / pdb_00006em1
EMDB ID : EMD-3893
Title : State C (Nsa1-TAP Flag-Ytm1) - Visualizing the assembly pathway of nuclear pre-60S ribosomes
Authors : Kater, L.; Cheng, J.; Barrio-Garcia, C.; Hurt, E.; Beckmann, R.
Deposited on : 2017-10-01
Resolution : 3.60 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

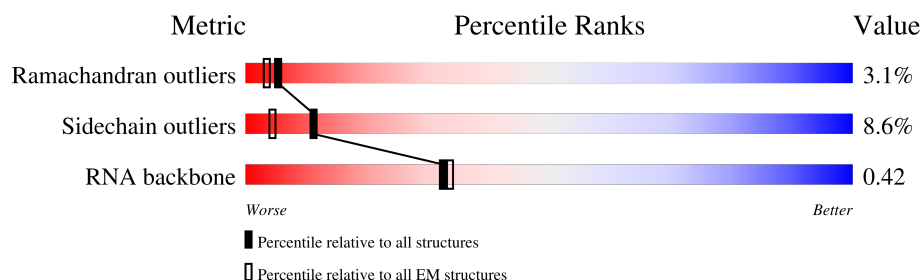
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



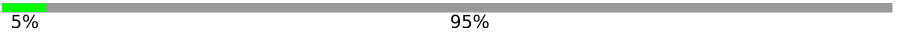
















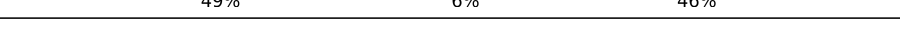







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	x	295	72% 17% 9%
2	F	244	91% 8%
3	3	306	44% 12% 43%
4	4	278	64% 14% 22%
5	5	463	78% 5% 17%
6	A	291	45% 50%
7	b	647	59% 6% 35%
8	J	427	15% 85%
9	r	261	26% 72%









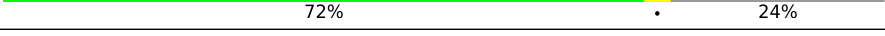
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Mol	Chain	Length	Quality of chain
10	s	520	 5% 95%
11	u	199	 55% 42%
12	v	231	 52% 5% 44%
13	W	236	 93% 5%
14	y	245	 88% 8%
15	z	106	 52% 48%
16	B	387	 78% 8% 14%
17	C	362	 80% 15% 5%
18	e	130	 83% 13%
19	E	176	 81% 5% 14%
20	f	107	 86% 12% ..
21	G	256	 54% 9% 38%
22	h	120	 88% 10% ..
23	H	191	 91% 8%
24	i	100	 64% 10% 26%
25	j	88	 69% 10% 19%
26	L	199	 49% 6% 46%
27	M	138	 92% 5%
28	N	204	 74% 13% 13%
29	O	199	 42% 47% 10%
30	P	184	 65% 9% 26%
31	Q	186	 65% 6% 30%
32	S	172	 87% 11% ..
33	V	137	 90% 8%
34	Y	127	 87% 10% ..

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Mol	Chain	Length	Quality of chain
35	1	3396	
36	2	158	
37	6	232	
38	K	376	
39	m	807	
40	D	505	
41	o	220	
42	n	605	
43	t	322	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 99980 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 Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	x	267	Total	C	N	O	S	0	0
			2268	1444	413	407	4		

- Molecule 2 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	241	Total	C	N	O	S	0	0
			1936	1246	351	338	1		

- Molecule 3 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	173	Total	C	N	O	S	0	0
			1434	901	274	250	9		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	217	Total	C	N	O	S	0	0
			1853	1208	319	323	3		

- Molecule 5 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	385	Total	C	N	O	S	0	0
			3055	1957	514	573	11		

- Molecule 6 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	145	Total	C	N	O	S	0	0
			1211	780	218	210	3		

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	b	421	Total	C	N	O	S	0	0
			3410	2180	585	627	18		

- Molecule 8 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	66	Total	C	N	O	S	0	0
			549	341	97	110	1		

- Molecule 9 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	r	73	Total	C	N	O	S	0	0
			628	388	133	106	1		

- Molecule 10 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	s	27	Total	C	N	O	0	0
			224	136	51	37		

- Molecule 11 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	u	116	Total	C	N	O	S	0	0
			976	612	200	155	9		

- Molecule 12 is a protein called Nucleolar protein 16.

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

- Molecule 13 is a protein called Ribosome assembly factor MRT4.

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

- Molecule 14 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 15 is a protein called UPF0642 protein YBL028C.

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

- Molecule 16 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	333	Total	C	N	O	S	0	0
			2646	1680	490	470	6		

- Molecule 17 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	C	343	Total	C	N	O	S	0	0
			2611	1643	499	466	3		

- Molecule 18 is a protein called 60S ribosomal protein L32.

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

- Molecule 19 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	E	151	Total	C	N	O	S	0	0
			1205	780	215	209	1		

- Molecule 20 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	G	159	Total	C	N	O	S	0	0
			1231	794	209	226	2		

- Molecule 22 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	74	Total	C	N	O	S	0	0
			594	367	125	101	1		

- Molecule 25 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	71	Total	C	N	O	S	0	0
			566	344	123	94	5		

- Molecule 26 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L	108	Total	C	N	O		0	0
			864	541	180	143			

- Molecule 27 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	M	134	Total	C	N	O	S	0	0
			1041	668	197	174	2		

- Molecule 28 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N	177	Total	C	N	O	S	0	0
			1513	948	320	244	1		

- Molecule 29 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	P	137	Total	C	N	O	S	0	0
			1062	666	198	198			

- Molecule 31 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Q	131	Total	C	N	O	S	0	0
			1009	645	190	173	1		

- Molecule 32 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	V	126	Total	C	N	O	S	0	0
			936	588	176	165	7		

- Molecule 34 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	125	Total	C	N	O	S	0	0
			984	620	191	173			

- Molecule 35 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1	1785	Total	C	N	O	P	0	0
			38221	17064	6918	12454	1785		

- Molecule 36 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 37 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 38 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	K	257	Total	C	N	O	S	0	0
			2073	1337	341	392	3		

- Molecule 39 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	161	Total	C	N	O	S	0	0
			1362	867	238	253	4		

- Molecule 40 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	D	194	Total	C	N	O	S	0	0
			1590	1030	268	287	5		

- Molecule 41 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 42 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	334	Total	C	N	O	S	0	0
			2734	1787	457	482	8		

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	244	Total	C	N	O	S	0	0
			1935	1233	345	354	3		

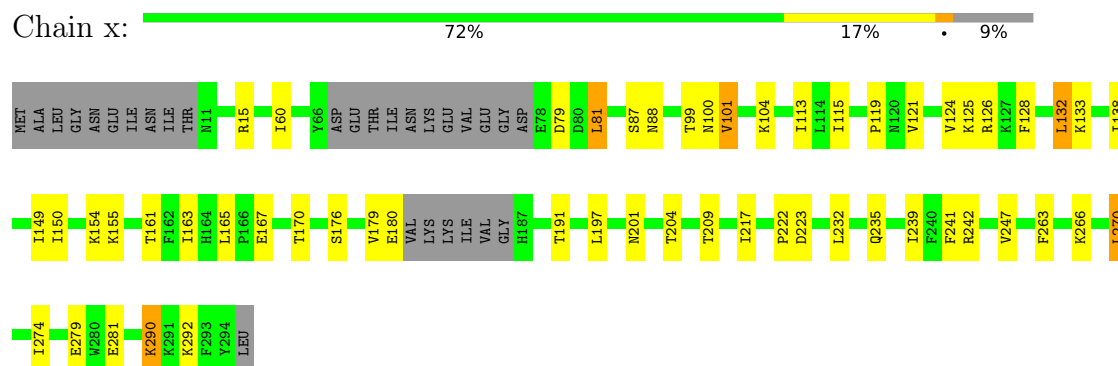
- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	u	1	Total	Zn	0
			1	1	
44	j	1	Total	Zn	0
			1	1	

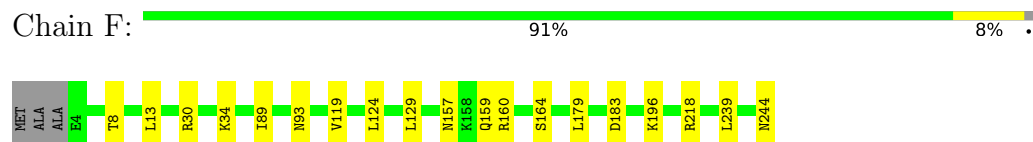
3 Residue-property plots

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. 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. 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.

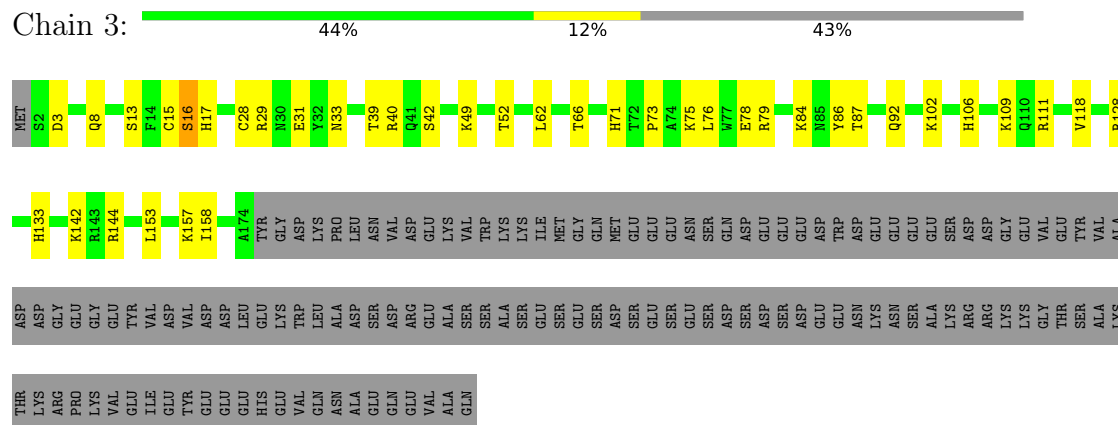
- Molecule 1: Ribosome production factor 1



- Molecule 2: 60S ribosomal protein L7-A

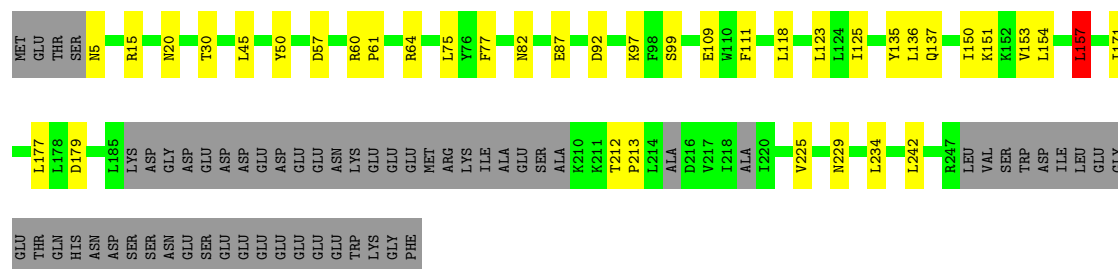


- Molecule 3: Protein MAK16



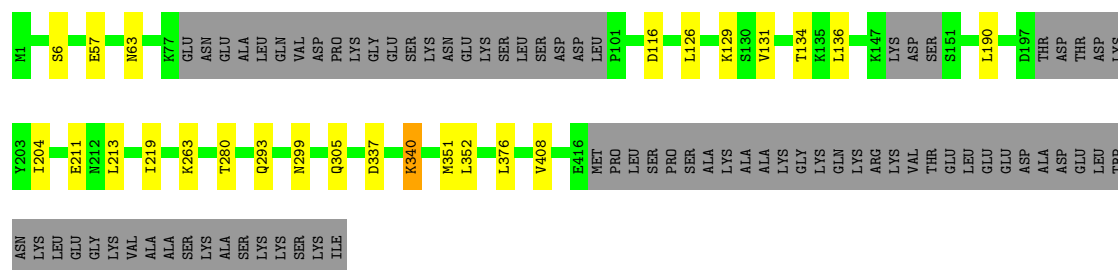
- Molecule 4: Ribosomal RNA-processing protein 1





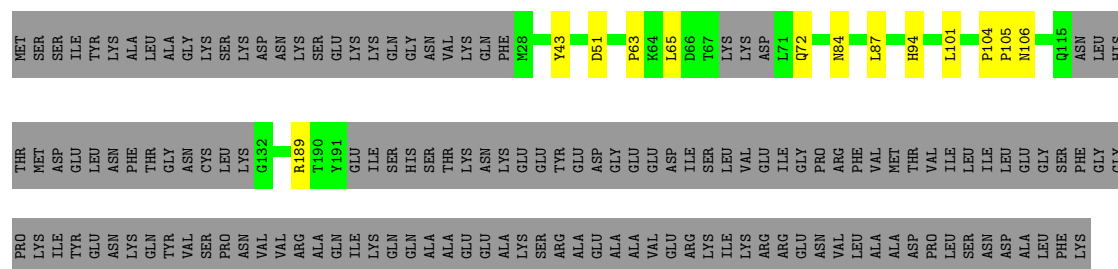
• Molecule 5: Ribosome biogenesis protein NSA1

Chain 5: 78% 5% 17%



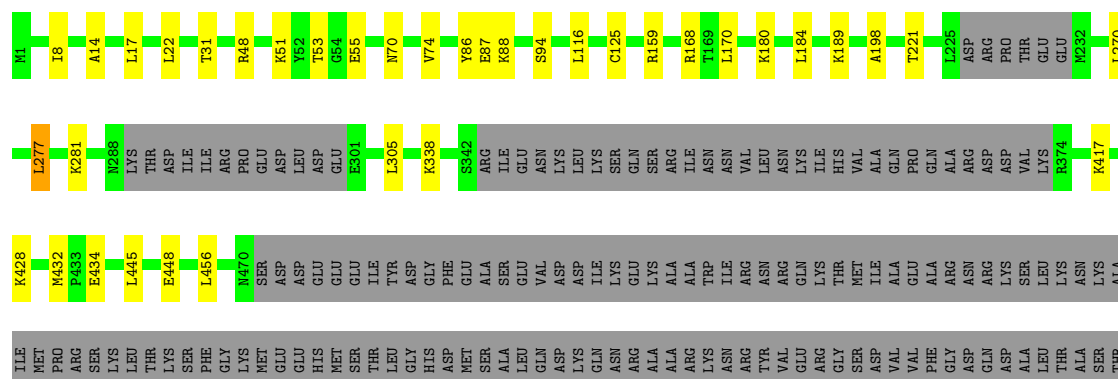
• Molecule 6: Ribosome biogenesis protein BRX1

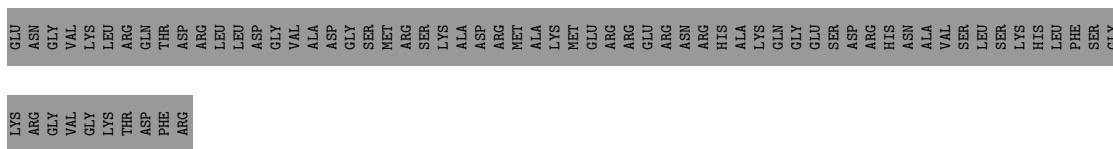
Chain A: 45% 50%



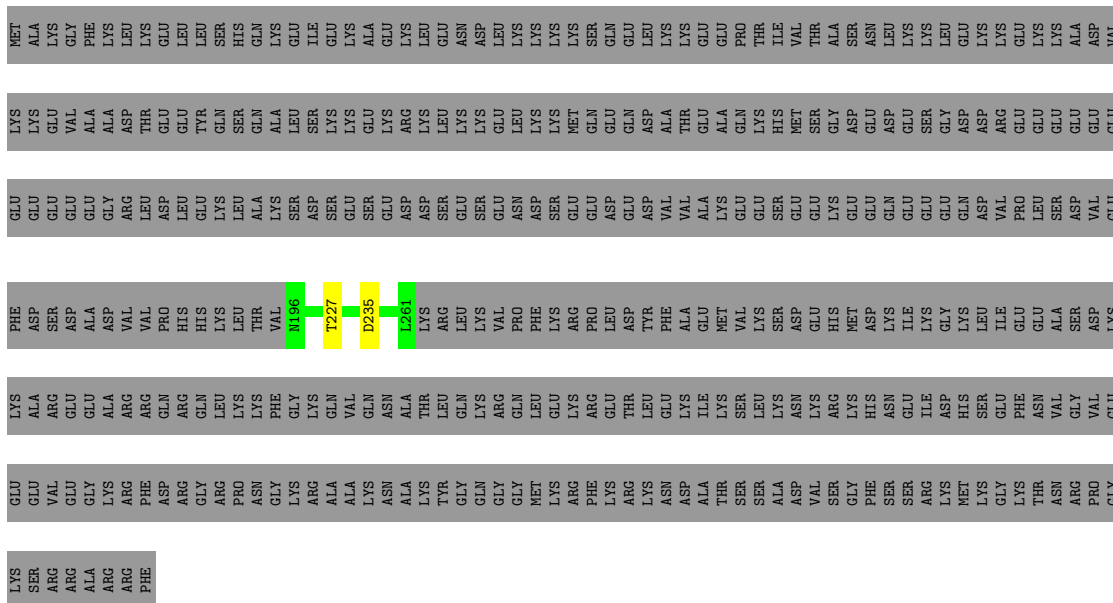
• Molecule 7: Nucleolar GTP-binding protein 1

Chain b: 59% 6% 35%

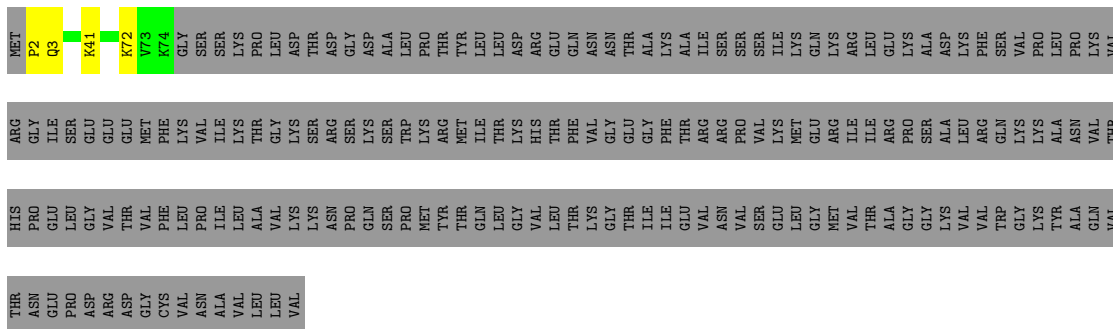




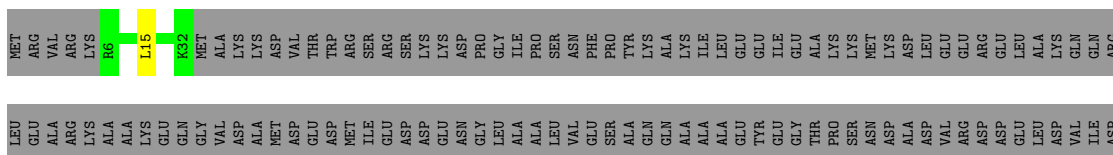
- Molecule 8: rRNA-processing protein EBP2

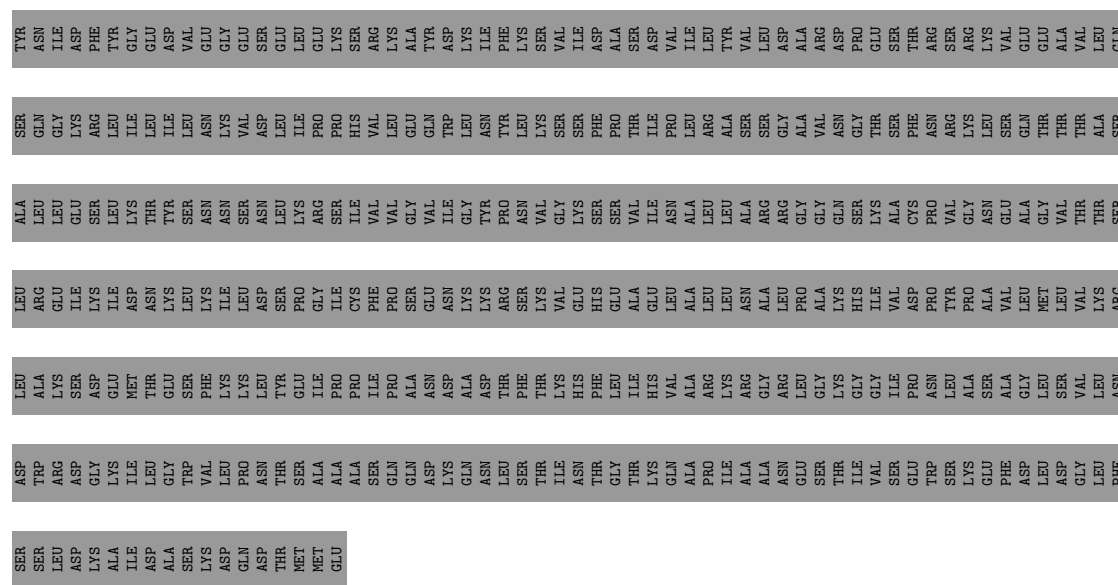


- Molecule 9: Ribosome biogenesis protein NSA2

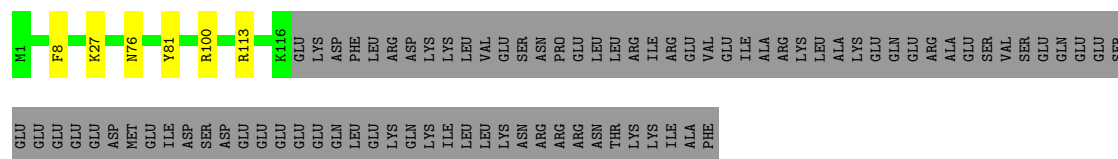


- Molecule 10: Nuclear GTP-binding protein NUG1

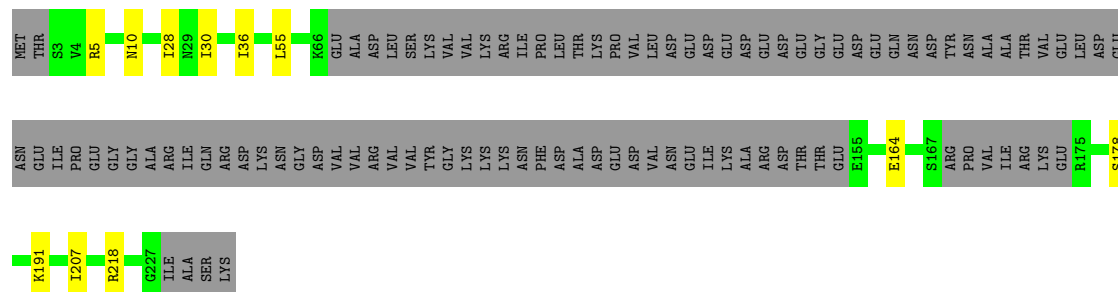




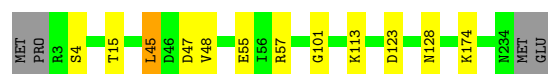
- Molecule 11: Ribosome biogenesis protein RLP24



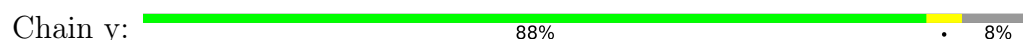
- Molecule 12: Nucleolar protein 16

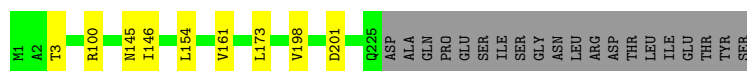


- Molecule 13: Ribosome assembly factor MRT4

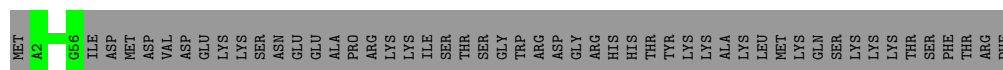


- Molecule 14: Eukaryotic translation initiation factor 6

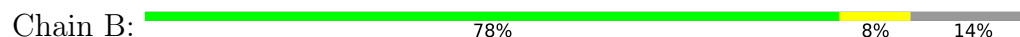




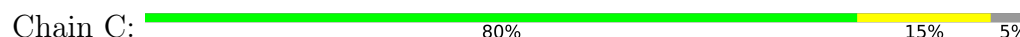
- Molecule 15: UPF0642 protein YBL028C



- Molecule 16: 60S ribosomal protein L3

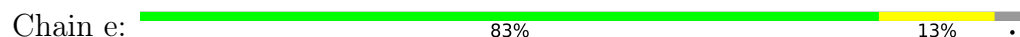


- Molecule 17: 60S ribosomal protein L4-A

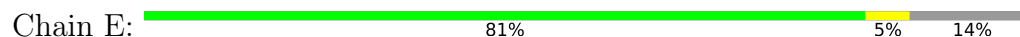


ASP

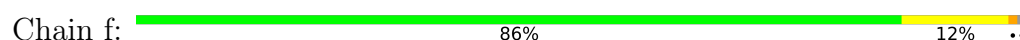
- Molecule 18: 60S ribosomal protein L32



- Molecule 19: 60S ribosomal protein L6-A



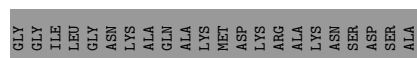
- Molecule 20: 60S ribosomal protein L33-A





- Molecule 21: 60S ribosomal protein L8-A

Chain G: 54% 9% 38%



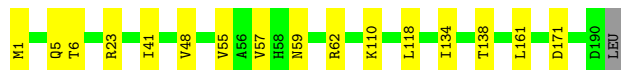
- Molecule 22: 60S ribosomal protein L35-A

Chain h: 88% 10% ..



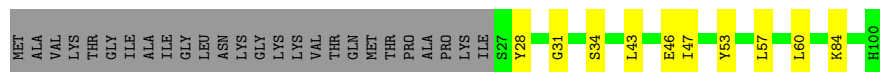
- Molecule 23: 60S ribosomal protein L9-A

Chain H: 91% 8% .



- Molecule 24: 60S ribosomal protein L36-B

Chain i: 64% 10% 26%



- Molecule 25: 60S ribosomal protein L37-A

Chain j: 69% 10% . 19%



- Molecule 26: 60S ribosomal protein L13-A

Chain L: 49% 6% 46%



PRO ILE ALA GLN PRO PRO THR ASP VAL GLU ALA ARG ALA VAL ASP GLN ASP ASN GLY GLU SER ALA PHE ARG THR LEU ARG ALA ALA SER SER GLY LYS PHE ARG GLY ILE ARG GLU LYS ALA ARG ALA ARG GLU LYS LYS ALA GLU ALA GLU ALA GLU LYS LYS

• Molecule 27: 60S ribosomal protein L14-A

Chain M:  92% 5%

MET SER THR D4 V15 A29 I39 V63 T69 T80 K125 K137 ALA

• Molecule 28: 60S ribosomal protein L15-A

Chain N:  74% 13% 13%

MET G2 L7 L10 L19 L22 L29 R38 D46 R49 V66 G69 ASN ARG LYS ARG VAL PRO LYS GLY ALA THR TYR GLY LYS PRO THR ASN GLN GLY VAL ASN GLU LEU LYS TYR R96 R105 R108 L116 V121 M122 T126

V132 I133 I142 R143 R144 D145 D153 P154 V155 T167 S171 A20 K179 G186 R187 K204

• Molecule 29: 60S ribosomal protein L16-A

Chain O:  42% 47% 10%

MET SER V3 V7 V8 A83 I9 D10 G11 K12 L15 L16 G17 R18 A19 S21 A20 V22 K25 Q26 L27 L28 N29 G30 Q31 V34 R37 R38 E39 M42 I43 E46 F47 F48 R49 N50 K53 P56 R59 K60 A61 T62 A63 F64 P70 R74 A75 P76 S77

R78 I79 F80 Y81 K82 A83 L84 R85 G86 M87 V88 S89 H90 K91 T92 A93 R94 S21 G95 L99 E100 R101 L102 F105 K116 R117 V118 P121 Q122 A123 L124 R125 V126 I127 R128 G132 R133 K134 L138 G139 K140 L141 S142 T143 S144 V145 Y149 E150 D151 V152 V153 A154 K155 L156

E157 A158 K159 R160 V162 K161 S163 S164 A166 E167 Y168 Y169 A169 K170 F174 T175 K176 K177 V178 A179 T184 A185 A186 E187 S188 D189 V190 A191 K192 Q193 L194 Y199

• Molecule 30: 60S ribosomal protein L17-A

Chain P:  65% 9% 26%

MET ALA ARG THR ALA THR N10 S16 V24 T29 R30 L41 T42 L52 K74 V78 P84 S87 Q86 V119 N120 K124 GLN ARG ARG ARG THR TYR ARG ALA HIS GLY ILE ARG MET ARG ASN LYS TYR E140 A156 V157 A158 K159 A160 A161

GLU LYS VAL VAL ARG LEU THR SER ARG GLN ARG GLY ARG ILE ALA ALA GLN LYS ARG ILE ALA

• Molecule 31: 60S ribosomal protein L18-A

Chain Q:  65% 6% 30%

MET GLY ILE ASP HIS THR SER LYS GLN HIS LYS ARG ARG GLY H15 K20 S21 D22 V23 V24 L28 L49 S55 K56 V64 R69 R92 N136 H145 SER ARG GLU PHE ALA VAL ARG HIS PHE GLY MET GLY PRO LYS LYS GLY LYS ALA PRO ARG ARG ILE LEU SER

THR
GLY
ARG
LYS
PHE
GLU
ARG
ALA
ARG
GLY
P22
ARG
ARG
SER
LYS
GLY
PHE
LYS
VAL

• Molecule 32: 60S ribosomal protein L20-A

Chain S: 87% 11% ..

MET
ALA
R3
R12
R13
L14
E21
P22
R23
L24
S32
S80
K71
I94
R95
D96
L106
R115
H122
D134
H154
K158
R167
P168
S169
Y172

• Molecule 33: 60S ribosomal protein L23-A

Chain V: 90% 8% ..

MET
SER
GLY
ASN
GLY
ALA
GLN
THR
LYS
PHE
R12
L54
K64
L93
Y137

• Molecule 34: 60S ribosomal protein L26-A

Chain Y: 87% 10% ..

MET
A2
S5
K17
K37
R51
R52
D53
D54
E55
V56
L57
V58
Y59
K64
Y74
T107
L111
L126
GLU

• Molecule 35: 25S ribosomal RNA

Chain 1: 37% 15% 47%

G1
U2
U3
A6
C7
A11
G18
A26
G30
A39
A40
C41
C42
A43
A48
A49
U50
A57
G58
G59
A60
A65
A66
C72
C73
G74
G75
G92
C93
C94
A95
G96
C105
G110
C111
A116
U117
U118
U119
G120
A121
A122
C125
U133

U134
C135
G136
G143
A146
U147
G148
G155
G156
A157
G161
A164
A165
C166
G170
G171
G172
G173
U190
U191
C200
G206
U210
A211
G212
A213
G218
A219
G220
C221
G239
U240
G241
C242
G243
U249
U250
G251
A255
A256
G267
A268
G269
U270
G277

G281
G282
G283
A284
A285
U286
G287
A295
A296
G297
U298
G299
G304
U305
A
A
U
U310
C311
C315
A323
A324
U329
A336
C346
A349
A352
G353
U354
C368
A369
U370
A374
G376
A377
G383
A384
A385
A386
A387
C388
A389
G390
A395

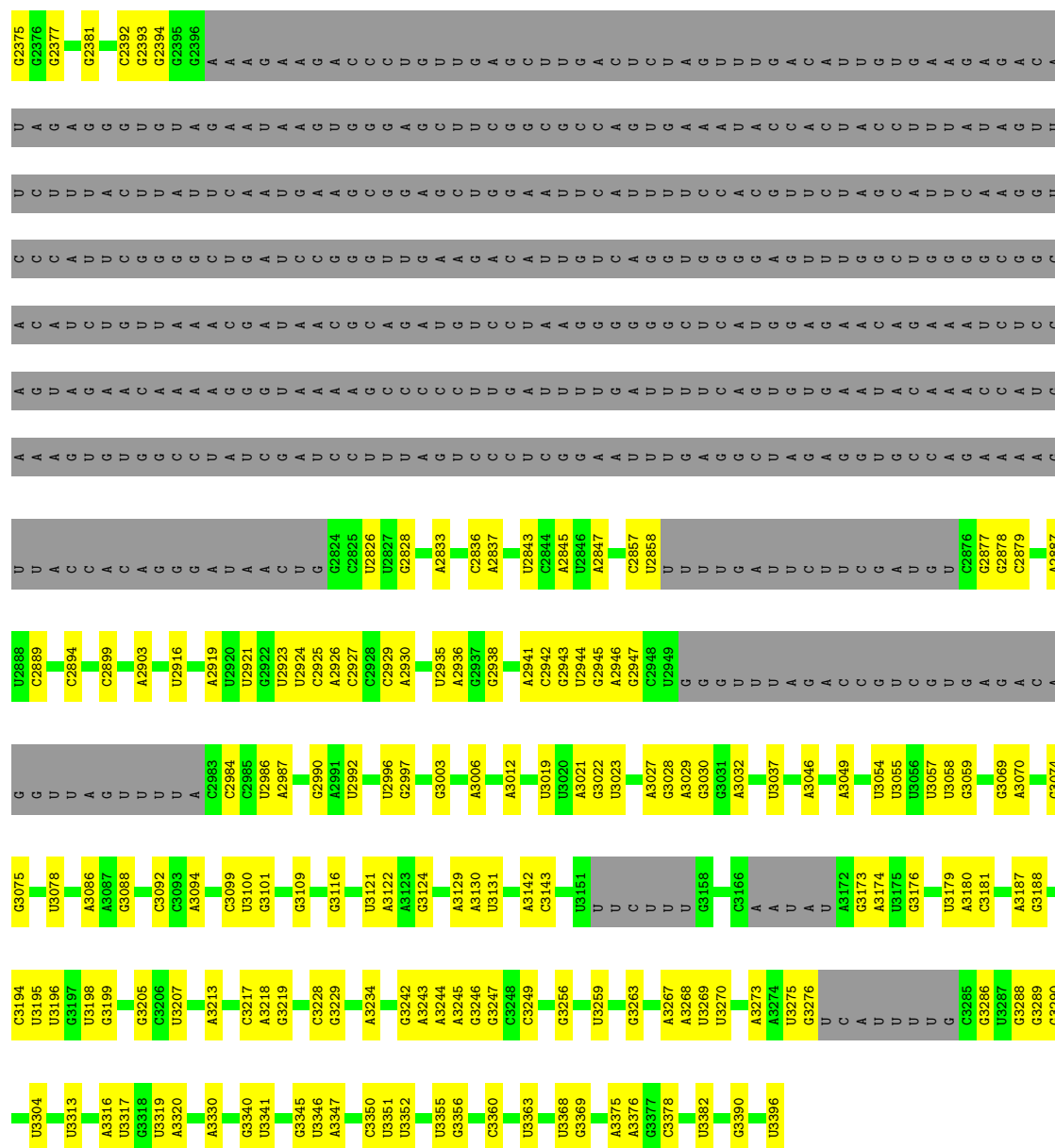
A398
A399
G400
U401
A402
C403
G406
G421
A422
U429
A436
A437
A438
C439
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U441
G442
U449
G452
C453
U454
A455
U456
C457
U458
G459
C462
C463
U464
U465
G466
U467
G468
G474
A478
U479
C480
U481
C482
G494
G495
A498
A611
C503
G510
C515

A516
G517
G518
A519
U520
A521
A522
A523
A527
A533
U534
G535
C543
C544
U545
C546
G547
G548
U549
A551
G552
U555
U556
A557
U558
A559
A569
U570
A571
A572
A578
G579
G588
A589
G590
G591
A592
G597
A602
A603
G604
A607
A780
G781
U782
A783
A784
G785
A786

C636
U642
U643
U644
A645
A646
A647
C648
A649
C650
A660
G661
C675
G676
A677
U681
A691
C694
C695
U704
A705
A720
G721
G722
G742
G750
U756
C757
U761
U
U
U
C
U
C
U
C
G769
U776
A780
G781
U782
A783
A784
G785
A786

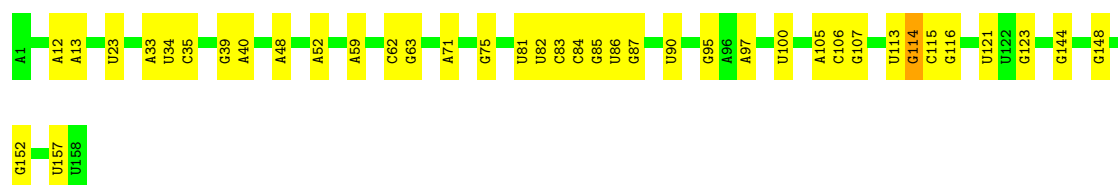
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G799
A806
A807
A808
G813
U814
G815
A816
A817
C
U
A
U
U
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C
C
C
G
U
A
A
U
A
G
G
G
U
U
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G
G
U
G
G
G
A
G
G
C
C





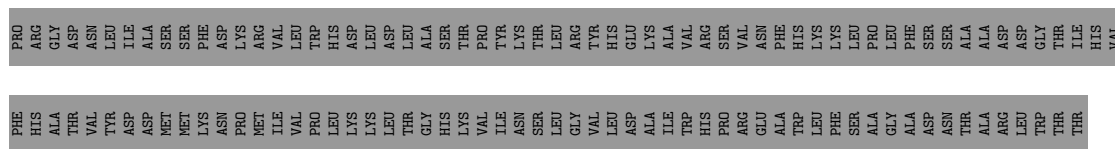
• Molecule 36: 5.8S ribosomal RNA

Chain 2: 75% 24%

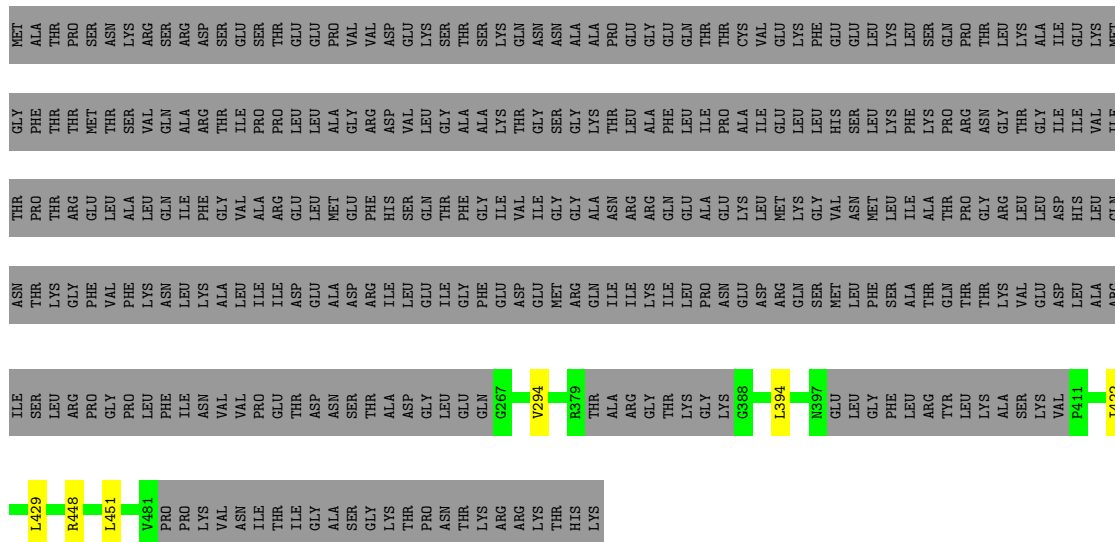


• Molecule 37: 5.8S ribosomal RNA

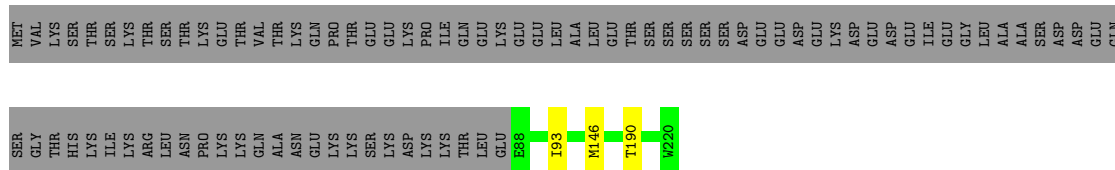
Chain 6: 15% 13% 72%



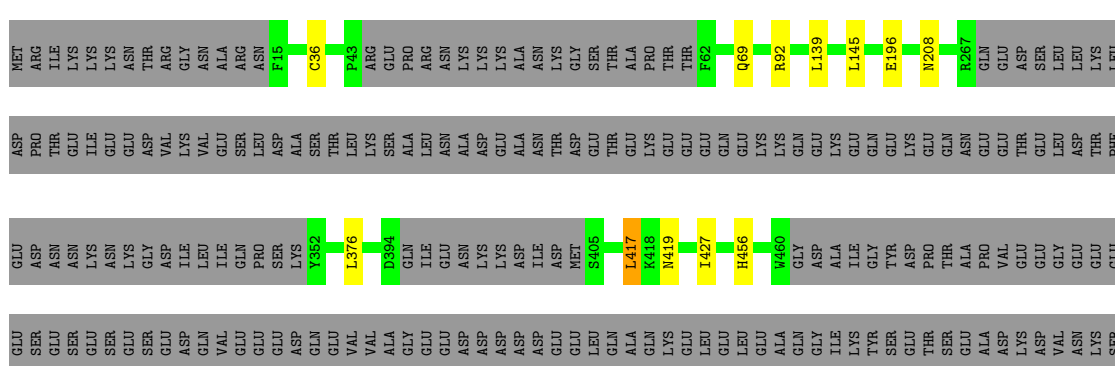
- Molecule 40: ATP-dependent RNA helicase HAS1



- Molecule 41: Ribosome biogenesis protein 15



- Molecule 42: Pescadillo homolog



[illegible]

- Molecule 43: Ribosome biogenesis protein RLP7

Chain t:  72% • 24%

GLY	ALA	GLU	GLU	GLU	THR	ASN	ASP	SER	VAL	ASP	ASP	LEU	GLU	GLU	THR	LEU	ASN	SER	ASN	GLU	ILE	LEU	LEU	ARG	LYS	ARG	ARG	ASN	ALA	ASP	ARG	THR	ARG	ILE	GLU	GLN	GLU	LEU	ALA	LYS	LYS	ARG	GLU	GLU	GLN	ILE	LYS	LYS	LYS	ARG	SER	ASN	LYS	ME3	L66	L106	LYS	ALA	ASN
GLY	ALA	GLU	GLU	GLU	THR	ASN	ASP	SER	VAL	ASP	ASP	LEU	GLU	GLU	THR	LEU	ASN	SER	ASN	GLU	ILE	LEU	LEU	ARG	LYS	ARG	ARG	ASN	ALA	ASP	ARG	THR	ARG	ILE	GLU	GLN	GLU	LEU	ALA	LYS	LYS	ARG	GLU	GLU	GLN	ILE	LYS	LYS	LYS	ARG	SER	ASN	LYS	ME3	L66	L106	LYS	ALA	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	156937	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 ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	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	x	0.55	1/2312 (0.0%)	0.80	1/3097 (0.0%)
2	F	0.49	0/1974	0.73	2/2654 (0.1%)
3	3	0.64	0/1461	0.93	2/1958 (0.1%)
4	4	0.47	0/1895	0.81	2/2549 (0.1%)
5	5	0.44	0/3109	0.68	0/4187
6	A	0.47	0/1243	0.64	0/1679
7	b	0.43	0/3474	0.64	1/4683 (0.0%)
8	J	0.44	0/559	0.58	0/754
9	r	0.41	0/638	0.61	0/837
10	s	0.44	0/224	0.64	0/288
11	u	0.42	0/996	0.61	0/1324
12	v	0.46	0/1100	0.63	0/1456
13	W	0.42	0/1902	0.62	1/2564 (0.0%)
14	y	0.41	0/1722	0.63	0/2343
15	z	0.39	0/445	0.60	0/585
16	B	0.44	0/2699	0.70	1/3626 (0.0%)
17	C	0.56	0/2660	0.86	4/3601 (0.1%)
18	e	0.56	0/1030	0.82	2/1379 (0.1%)
19	E	0.47	0/1226	0.72	0/1648
20	f	0.56	0/868	0.79	0/1168
21	G	0.44	0/1252	0.71	0/1695
22	h	0.42	0/978	0.70	1/1301 (0.1%)
23	H	0.43	0/1531	0.65	0/2062
24	i	0.41	0/599	0.70	0/793
25	j	0.55	0/578	0.85	0/767
26	L	0.51	0/877	0.84	0/1179
27	M	0.42	0/1056	0.69	0/1421
28	N	0.56	2/1544 (0.1%)	0.78	3/2065 (0.1%)
29	O	0.70	1/1585 (0.1%)	0.88	2/2128 (0.1%)
30	P	0.49	0/1080	0.70	0/1455
31	Q	0.47	0/1024	0.74	0/1385
32	S	0.47	0/1468	0.69	0/1973

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	V	0.41	0/950	0.61	0/1279
34	Y	0.59	1/995 (0.1%)	0.77	0/1329
35	1	0.35	0/42777	0.69	10/66679 (0.0%)
36	2	0.35	0/3740	0.69	1/5808 (0.0%)
37	6	0.27	0/1527	0.75	0/2371
38	K	0.42	0/2107	0.65	0/2845
39	m	0.40	0/1401	0.64	0/1895
40	D	0.44	0/1626	0.65	0/2193
41	o	0.42	0/1129	0.65	0/1502
42	n	0.42	0/2802	0.62	1/3791 (0.0%)
43	t	0.40	0/1961	0.65	0/2639
All	All	0.42	5/106124 (0.0%)	0.70	34/152935 (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
3	3	0	1
4	4	0	3
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	Y	126	LEU	C-O	11.24	1.44	1.23
29	O	100	GLU	CD-OE2	8.32	1.34	1.25
28	N	105	ARG	CZ-NH1	7.06	1.42	1.33
1	x	180	GLU	C-O	5.37	1.33	1.23
28	N	105	ARG	NE-CZ	5.00	1.39	1.33

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	1	649	A	C2'-C3'-O3'	8.99	129.27	109.50
29	O	19	LEU	CA-CB-CG	-8.57	95.58	115.30
17	C	313	LEU	CA-CB-CG	8.43	134.69	115.30
35	1	1347	U	C4'-C3'-O3'	7.64	128.28	113.00
28	N	105	ARG	NE-CZ-NH1	7.48	124.04	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	118	VAL	Peptide
4	4	135	TYR	Peptide
4	4	136	LEU	Mainchain
4	4	225	VAL	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	
1	x	259/295 (88%)	203 (78%)	44 (17%)	12 (5%)	2	18
2	F	239/244 (98%)	212 (89%)	23 (10%)	4 (2%)	7	37
3	3	171/306 (56%)	122 (71%)	38 (22%)	11 (6%)	1	13
4	4	209/278 (75%)	173 (83%)	26 (12%)	10 (5%)	2	17
5	5	377/463 (81%)	338 (90%)	33 (9%)	6 (2%)	8	38
6	A	139/291 (48%)	122 (88%)	12 (9%)	5 (4%)	3	23
7	b	413/647 (64%)	381 (92%)	27 (6%)	5 (1%)	11	43
8	J	64/427 (15%)	58 (91%)	4 (6%)	2 (3%)	3	26
9	r	71/261 (27%)	65 (92%)	4 (6%)	2 (3%)	4	27
10	s	25/520 (5%)	25 (100%)	0	0	100	100
11	u	114/199 (57%)	109 (96%)	4 (4%)	1 (1%)	14	48
12	v	124/231 (54%)	115 (93%)	9 (7%)	0	100	100
13	W	230/236 (98%)	213 (93%)	15 (6%)	2 (1%)	14	48
14	y	223/245 (91%)	210 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	z	53/106 (50%)	49 (92%)	4 (8%)	0	100	100
16	B	329/387 (85%)	289 (88%)	30 (9%)	10 (3%)	3	26
17	C	341/362 (94%)	295 (86%)	30 (9%)	16 (5%)	2	18
18	e	123/130 (95%)	113 (92%)	9 (7%)	1 (1%)	16	51
19	E	147/176 (84%)	131 (89%)	16 (11%)	0	100	100
20	f	104/107 (97%)	98 (94%)	4 (4%)	2 (2%)	6	35
21	G	155/256 (60%)	134 (86%)	17 (11%)	4 (3%)	4	28
22	h	117/120 (98%)	104 (89%)	8 (7%)	5 (4%)	2	19
23	H	188/191 (98%)	167 (89%)	20 (11%)	1 (0%)	25	59
24	i	72/100 (72%)	66 (92%)	4 (6%)	2 (3%)	4	27
25	j	69/88 (78%)	62 (90%)	5 (7%)	2 (3%)	3	27
26	L	106/199 (53%)	97 (92%)	7 (7%)	2 (2%)	6	35
27	M	132/138 (96%)	121 (92%)	9 (7%)	2 (2%)	8	39
28	N	173/204 (85%)	150 (87%)	22 (13%)	1 (1%)	22	55
29	O	195/199 (98%)	66 (34%)	44 (23%)	85 (44%)	0	0
30	P	133/184 (72%)	118 (89%)	13 (10%)	2 (2%)	8	39
31	Q	129/186 (69%)	117 (91%)	12 (9%)	0	100	100
32	S	168/172 (98%)	143 (85%)	18 (11%)	7 (4%)	2	20
33	V	124/137 (90%)	113 (91%)	11 (9%)	0	100	100
34	Y	123/127 (97%)	110 (89%)	11 (9%)	2 (2%)	8	38
38	K	253/376 (67%)	231 (91%)	20 (8%)	2 (1%)	16	51
39	m	159/807 (20%)	144 (91%)	14 (9%)	1 (1%)	22	55
40	D	188/505 (37%)	167 (89%)	21 (11%)	0	100	100
41	o	131/220 (60%)	121 (92%)	9 (7%)	1 (1%)	16	51
42	n	326/605 (54%)	302 (93%)	22 (7%)	2 (1%)	22	55
43	t	240/322 (74%)	214 (89%)	20 (8%)	6 (2%)	4	29
All	All	6936/11047 (63%)	6068 (88%)	652 (9%)	216 (3%)	5	26

5 of 216 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	x	119	PRO
1	x	128	PHE

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Mol	Chain	Res	Type
1	x	222	PRO
2	F	160	ARG
2	F	164	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	252/276 (91%)	206 (82%)	46 (18%)	1	8
2	F	204/205 (100%)	191 (94%)	13 (6%)	14	43
3	3	155/274 (57%)	129 (83%)	26 (17%)	1	11
4	4	203/257 (79%)	177 (87%)	26 (13%)	3	19
5	5	343/410 (84%)	323 (94%)	20 (6%)	17	46
6	A	137/263 (52%)	129 (94%)	8 (6%)	17	46
7	b	377/573 (66%)	345 (92%)	32 (8%)	8	33
8	J	61/383 (16%)	61 (100%)	0	100	100
9	r	65/229 (28%)	63 (97%)	2 (3%)	35	62
10	s	24/445 (5%)	23 (96%)	1 (4%)	25	54
11	u	101/180 (56%)	96 (95%)	5 (5%)	20	49
12	v	116/205 (57%)	105 (90%)	11 (10%)	7	30
13	W	209/213 (98%)	199 (95%)	10 (5%)	21	51
14	y	193/211 (92%)	184 (95%)	9 (5%)	22	51
15	z	48/95 (50%)	48 (100%)	0	100	100
16	B	280/323 (87%)	259 (92%)	21 (8%)	11	37
17	C	273/289 (94%)	238 (87%)	35 (13%)	3	19
18	e	108/111 (97%)	94 (87%)	14 (13%)	3	19
19	E	131/153 (86%)	123 (94%)	8 (6%)	15	44
20	f	90/91 (99%)	77 (86%)	13 (14%)	2	16
21	G	128/208 (62%)	110 (86%)	18 (14%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	h	104/105 (99%)	96 (92%)	8 (8%)	10	36
23	H	170/171 (99%)	155 (91%)	15 (9%)	8	32
24	i	61/81 (75%)	53 (87%)	8 (13%)	3	19
25	j	59/71 (83%)	50 (85%)	9 (15%)	2	14
26	L	87/159 (55%)	78 (90%)	9 (10%)	6	27
27	M	106/109 (97%)	101 (95%)	5 (5%)	22	51
28	N	153/176 (87%)	128 (84%)	25 (16%)	2	12
29	O	160/162 (99%)	114 (71%)	46 (29%)	0	2
30	P	109/146 (75%)	94 (86%)	15 (14%)	3	17
31	Q	107/151 (71%)	96 (90%)	11 (10%)	6	27
32	S	155/156 (99%)	141 (91%)	14 (9%)	8	32
33	V	98/105 (93%)	95 (97%)	3 (3%)	35	62
34	Y	108/110 (98%)	96 (89%)	12 (11%)	5	25
38	K	238/346 (69%)	233 (98%)	5 (2%)	48	71
39	m	150/723 (21%)	146 (97%)	4 (3%)	40	65
40	D	175/440 (40%)	169 (97%)	6 (3%)	32	60
41	o	118/199 (59%)	116 (98%)	2 (2%)	56	75
42	n	302/548 (55%)	292 (97%)	10 (3%)	33	61
43	t	216/287 (75%)	210 (97%)	6 (3%)	38	64
All	All	6174/9639 (64%)	5643 (91%)	531 (9%)	11	33

5 of 531 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	Q	55	SER
32	S	115	ARG
31	Q	49	LEU
42	n	208	ASN
13	W	55	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
32	S	62	ASN

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Mol	Chain	Res	Type
32	S	142	GLN
41	o	113	GLN
12	v	33	ASN
8	J	228	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	1	1772/3396 (52%)	498 (28%)	49 (2%)
36	2	152/158 (96%)	36 (23%)	6 (3%)
37	6	63/232 (27%)	30 (47%)	2 (3%)
All	All	1987/3786 (52%)	564 (28%)	57 (2%)

5 of 564 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	1	3	U
35	1	6	A
35	1	7	C
35	1	11	A
35	1	18	G

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	1	1307	G
37	6	16	U
35	1	2392	C
36	2	114	G
36	2	39	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	2	6
1	x	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	124:G	O3'	125:U	P	7.11
1	2	110:C	O3'	111:A	P	6.92
1	2	125:U	O3'	126:A	P	6.42
1	2	113:U	O3'	114:G	P	4.42
1	2	126:A	O3'	127:U	P	3.70

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3893. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.