



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2024 – 10:57 AM JST

PDB ID : 8I9R
EMDB ID : EMD-35281
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State 5S RNP
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.10 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:

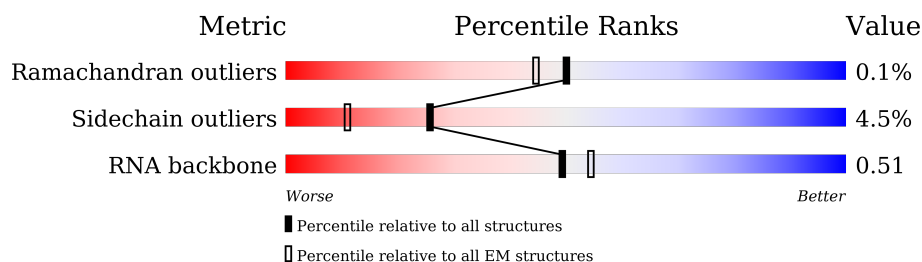
EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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.




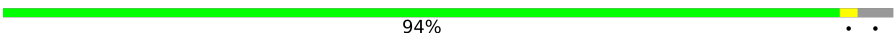
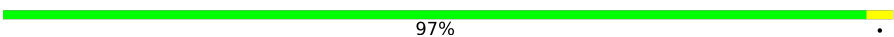







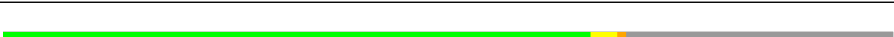


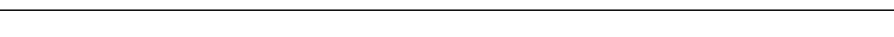
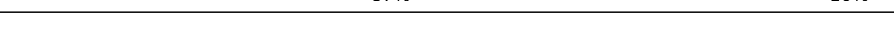
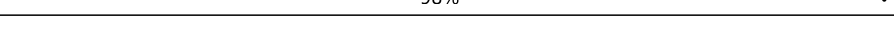


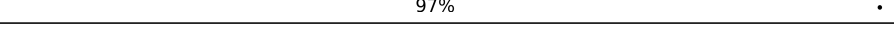
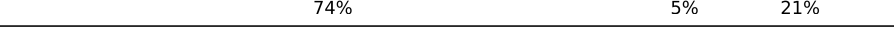
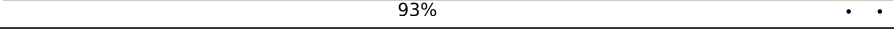
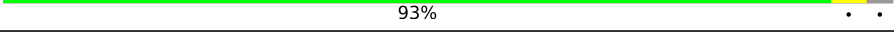
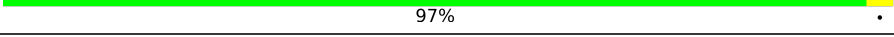
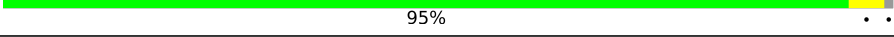

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	C1	3341	
2	C2	256	
3	CA	316	
4	CB	391	
5	CC	801	
6	CE	598	
7	CH	661	
8	CI	414	
9	CJ	679	














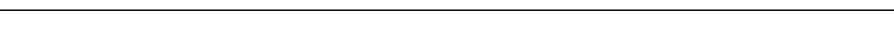
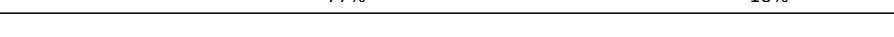
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Mol	Chain	Length	Quality of chain
10	CM	249	
10	LF	249	
11	CN	246	
12	CQ	225	
13	CR	237	
14	CU	451	
15	Ch	354	
16	LB	392	
17	LC	365	
18	LE	200	
19	LG	262	
20	LL	213	
21	LM	142	
22	LN	203	
23	LO	204	
24	LP	187	
25	LQ	213	
26	LS	174	
27	LT	160	
28	LV	139	
29	LY	138	
30	Le	131	
31	Lf	109	
32	Lh	935	
33	Li	110	

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Mol	Chain	Length	Quality of chain
34	Lj	95	 77% 22%
35	Cc	282	 80% 16%
36	Cd	436	 76% 20%
37	Ce	336	 56% 42%
38	Cf	570	 25% 74%
39	Cy	350	 70% 30%
40	Cg	478	 46% 51%
41	CP	751	 43% 57%
42	CG	184	 96%
43	Lq	217	 94% 5%
44	Cx	202	 50% 50%
45	LJ	173	 98%
46	LD	304	 90% 10%
47	C4	119	 77% 18%
48	CX	203	 31% 69%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 117417 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 RNA (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	2048	Total	C	N	O	P	0	0
			43814	19561	7931	14274	2048		

- Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	228	Total	C	N	O	P	0	0
			4846	2162	864	1592	228		

- Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CA	260	Total	C	N	O	S	0	0
			2144	1371	393	373	7		

- Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	260	Total	C	N	O	S	0	0
			2063	1322	367	371	3		

- Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CC	272	Total	C	N	O	S	0	0
			2258	1438	379	434	7		

- Molecule 6 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CE	463	Total	C	N	O	S	0	0
			3673	2352	643	667	11		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CH	108	Total	C	N	O	S	0	0
			891	561	146	183	1		

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 9 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CJ	380	Total	C	N	O	S	0	0
			3109	2003	547	549	10		

- Molecule 10 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CM	187	Total	C	N	O	S	0	0
			1525	987	278	257	3		
10	LF	240	Total	C	N	O	S	0	0
			1967	1264	368	332	3		

- Molecule 11 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CN	246	Total	C	N	O	S	0	0
			1856	1158	322	369	7		

- Molecule 12 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CQ	112	Total	C	N	O	S	0	0
			960	607	195	148	10		

- Molecule 13 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 14 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CU	121	Total	C	N	O	S	0	0
			969	604	179	183	3		

- Molecule 15 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ch	71	Total	C	N	O	S	0	0
			562	350	109	102	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LB	341	Total	C	N	O	S	0	0
			2708	1721	493	482	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LC	362	Total	C	N	O	S	0	0
			2752	1738	526	479	9		

- Molecule 18 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LE	170	Total	C	N	O	S	0	0
			1338	861	241	233	3		

- Molecule 19 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LG	183	Total	C	N	O	S	0	0
			1470	951	263	252	4		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	117	Total	C	N	O	S	0	0
			964	608	206	148	2		

- Molecule 21 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	137	Total	C	N	O	S	0	0
			1101	699	211	190	1		

- Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	183	Total	C	N	O	S	0	0
			1563	974	332	253	4		

- Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	204	Total	C	N	O	S	0	0
			1618	1039	306	267	6		

- Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	154	Total	C	N	O	S	0	0
			1212	758	233	218	3		

- Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	129	Total	C	N	O	S	0	0
			1021	646	200	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	174	Total	C	N	O	S	0	0
			1433	922	267	239	5		

- Molecule 27 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	126	Total	C	N	O	S	0	0
			1014	643	196	173	2		

- Molecule 28 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	135	Total	C	N	O	S	0	0
			995	633	185	170	7		

- Molecule 29 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 30 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Le	131	Total	C	N	O	S	0	0
			1055	663	213	172	7		

- Molecule 31 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 32 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Lh	121	Total	C	N	O	0	0
			995	633	196	166		

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Li	88	Total	C	N	O	S	0	0
			731	449	162	119	1		

- Molecule 34 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lj	74	Total	C	N	O	S	0	0
			595	365	132	93	5		

- Molecule 35 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Cc	236	Total	C	N	O	S	0	0
			1898	1208	337	343	10		

- Molecule 36 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Cd	347	Total	C	N	O	S	0	0
			2800	1764	538	494	4		

- Molecule 37 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ce	194	Total	C	N	O	S	0	0
			1609	1020	304	276	9		

- Molecule 38 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cf	147	Total	C	N	O	S	0	0
			1225	755	245	224	1		

- Molecule 39 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cy	244	Total	C	N	O		0	0
			1210	722	244	244			

- Molecule 40 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Cg	233	Total	C	N	O	S	0	0
			1850	1168	348	324	10		

- Molecule 41 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CP	324	Total	C	N	O		0	0
			1596	948	324	324			

- Molecule 42 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	CG	177	Total	C	N	O	0	0
			873	519	177	177		

- Molecule 43 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	Lq	207	Total	C	N	O	0	0
			1021	607	207	207		

- Molecule 44 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Cx	102	Total	C	N	O	0	0
			565	340	114	111		

- Molecule 45 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	LJ	169	Total	C	N	O	0	0
			831	492	169	170		

- Molecule 46 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	LD	273	Total	C	N	O	0	0
			1346	801	273	272		

- Molecule 47 is a RNA chain called RNA (119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	C4	119	Total	C	N	O	P	0	0
			2536	1131	453	833	119		

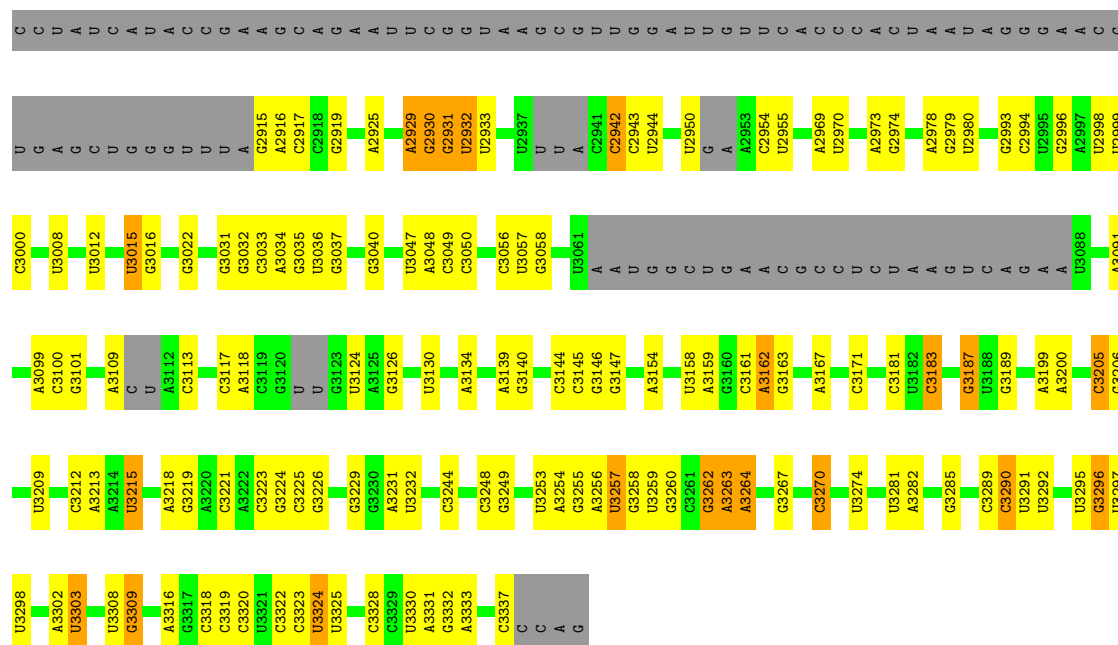
- Molecule 48 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	CX	63	Total	C	N	O	0	0
			375	233	68	74		

- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

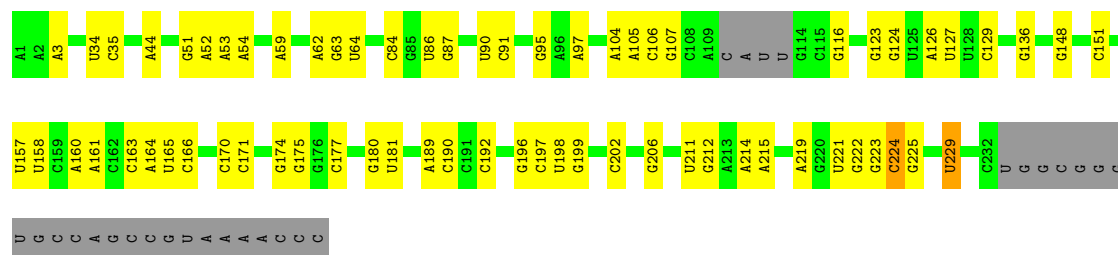
Mol	Chain	Residues	Atoms		AltConf
49	C1	1	Total 1	Zn 1	0
49	Lj	1	Total 1	Zn 1	0
49	Ce	1	Total 1	Zn 1	0





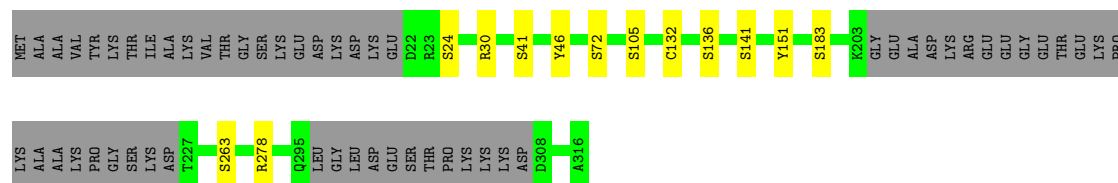
• Molecule 2: RNA (256-MER)

Chain C2: 63% 25% 11%



• Molecule 3: Brix domain-containing protein

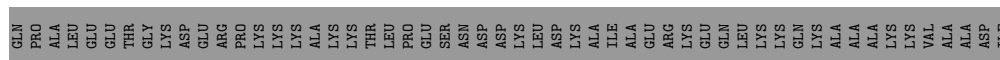
Chain CA: 78% 18%



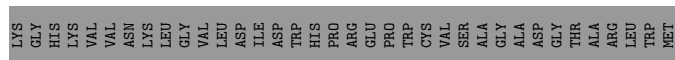
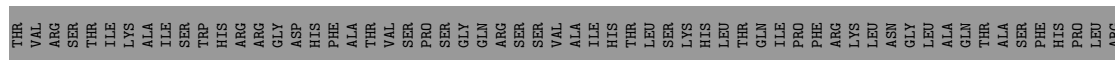
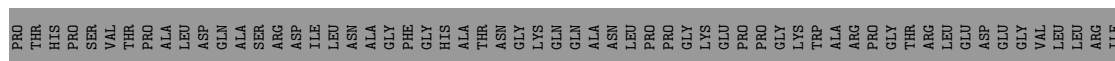
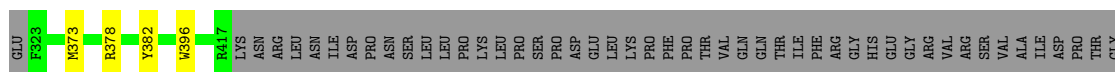
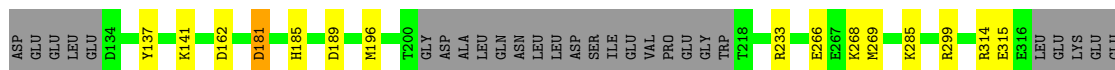
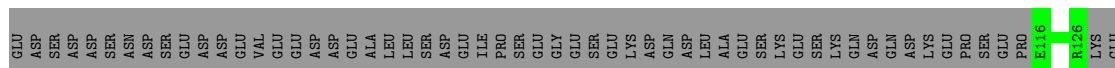
• Molecule 4: Ribosome biogenesis protein C8F11.04

Chain CB: 62% 5% 34%

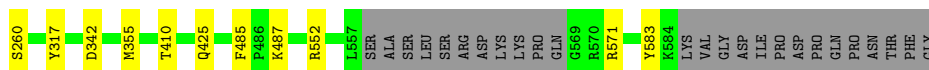
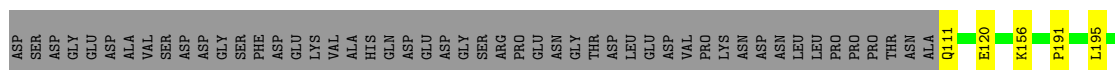
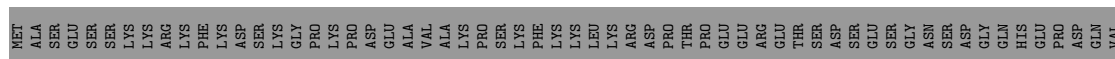




Chain CC:  32% . 66%



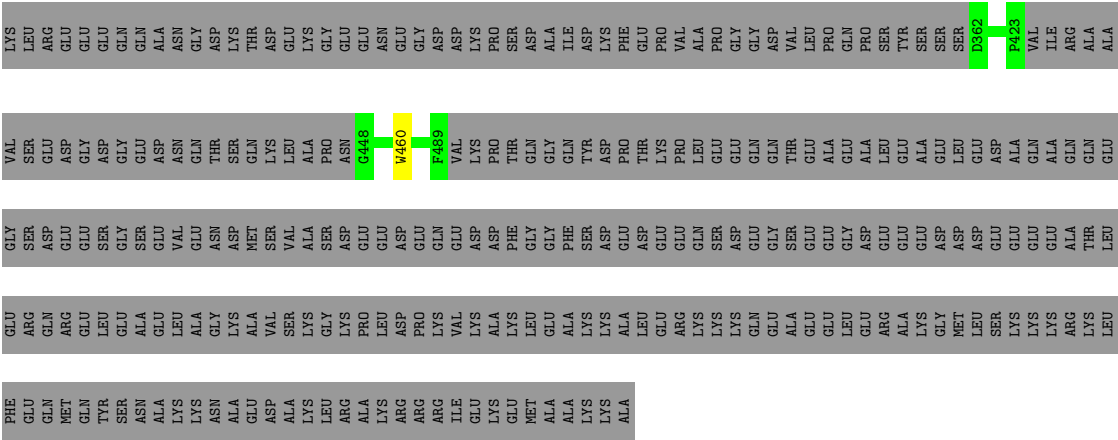
Chain CE: 75% . 23%



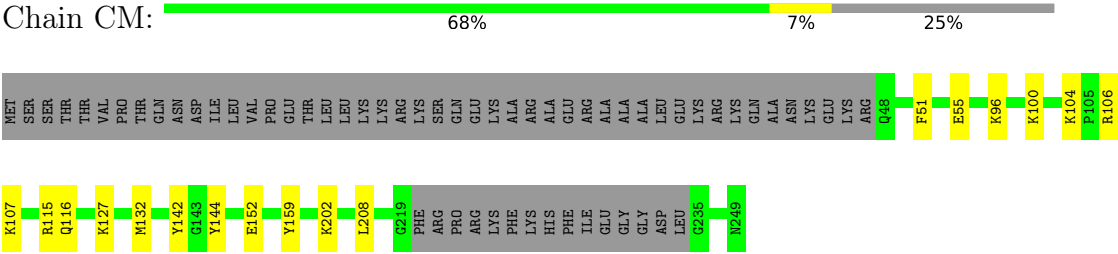
[illegible]

GLU	GLU	GLY	ALA	ASP	VAL	MET
GLU	VAL	GLY	GLY	GLU	VAL	ALA
GLU	ASP	\$184		SER	LYS	ALA
GLU	GLU		F198	LEU	ALA	ARG
LYS	ALA			ASP	VAL	LYS
PRO	PRO	R261		GLU	ALA	LYS
ALA	ALA	V268		GLN	GLU	LYS
PRO	PRO			THR	GLU	SER
LYS	LYS	R291		LYS	ASP	SER
THR	THR			ALA	LYS	ALA
LYS	LYS	E318		LEU	ILE	ALA
VAL	VAL			MET	ALA	VAL
GLU	GLY	A329		THR	GLU	ASP
LYS	LYS		PRO	LEU	PRO	LYS
ASP	ASP	ALA	ALA	ASP	VAL	ASP
LYS	LYS	LEU	ALA	ASP	LYS	ALA
PRO	PRO	LYS	LYS	GLY	SER	ALA
ALA	ALA	VAL	PRO	GLU	VAL	ILE
THR	THR	ILE	PRO	GLU	LEU	SER
SER	SER	LEU	LEU	SER	LYS	LYS
ALA	ALA	GLU	ASN	GLN	LYS	GLU
PRO	PRO	ASN	GLY	VAL	ALA	VAL
LYS	LYS	GLY	GLU	VAL	LYS	THR
LYS	GLY	GLU	GLU	THR	GLU	LYS
LYS	LYS	ILE	ILE	PHE	ALA	ALA
THR	THR	GLU	GLU	LYS	ALA	THR
LYS	LYS	THR	LYS	LYS	LYS	PRO
SER	SER	LYS	LYS	LYS	PRO	LYS
LYS	LYS	ALA	GLY	GLY	LYS	ALA
LYS	LYS	ILE	GLN	GLN	LYS	LYS
THR	THR	GLU	ASP	VAL	GLN	ARG
LYS	LYS	THR	THR	GLY	GLU	LYS
SER	SER	ALA	PRO	LYS	LYS	ALA
		ALA	ALA	ILE	VAL	PRO
		PRO	PRO	PRO	GLU	GLU
		VAL	VAL	PRO	GLU	ALA
		GLU	GLU	LYS	GLU	SER
		GLU	GLU	LYS	GLU	PRO
		LYS	LYS	ALA	GLU	VAL
		SER	SER	GLN	ASN	LYS
		VAL	VAL	THR	ALA	GLN
		ALA	ALA	ASN	ASP	LYS
		ARG	LYS	GLY	ALA	LYS
		ALA	THR	ASP	ALA	ASP
		GLN	GLN	SER	PHE	LYS
		THR	LYS	LYS	GLY	ASP
		GLU	PRO	PRO	SER	ALA

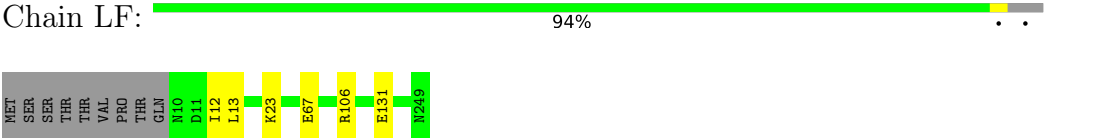
MET
G2
K34
R35
L38
C37
V39
R105
R108
K115
R170
Y243
R244
F257
K261
E267
N277
LEU
ALA
GLN
SR
ASN
GLY
GLU
GLN
LYS
ALA
ILE
THR
ASN
ASP
GLY
GLU
GLU
HIS
GLY
PRO
ASP
PRO
VAL
GLM
ALA
GLU
VAL
ASP
LYS
LEU
VAL



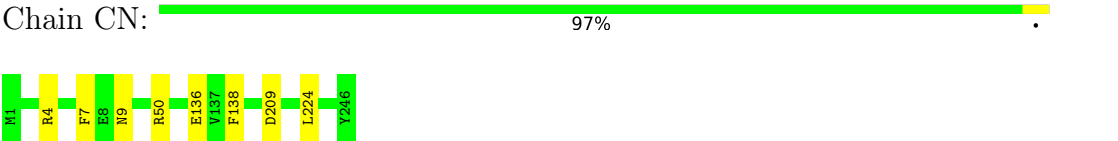
• Molecule 10: 60S ribosomal protein l7-like protein



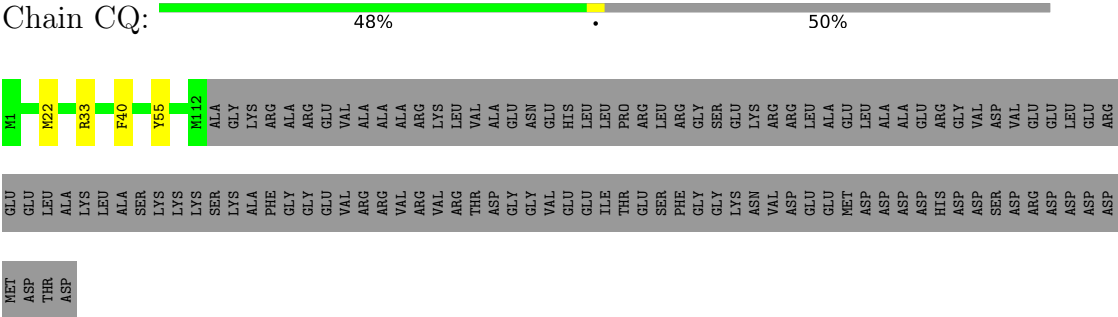
• Molecule 10: 60S ribosomal protein l7-like protein



• Molecule 11: Eukaryotic translation initiation factor 6



• Molecule 12: Ribosome biogenesis protein RLP24





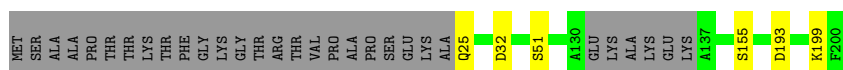
- Molecule 17: 60S ribosomal protein L4-like protein

Chain LC: 97%



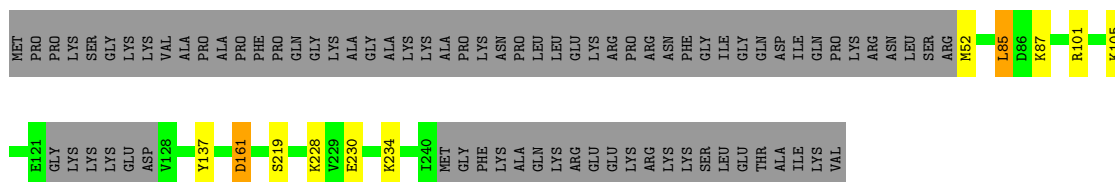
- Molecule 18: 60S ribosomal protein L6

Chain LE: 82%



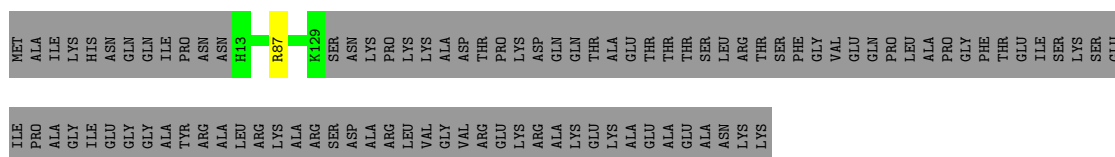
- Molecule 19: 60S ribosomal protein L8

Chain LG: 66%



- Molecule 20: 60S ribosomal protein L13

Chain LL: 54%



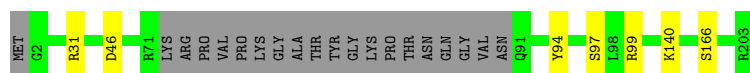
- Molecule 21: 60S ribosomal protein L14-like protein

Chain LM: 92%



- Molecule 22: Ribosomal protein L15

Chain LN: 87%



- Molecule 23: 60S ribosomal protein L16-like protein

Chain LO: 98%



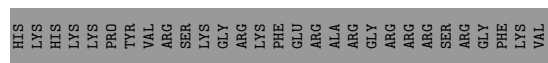
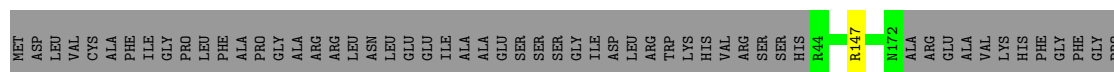
- Molecule 24: 60S ribosomal protein l17-like protein

Chain LP: 81%



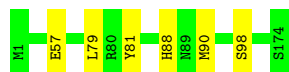
- Molecule 25: Ribosomal protein L18-like protein

Chain LQ: 60%



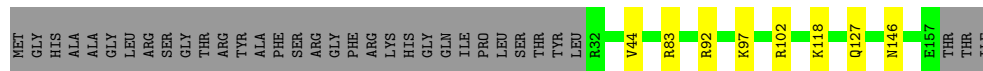
- Molecule 26: 60S ribosomal protein L20

Chain LS: 97%



- Molecule 27: 60S ribosomal protein l21-like protein

Chain LT: 74%



- Molecule 28: 60S ribosomal protein l23-like protein

Chain LV: 93%



- Molecule 29: 60S ribosomal protein L26-like protein



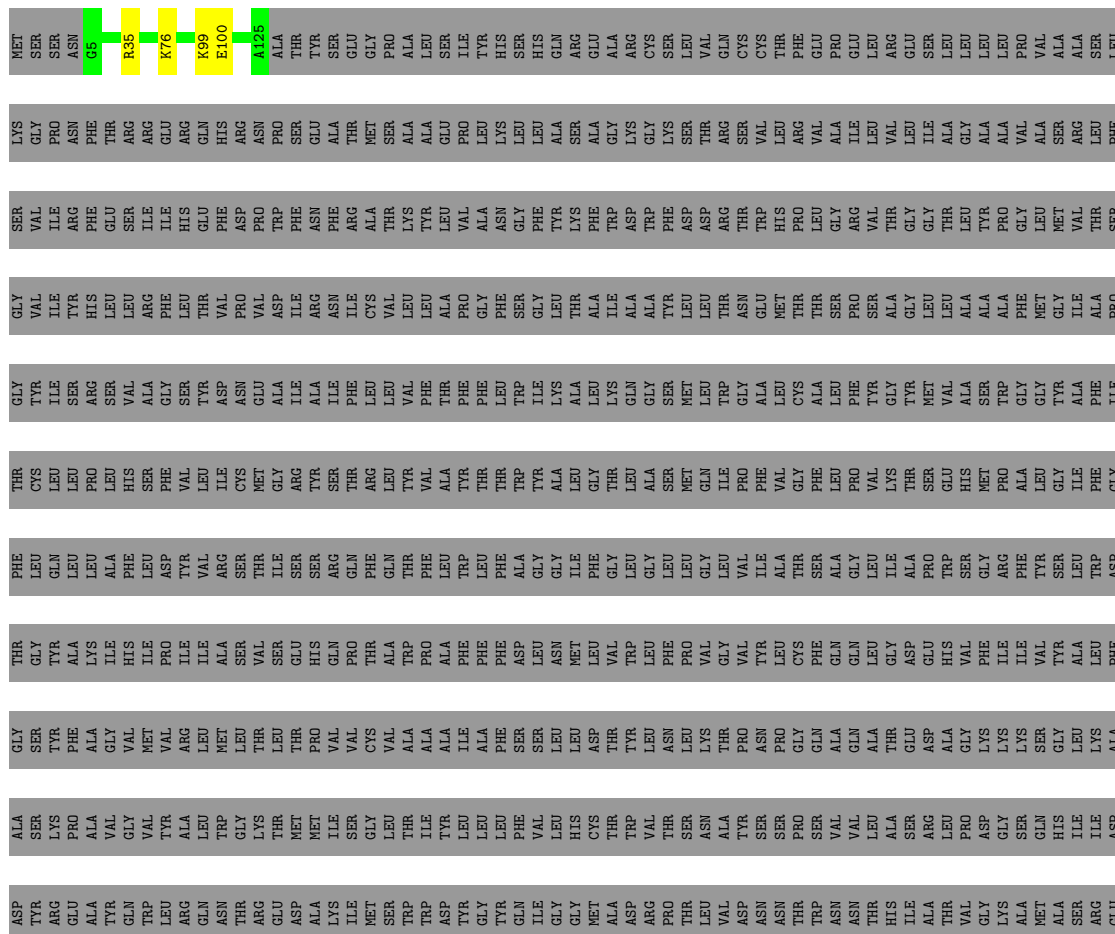
- Molecule 30: 60S ribosomal protein L32-like protein

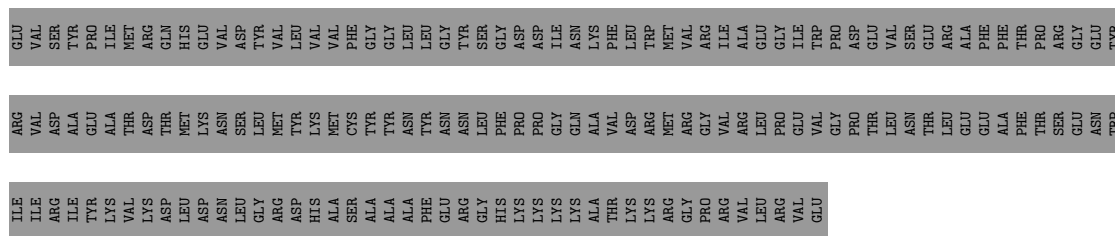


- Molecule 31: 60S ribosomal protein l33-like protein

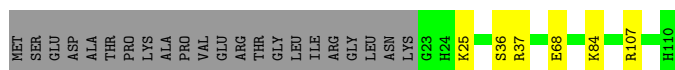
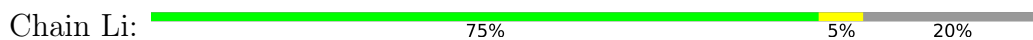


- Molecule 32: dolichyl-diphosphooligosaccharide--protein glycotransferase

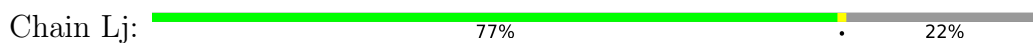




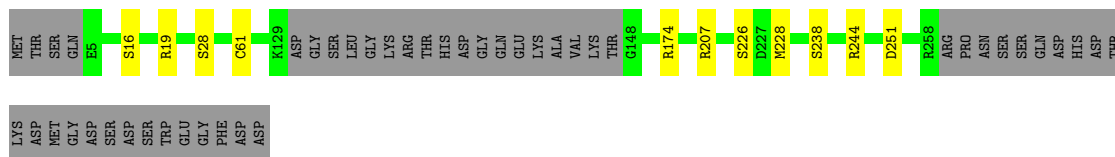
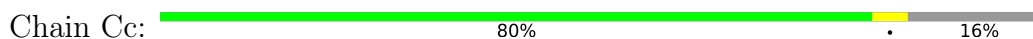
- Molecule 33: 60S ribosomal protein L36



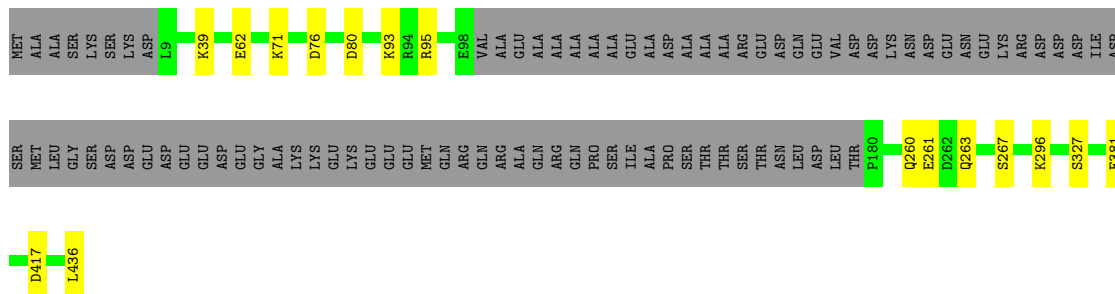
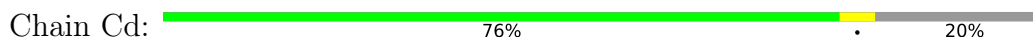
- Molecule 34: Ribosomal protein L37



- Molecule 35: Ribosomal RNA-processing protein 1

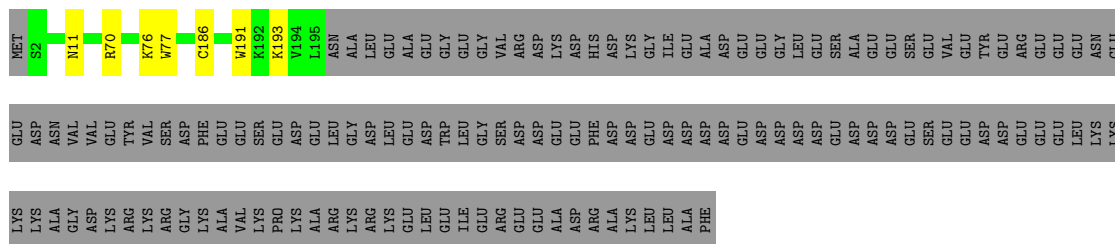


- Molecule 36: Brix domain-containing protein

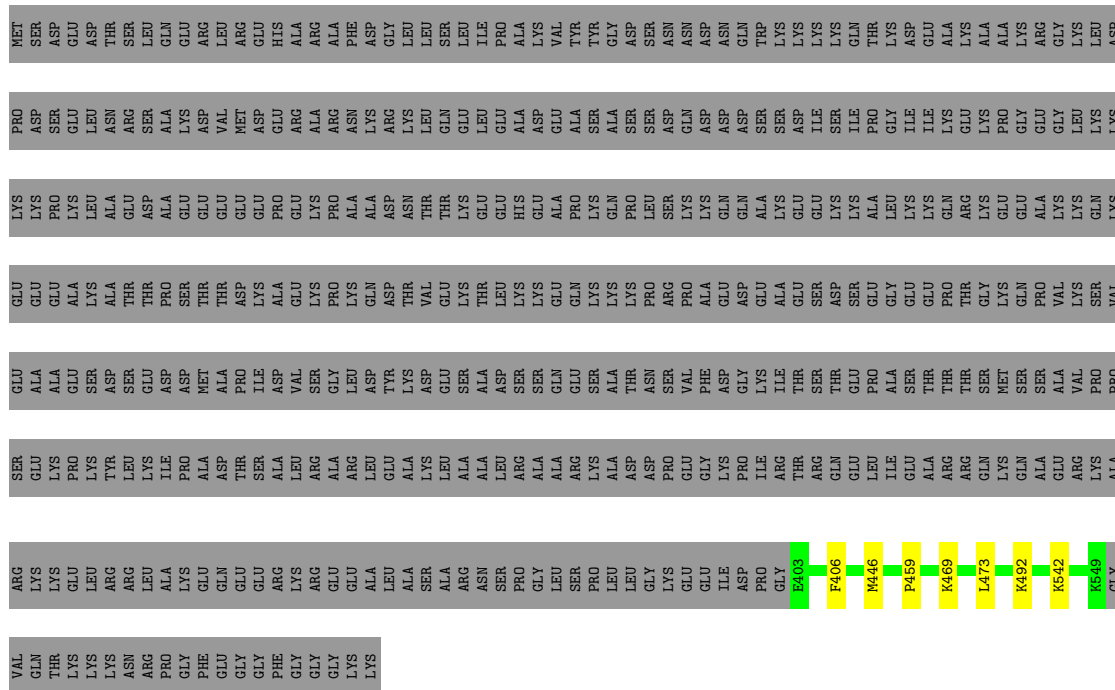


- Molecule 37: Protein MAK16

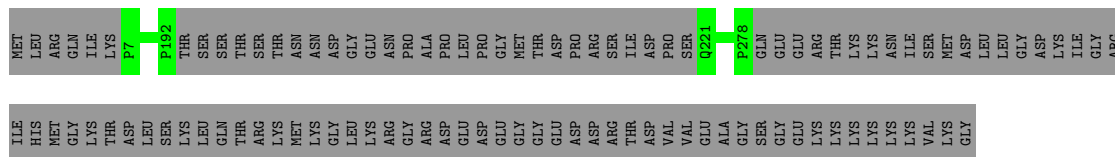




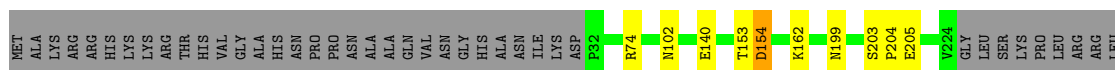
- Molecule 38: 60S ribosome biogenesis protein Rrp14

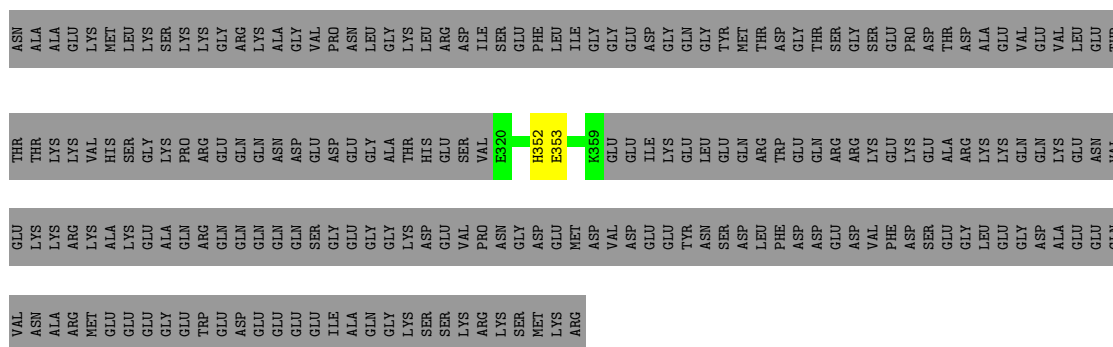


- Molecule 39: Ribosome production factor 2 homolog

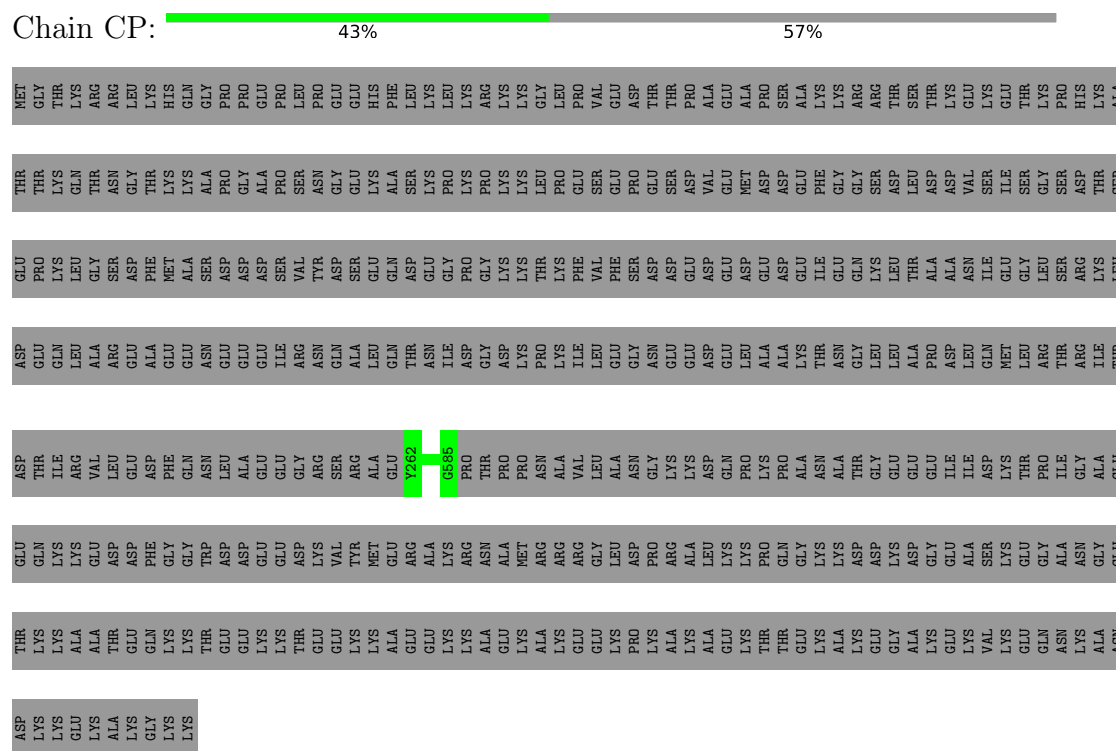


- Molecule 40: Brix domain-containing protein

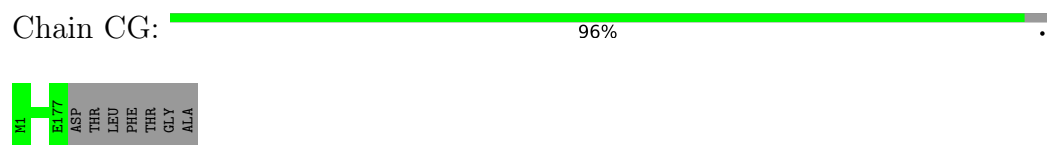




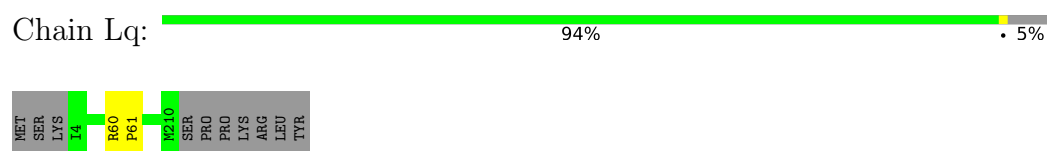
- Molecule 41: RNA methyltransferase nop2-like protein



- Molecule 42: 60S ribosome subunit biogenesis protein NIP7



- Molecule 43: Ribosomal protein



- Molecule 44: Ribosome biogenesis regulatory protein

[illegible]

- Chain LJ: 98%

MET
SER
SER
GLU
K5
R173

- Chain LD: 

MET	ALA	PHE	HIS	K5	D116	LYS	THR	PHE	THR	GLY	VAL	GLU	GLU	PRO	ASN	G127	R287	LYS	ALA	ARG	VAL	GLU	ALA	ALA	LYS	ILE	LYS	GLN	LEU	LEU	ALA	GLU	GLN	ASP	GLU
-----	-----	-----	-----	----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain C4: 77% 18% .

A1	G7	A8	C9	C15	A22	C26	G29	C42	U54	A55	A64	G65	G66	A75	G76	G82	G83	G84	U85	C96	U89	C92	G93	A94	C95	C99	G100	A101	G111	U119
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------

- Chain CX:  31% 69%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41599	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)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (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, OMU

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	C1	0.55	1/48945 (0.0%)	1.02	181/76270 (0.2%)
2	C2	0.57	0/5415	0.96	11/8436 (0.1%)
3	CA	0.34	0/2190	0.68	0/2940
4	CB	0.34	0/2109	0.65	2/2866 (0.1%)
5	CC	0.33	0/2325	0.67	4/3164 (0.1%)
6	CE	0.35	0/3743	0.61	1/5045 (0.0%)
7	CH	0.31	0/909	0.68	0/1229
8	CI	0.34	0/1225	0.64	0/1645
9	CJ	0.28	0/3189	0.58	2/4309 (0.0%)
10	CM	0.31	0/1555	0.65	1/2091 (0.0%)
10	LF	0.37	0/2004	0.60	1/2686 (0.0%)
11	CN	0.30	0/1881	0.66	1/2560 (0.0%)
12	CQ	0.34	0/981	0.70	0/1301
13	CR	0.33	0/1369	0.62	0/1828
14	CU	0.28	0/980	0.64	1/1314 (0.1%)
15	Ch	0.26	0/563	0.68	1/746 (0.1%)
16	LB	0.35	0/2760	0.72	5/3701 (0.1%)
17	LC	0.36	0/2809	0.58	0/3787
18	LE	0.34	0/1363	0.57	0/1833
19	LG	0.36	0/1492	0.59	1/2003 (0.0%)
20	LL	0.36	0/983	0.66	0/1318
21	LM	0.34	0/1120	0.64	1/1507 (0.1%)
22	LN	0.37	0/1595	0.63	1/2132 (0.0%)
23	LO	0.36	0/1652	0.64	1/2215 (0.0%)
24	LP	0.29	0/1231	0.56	0/1658
25	LQ	0.35	0/1033	0.61	0/1391
26	LS	0.35	0/1468	0.63	0/1975
27	LT	0.31	0/1033	0.62	0/1389
28	LV	0.32	0/1013	0.66	2/1361 (0.1%)
29	LY	0.34	0/1079	0.59	0/1443
30	Le	0.34	0/1073	0.57	0/1431
31	Lf	0.38	0/883	0.62	0/1187

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lh	0.30	0/1006	0.56	0/1338
33	Li	0.32	0/738	0.63	0/971
34	Lj	0.37	0/606	0.64	0/803
35	Cc	0.33	0/1934	0.58	1/2614 (0.0%)
36	Cd	0.33	0/2857	0.59	0/3843
37	Ce	0.38	0/1638	0.63	1/2196 (0.0%)
38	Cf	0.31	0/1238	0.67	2/1631 (0.1%)
39	Cy	0.24	0/1208	0.43	0/1682
40	Cg	0.51	2/1887 (0.1%)	0.85	4/2544 (0.2%)
41	CP	0.24	0/1595	0.46	0/2217
42	CG	0.26	0/872	0.50	0/1212
43	Lq	0.26	0/1020	0.49	0/1418
44	Cx	0.25	0/567	0.49	0/783
45	LJ	0.24	0/830	0.44	0/1150
46	LD	0.23	0/1344	0.41	0/1868
47	C4	0.30	0/2833	1.08	19/4414 (0.4%)
48	CX	0.58	0/377	0.66	0/518
All	All	0.44	3/124520 (0.0%)	0.84	244/179963 (0.1%)

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	CB	0	1
15	Ch	0	1
16	LB	0	1
19	LG	0	1
25	LQ	0	1
40	Cg	0	1
43	Lq	0	1
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	Cg	204	PRO	CG-CD	-15.22	1.00	1.50
40	Cg	204	PRO	N-CD	6.92	1.57	1.47
1	C1	3215	U	C1'-N1	6.65	1.58	1.48

The worst 5 of 244 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	Cg	204	PRO	N-CD-CG	-16.54	78.39	103.20
1	C1	1050	C	N3-C2-O2	-12.57	113.10	121.90
1	C1	1050	C	N1-C2-O2	10.13	124.98	118.90
37	Ce	186	CYS	C-N-CA	10.04	146.80	121.70
1	C1	625	C	C6-N1-C2	-10.02	116.29	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CB	42	ARG	Peptide
15	Ch	282	LEU	Peptide
16	LB	58	ARG	Sidechain
19	LG	161	ASP	Peptide
25	LQ	147	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CA	254/316 (80%)	236 (93%)	18 (7%)	0	100	100
4	CB	256/391 (66%)	235 (92%)	20 (8%)	1 (0%)	30	63
5	CC	264/801 (33%)	250 (95%)	14 (5%)	0	100	100
6	CE	459/598 (77%)	440 (96%)	19 (4%)	0	100	100
7	CH	106/661 (16%)	101 (95%)	4 (4%)	1 (1%)	14	45
8	CI	144/414 (35%)	133 (92%)	10 (7%)	1 (1%)	19	51
9	CJ	374/679 (55%)	357 (96%)	16 (4%)	1 (0%)	37	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	CM	183/249 (74%)	171 (93%)	12 (7%)	0	100	100
10	LF	238/249 (96%)	230 (97%)	7 (3%)	1 (0%)	30	63
11	CN	244/246 (99%)	228 (93%)	16 (7%)	0	100	100
12	CQ	110/225 (49%)	107 (97%)	3 (3%)	0	100	100
13	CR	159/237 (67%)	153 (96%)	6 (4%)	0	100	100
14	CU	119/451 (26%)	113 (95%)	6 (5%)	0	100	100
15	Ch	69/354 (20%)	66 (96%)	3 (4%)	0	100	100
16	LB	337/392 (86%)	319 (95%)	18 (5%)	0	100	100
17	LC	360/365 (99%)	349 (97%)	11 (3%)	0	100	100
18	LE	166/200 (83%)	161 (97%)	5 (3%)	0	100	100
19	LG	179/262 (68%)	174 (97%)	5 (3%)	0	100	100
20	LL	115/213 (54%)	111 (96%)	4 (4%)	0	100	100
21	LM	135/142 (95%)	131 (97%)	4 (3%)	0	100	100
22	LN	179/203 (88%)	175 (98%)	4 (2%)	0	100	100
23	LO	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
24	LP	150/187 (80%)	148 (99%)	2 (1%)	0	100	100
25	LQ	127/213 (60%)	123 (97%)	4 (3%)	0	100	100
26	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
27	LT	124/160 (78%)	115 (93%)	8 (6%)	1 (1%)	16	48
28	LV	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
29	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
30	Le	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
31	Lf	106/109 (97%)	102 (96%)	2 (2%)	2 (2%)	6	27
32	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
33	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
34	Lj	72/95 (76%)	71 (99%)	1 (1%)	0	100	100
35	Cc	232/282 (82%)	222 (96%)	10 (4%)	0	100	100
36	Cd	343/436 (79%)	321 (94%)	22 (6%)	0	100	100
37	Ce	192/336 (57%)	188 (98%)	4 (2%)	0	100	100
38	Cf	145/570 (25%)	136 (94%)	9 (6%)	0	100	100
39	Cy	240/350 (69%)	238 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Cg	229/478 (48%)	215 (94%)	12 (5%)	2 (1%)	14	45
41	CP	322/751 (43%)	314 (98%)	8 (2%)	0	100	100
42	CG	175/184 (95%)	171 (98%)	4 (2%)	0	100	100
43	Lq	205/217 (94%)	183 (89%)	21 (10%)	1 (0%)	25	58
44	Cx	98/202 (48%)	98 (100%)	0	0	100	100
45	LJ	167/173 (96%)	167 (100%)	0	0	100	100
46	LD	269/304 (88%)	266 (99%)	3 (1%)	0	100	100
48	CX	59/203 (29%)	56 (95%)	3 (5%)	0	100	100
All	All	8678/14729 (59%)	8315 (96%)	352 (4%)	11 (0%)	50	79

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CB	117	PRO
8	CI	268	VAL
40	Cg	154	ASP
31	Lf	93	ALA
7	CH	403	LEU

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	
3	CA	231/276 (84%)	218 (94%)	13 (6%)	17	46
4	CB	222/329 (68%)	206 (93%)	16 (7%)	12	38
5	CC	252/710 (36%)	236 (94%)	16 (6%)	15	42
6	CE	398/517 (77%)	383 (96%)	15 (4%)	28	59
7	CH	95/575 (16%)	88 (93%)	7 (7%)	11	36
8	CI	121/336 (36%)	117 (97%)	4 (3%)	33	62
9	CJ	332/579 (57%)	321 (97%)	11 (3%)	33	62
10	CM	161/215 (75%)	145 (90%)	16 (10%)	6	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	LF	206/215 (96%)	202 (98%)	4 (2%)	52	75
11	CN	206/206 (100%)	199 (97%)	7 (3%)	32	62
12	CQ	100/192 (52%)	96 (96%)	4 (4%)	27	58
13	CR	144/206 (70%)	136 (94%)	8 (6%)	17	46
14	CU	104/376 (28%)	98 (94%)	6 (6%)	17	45
15	Ch	58/291 (20%)	56 (97%)	2 (3%)	32	62
16	LB	290/331 (88%)	267 (92%)	23 (8%)	10	34
17	LC	283/285 (99%)	274 (97%)	9 (3%)	34	63
18	LE	143/166 (86%)	137 (96%)	6 (4%)	25	56
19	LG	157/222 (71%)	146 (93%)	11 (7%)	12	39
20	LL	99/176 (56%)	98 (99%)	1 (1%)	73	86
21	LM	115/117 (98%)	110 (96%)	5 (4%)	25	55
22	LN	164/180 (91%)	158 (96%)	6 (4%)	29	59
23	LO	163/163 (100%)	160 (98%)	3 (2%)	54	76
24	LP	125/152 (82%)	122 (98%)	3 (2%)	44	70
25	LQ	110/178 (62%)	110 (100%)	0	100	100
26	LS	154/154 (100%)	148 (96%)	6 (4%)	27	58
27	LT	109/135 (81%)	102 (94%)	7 (6%)	14	42
28	LV	99/102 (97%)	95 (96%)	4 (4%)	27	58
29	LY	117/119 (98%)	112 (96%)	5 (4%)	25	55
30	Le	114/114 (100%)	110 (96%)	4 (4%)	31	61
31	Lf	89/90 (99%)	87 (98%)	2 (2%)	47	71
32	Lh	108/781 (14%)	104 (96%)	4 (4%)	29	59
33	Li	75/93 (81%)	69 (92%)	6 (8%)	10	34
34	Lj	61/78 (78%)	60 (98%)	1 (2%)	58	79
35	Cc	204/244 (84%)	194 (95%)	10 (5%)	21	51
36	Cd	295/367 (80%)	279 (95%)	16 (5%)	18	47
37	Ce	173/297 (58%)	167 (96%)	6 (4%)	31	61
38	Cf	127/482 (26%)	121 (95%)	6 (5%)	22	52
40	Cg	210/417 (50%)	202 (96%)	8 (4%)	28	59
44	Cx	14/176 (8%)	14 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	CX	22/172 (13%)	21 (96%)	1 (4%)	23	53
All	All	6250/10814 (58%)	5968 (96%)	282 (4%)	26	53

5 of 282 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	Li	68	GLU
35	Cc	61	CYS
36	Cd	436	LEU
10	CM	202	LYS
10	CM	144	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
40	Cg	100	ASN
32	Lh	47	ASN
12	CQ	45	ASN
10	CM	242	ASN
15	Ch	321	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2026/3341 (60%)	482 (23%)	17 (0%)
2	C2	225/256 (87%)	61 (27%)	1 (0%)
47	C4	118/119 (99%)	23 (19%)	0
All	All	2369/3716 (63%)	566 (23%)	18 (0%)

5 of 566 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3257	U
2	C2	123	G
1	C1	3297	U
1	C1	2569	U
1	C1	3255	G

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMU	C1	2682	1	19,22,23	2.97	8 (42%)	26,31,34	1.64	4 (15%)
1	OMU	C1	2687	1	19,22,23	2.96	8 (42%)	26,31,34	1.67	4 (15%)
1	OMU	C1	2689	1	19,22,23	2.98	8 (42%)	26,31,34	1.68	4 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	C1	2682	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2687	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2689	1	-	2/9/27/28	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2682	OMU	C2-N1	7.20	1.50	1.38
1	C1	2689	OMU	C2-N1	7.20	1.50	1.38
1	C1	2687	OMU	C2-N1	7.15	1.49	1.38
1	C1	2689	OMU	C2-N3	6.72	1.49	1.38
1	C1	2682	OMU	C2-N3	6.71	1.49	1.38

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	2689	OMU	C4-N3-C2	-5.14	119.80	126.58
1	C1	2687	OMU	C4-N3-C2	-5.12	119.83	126.58
1	C1	2682	OMU	C4-N3-C2	-4.98	120.01	126.58
1	C1	2689	OMU	N3-C2-N1	3.71	119.82	114.89
1	C1	2687	OMU	N3-C2-N1	3.67	119.77	114.89

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	2682	OMU	C1'-C2'-O2'-CM2
1	C1	2689	OMU	C3'-C4'-C5'-O5'
1	C1	2689	OMU	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 ⓘ

There are no chain breaks in this entry.