wwPDB EM Validation Summary Report ⓘ

May 21, 2024 – 10:27 AM JST

PDB ID	:	8I9V
EMDB ID	:	EMD-35285
Title	:	Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit - State Dbp10-2
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:

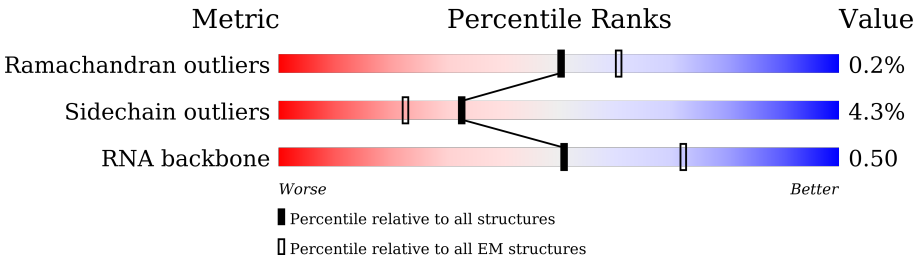
EMDB validation analysis	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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.



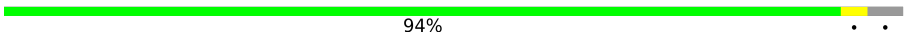
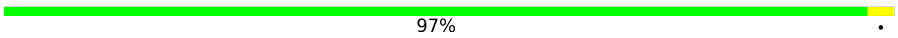
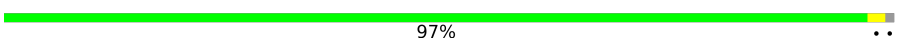
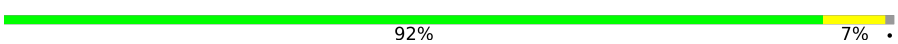
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	C1	3341	48% 15% • 36%
2	C2	256	49% 12% 38%
3	C3	161	37% 23% • 39%
4	CA	316	78% 5% 18%
5	CB	391	61% 5% • 34%
6	CC	801	34% • 64%
7	CE	598	73% 5% 23%
8	CF	270	86% • 9%
9	CG	184	91% 5% •

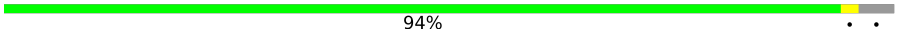
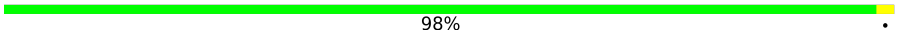
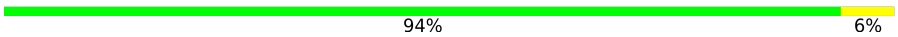
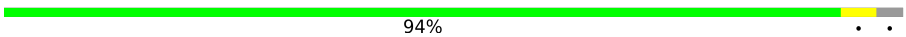
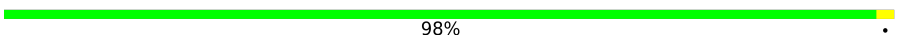
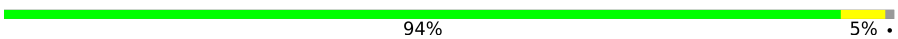
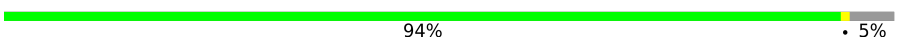
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	834	
22	CT	688	
23	CU	451	
24	CX	203	
25	CY	788	
26	Cz	123	
27	Cb	924	
28	LB	392	
29	LC	365	
30	LE	200	
31	LG	262	
32	LH	192	
33	LK	165	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	LL	213	
35	LM	142	
36	LN	203	
37	LO	204	
38	LP	187	
39	LQ	213	
40	LS	174	
41	LT	160	
42	LV	139	
43	LX	156	
44	LY	138	
45	Ld	120	
46	Le	131	
47	Lf	109	
48	Lh	935	
49	Li	110	
50	Lj	95	
51	Lq	217	
52	Cc	282	
53	Cd	436	
54	Ce	336	
55	Cf	570	

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 138001 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
			Total	C	N	O	P		
1	C1	2152	46025	20547	8331	14995	2152	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	C2	158	3359	1502	593	1106	158	0	0

- Molecule 3 is a RNA chain called RNA (161-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C3	98	2097	933	381	685	98	0	0

- Molecule 4 is a protein called Brix domain-containing protein.

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

- Molecule 5 is a protein called Ribosome biogenesis protein C8F11.04.

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

- Molecule 6 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	CC	289	2388	1520	399	462	7	0	0

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CF	245	Total	C	N	O	S	0	0
			1945	1222	352	362	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CG	177	Total	C	N	O	S	0	0
			1396	884	247	253	12		

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CH	476	Total	C	N	O	S	0	0
			3851	2451	669	716	15		

- Molecule 11 is a protein called Putative RNA-binding protein.

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

- Molecule 12 is a protein called Pescadillo homolog.

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

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	232	Total	C	N	O	S	0	0
			1855	1165	363	323	4		

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	CL	390	Total	C	N	O	0	0
			2173	1307	446	420		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 15 is a protein called 60S ribosomal protein l7-like protein.

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

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 17 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CP	324	Total	C	N	O	S	0	0
			2535	1618	445	457	15		

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

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

- Molecule 20 is a protein called Nucleolar protein 16.

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

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	298	Total	C	N	O	S	0	0
			1750	1072	330	347	1		

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	CT	458	Total	C	N	O	0	0
			2269	1353	458	458		

- Molecule 23 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CU	178	Total	C	N	O	S	0	0
			1415	876	265	271	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CX	88	Total	C	N	O	S	0	0
			701	435	128	135	3		

- Molecule 25 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	CY	324	Total	C	N	O	0	0
			1608	960	324	324		

- Molecule 26 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Cz	70	Total	C	N	O	S	0	0
			592	368	120	101	3		

- Molecule 27 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Cb	642	Total	C	N	O	S	0	0
			5058	3216	918	911	13		

- Molecule 28 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 30 is a protein called 60S ribosomal protein L6.

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

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LG	196	Total	C	N	O	S	0	0
			1583	1021	287	270	5		

- Molecule 32 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LH	190	Total	C	N	O	S	0	0
			1496	950	268	272	6		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 33 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LK	146	Total	C	N	O	S	0	0
			1112	701	203	206	2		

- Molecule 34 is a protein called 60S ribosomal protein L13.

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

- Molecule 35 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 36 is a protein called Ribosomal protein L15.

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

- Molecule 37 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 38 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 39 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 40 is a protein called 60S ribosomal protein L20.

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

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 42 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 43 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	LX	22	Total	C	N	O	0	0
			148	91	31	26		

- Molecule 44 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 45 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ld	109	Total	C	N	O	S	0	0
			890	563	171	155	1		

- Molecule 46 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 47 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 48 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 49 is a protein called 60S ribosomal protein L36.

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

- Molecule 50 is a protein called Ribosomal protein L37.

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

- Molecule 51 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lq	207	Total	C	N	O	S	0	0
			1600	1016	285	291	8		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 1.

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

- Molecule 53 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Cd	342	Total	C	N	O	S	0	0
			2763	1743	533	483	4		

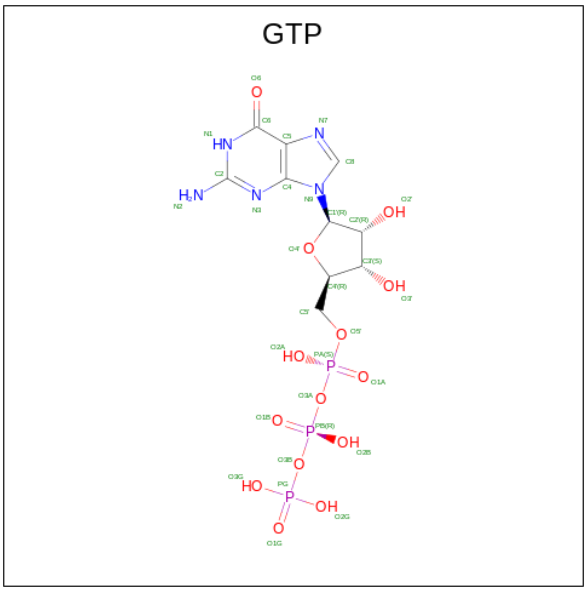
- Molecule 54 is a protein called Protein MAK16.

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

- Molecule 55 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	Cf	59	Total	C	N	O	0	0
			513	310	111	92		

- Molecule 56 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
56	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

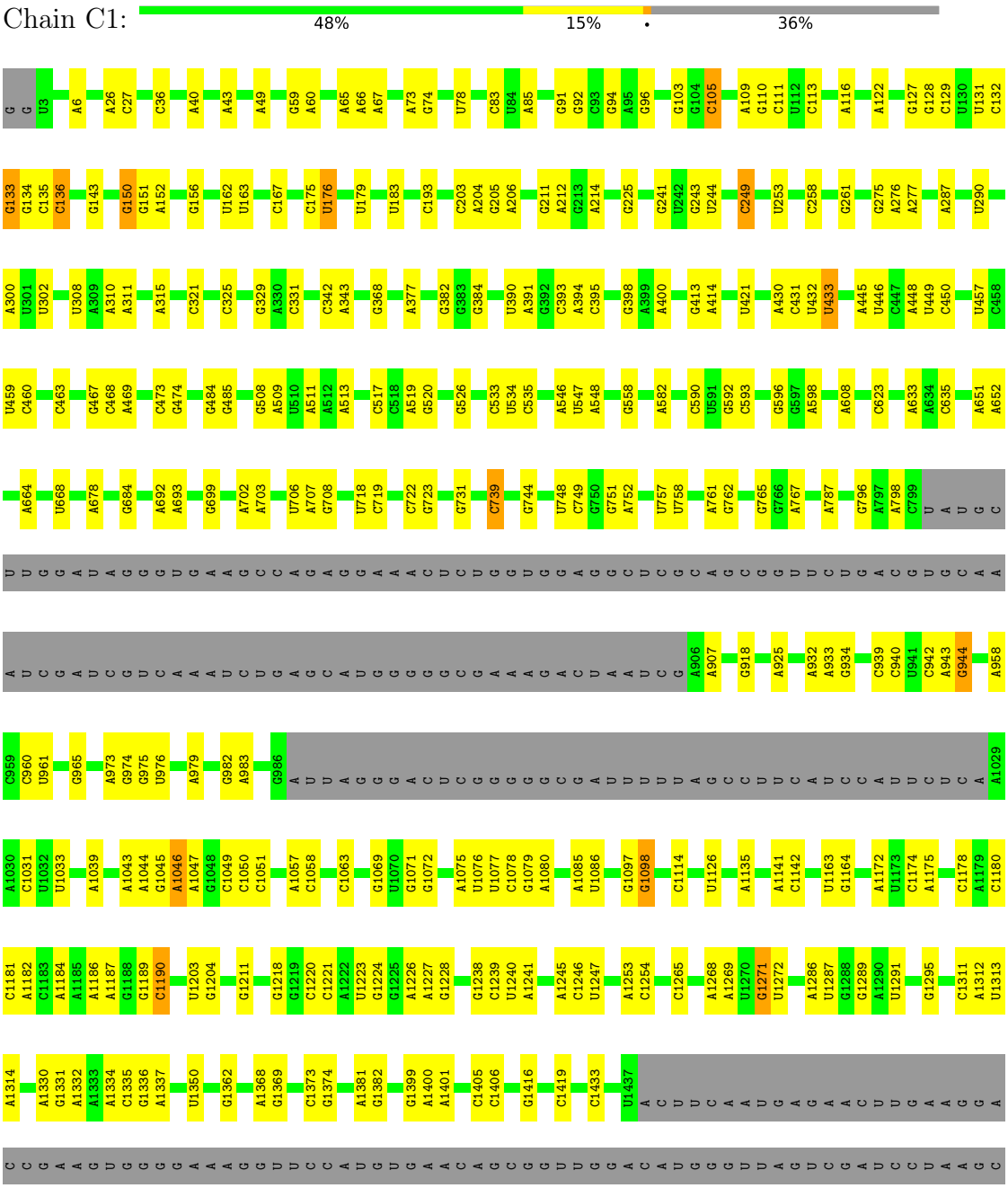
Mol	Chain	Residues	Atoms		AltConf
57	CQ	1	Total	Zn	0
			1	1	
57	Lj	1	Total	Zn	0
			1	1	
57	Ce	1	Total	Zn	0
			1	1	

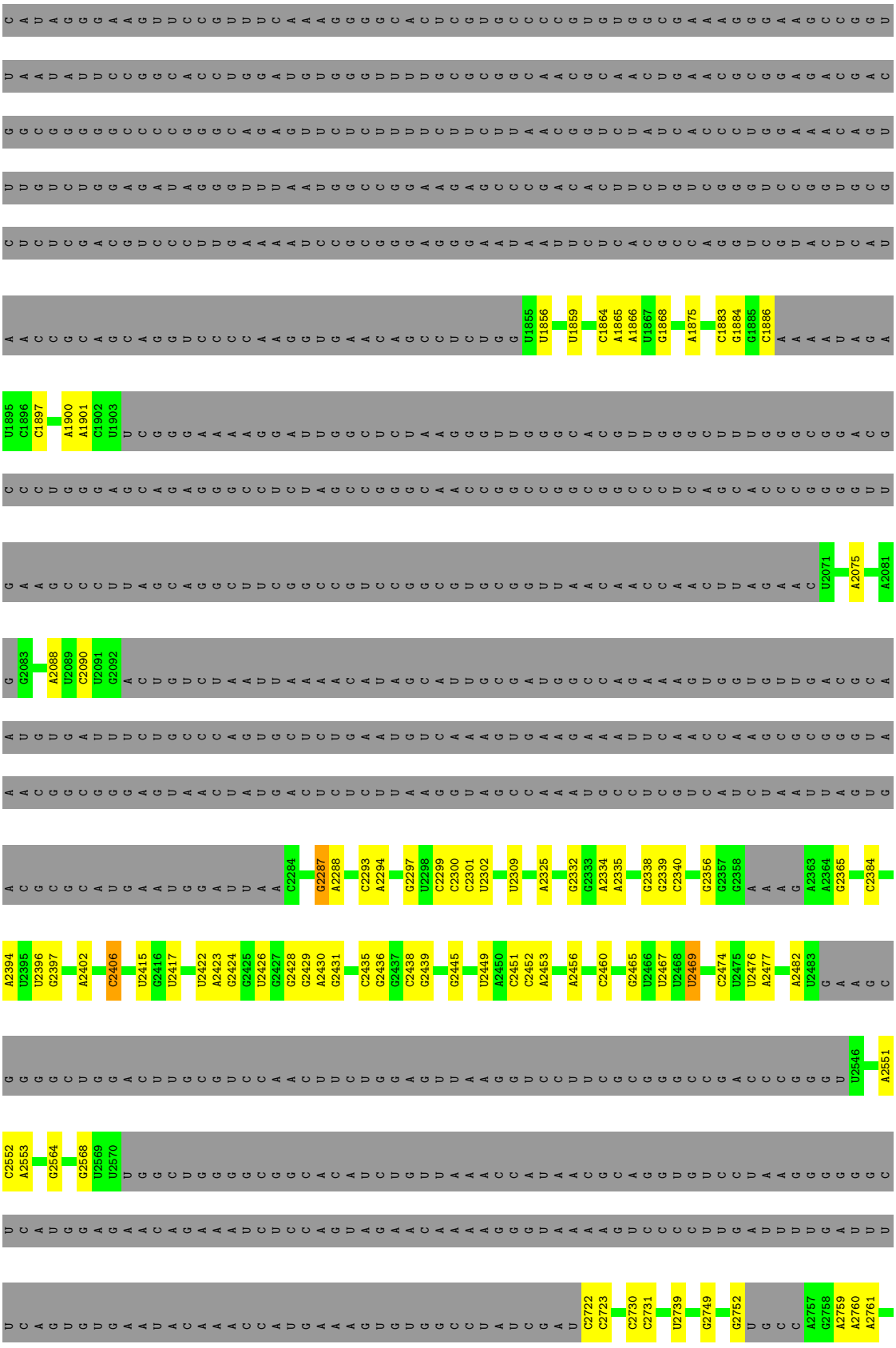
3 Residue-property plots (i)

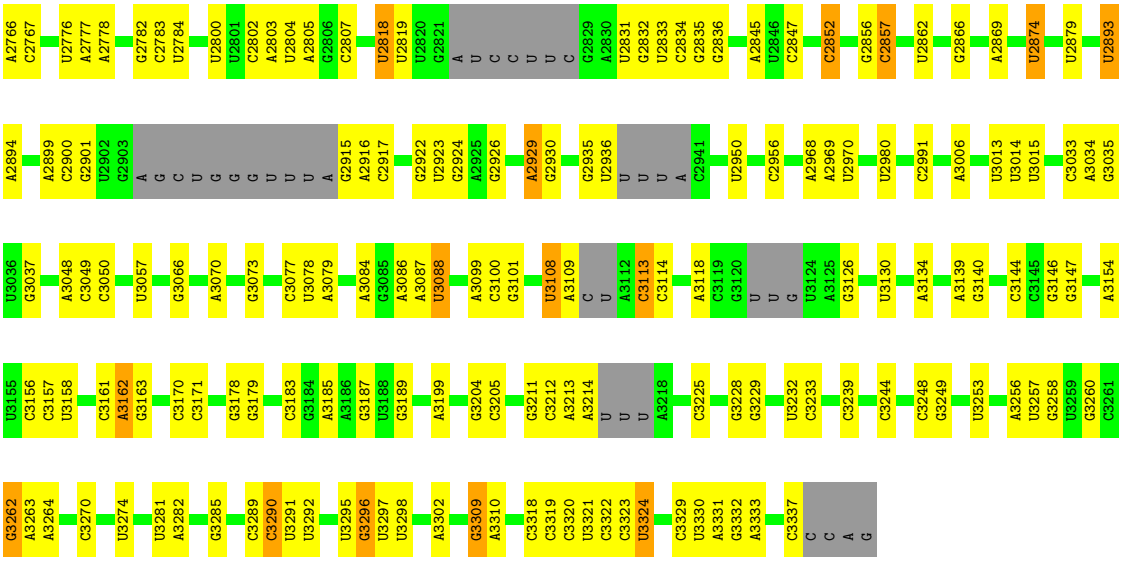
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: RNA (3341-MER)

Chain C1:

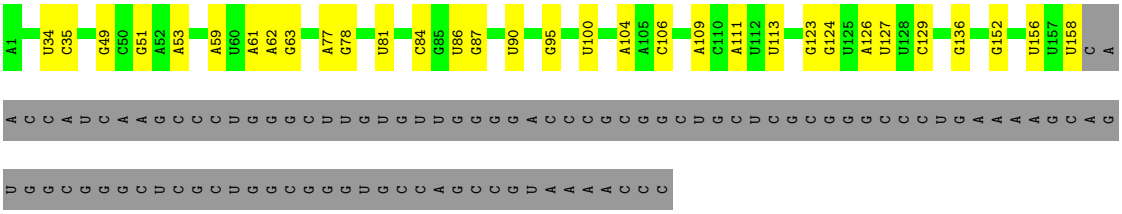



U1855
U1856
U1859
C1864
A1865
A1866
U1867
G1868
A1875
C1883
G1884
G1885
C1886
U1895
C1896
C1897
A1900
A1901
C1902
U1903
U2071
A2075
A2081
G2083
A2088
U2089
C2090
U2091
G2092
C2284
G2287
A2288
C2293
A2294
G2297
U2298
C2299
C2300
C2301
U2302
U2309
A2325
G2332
G2333
A2334
A2335
G2338
G2339
C2340
G2356
G2357
G2358
A2363
A2364
G2365
C2384
A2394
U2395
U2396
G2397
A2402
C2406
U2415
G2416
U2417
U2422
A2423
G2424
G2425
U2426
G2427
G2428
G2429
A2430
G2431
C2435
G2436
G2437
C2438
G2439
G2445
U2449
A2450
C2451
C2452
A2453
A2456
C2460
G2465
U2466
U2467
U2468
U2469
C2474
U2475
U2476
A2477
A2482
U2483
U2546
A2551
C2552
A2553
G2564
G2568
U2569
U2570
C2722
C2723
C2730
C2731
U2739
G2749
G2752
A2757
G2758
A2759
A2760
A2761



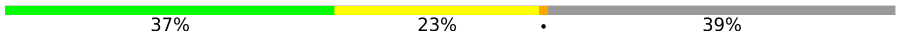
• Molecule 2: RNA (256-MER)

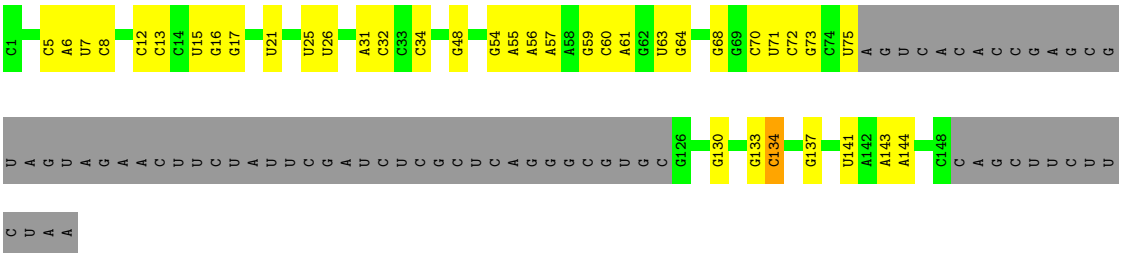
Chain C2:



• Molecule 3: RNA (161-MER)

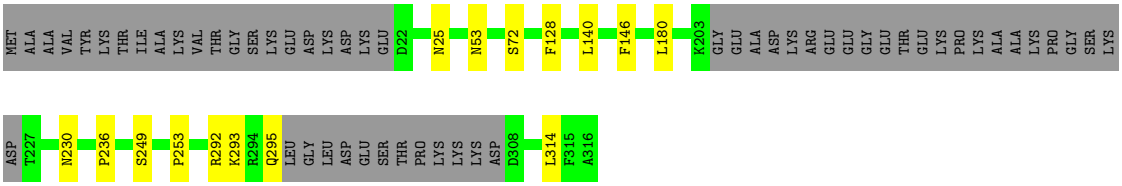
Chain C3:





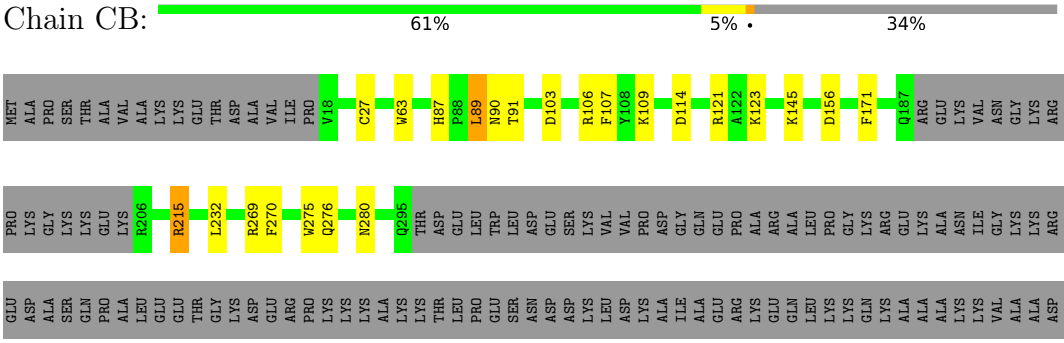
• Molecule 4: Brix domain-containing protein

Chain CA:



• Molecule 5: Ribosome biogenesis protein C8F11.04

Chain CB:

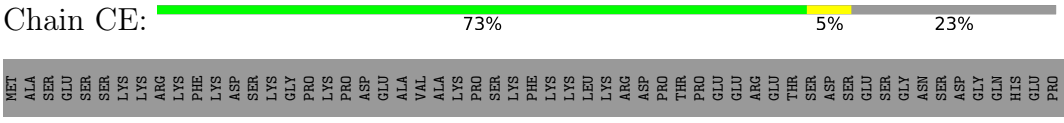


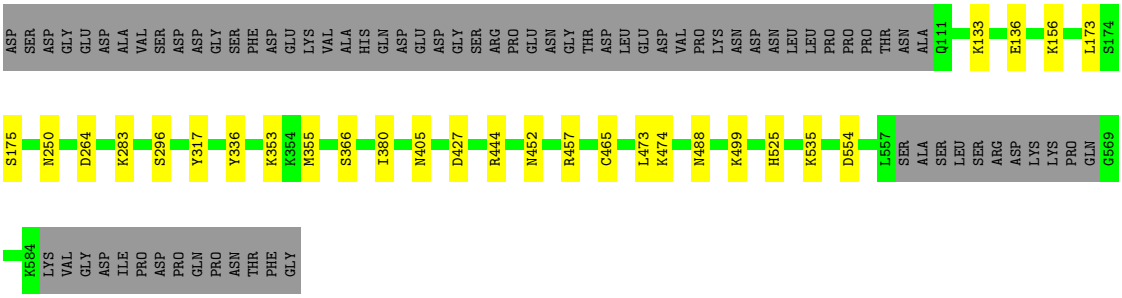
• Molecule 6: Ribosome biogenesis protein ERB1

Chain CC:

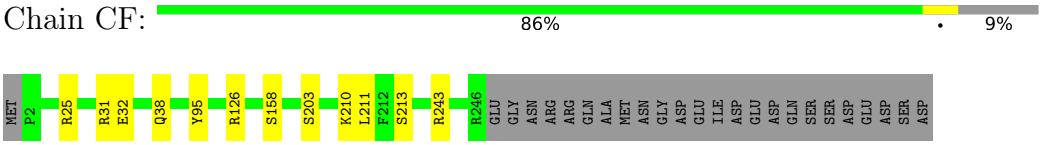
• Molecule 7: RNA helicase

Chain CE:

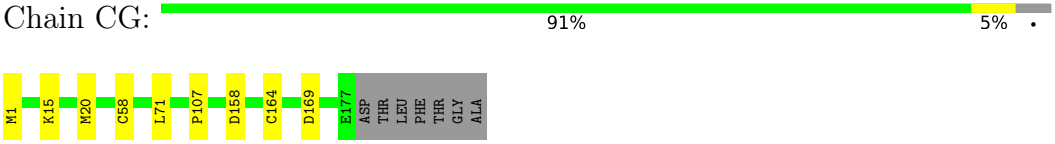




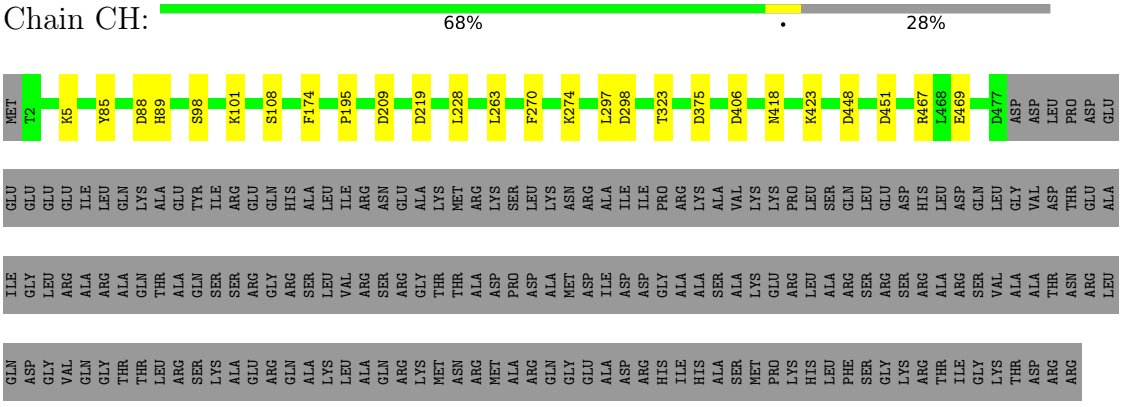
• Molecule 8: Ribosome assembly factor mrt4



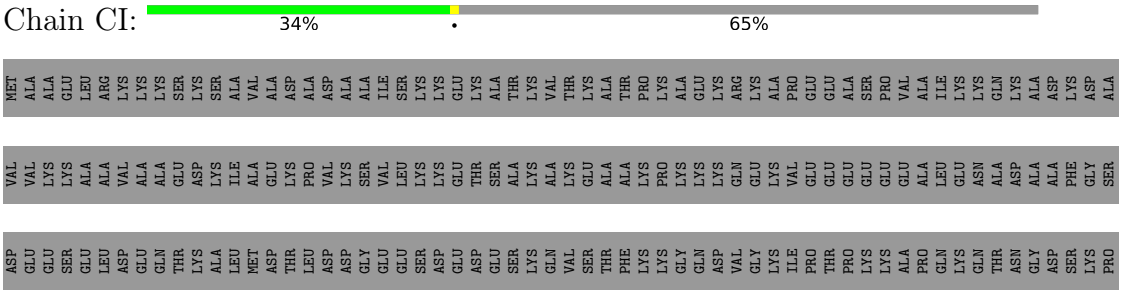
• Molecule 9: 60S ribosome subunit biogenesis protein NIP7

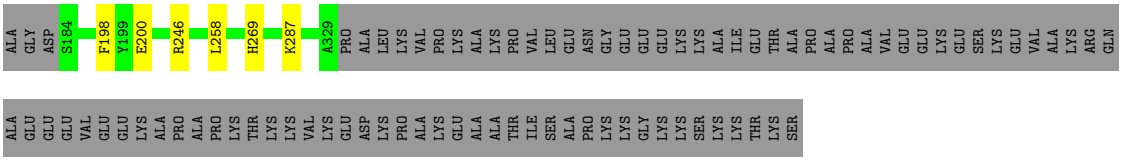


• Molecule 10: Nucleolar GTP-binding protein 1



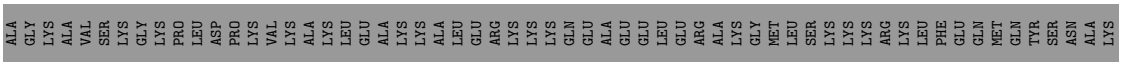
• Molecule 11: Putative RNA-binding protein





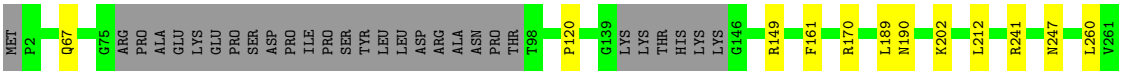
• Molecule 12: Pescadillo homolog

Chain CJ:



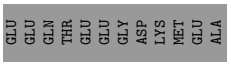
• Molecule 13: Ribosome biogenesis protein NSA2 homolog

Chain CK:



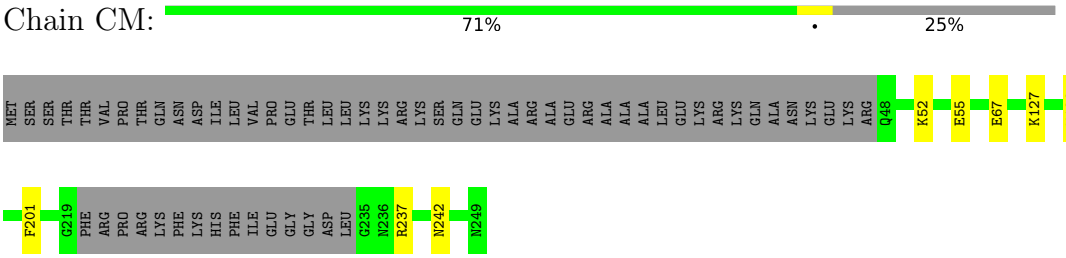
• Molecule 14: Putative GTP binding protein

Chain CL:



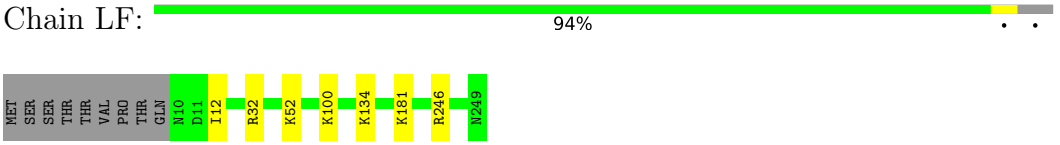
• Molecule 15: 60S ribosomal protein l7-like protein

Chain CM:



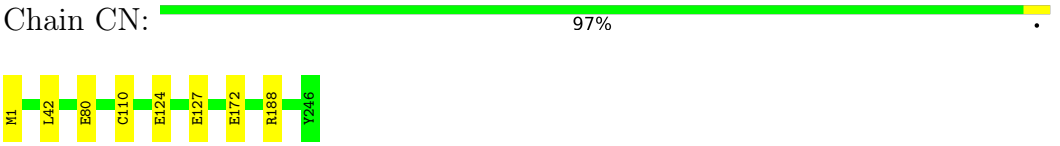
• Molecule 15: 60S ribosomal protein l7-like protein

Chain LF:



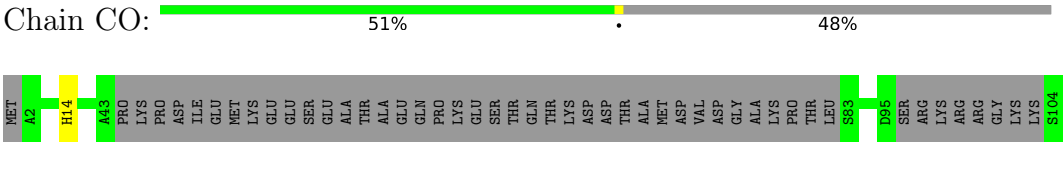
• Molecule 16: Eukaryotic translation initiation factor 6

Chain CN:



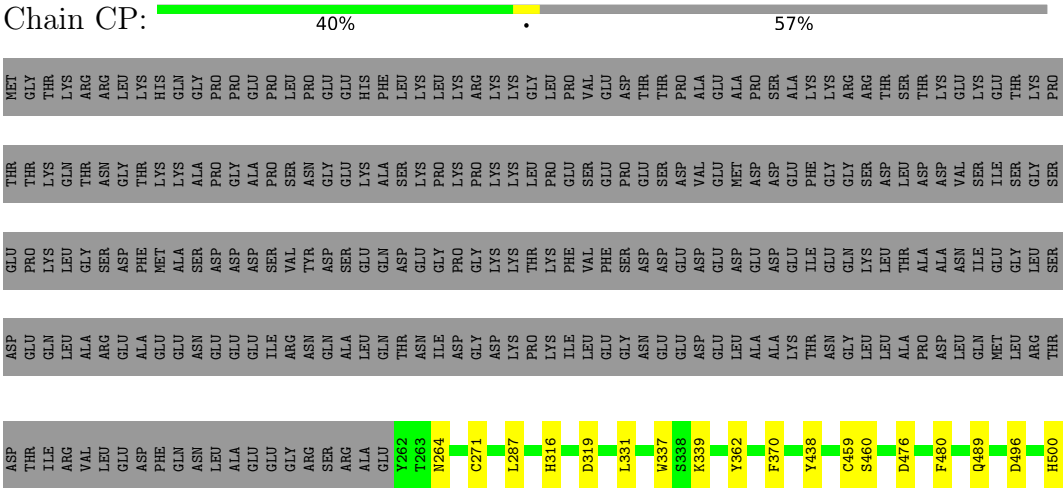
• Molecule 17: DUF2423 domain-containing protein

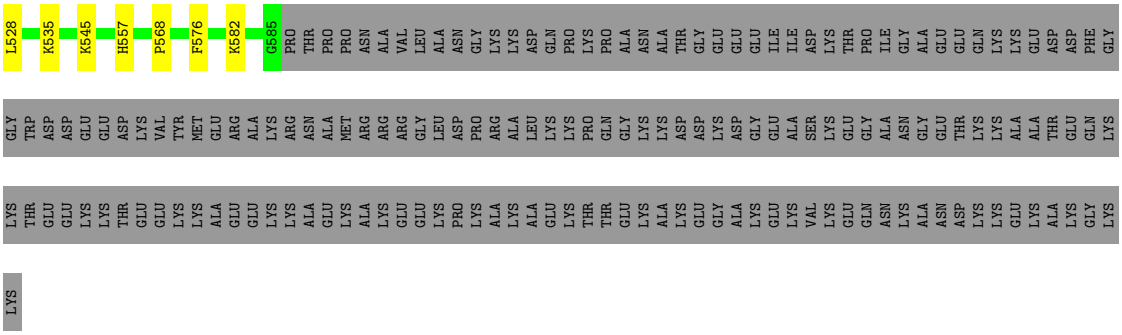
Chain CO:



• Molecule 18: RNA methyltransferase nop2-like protein

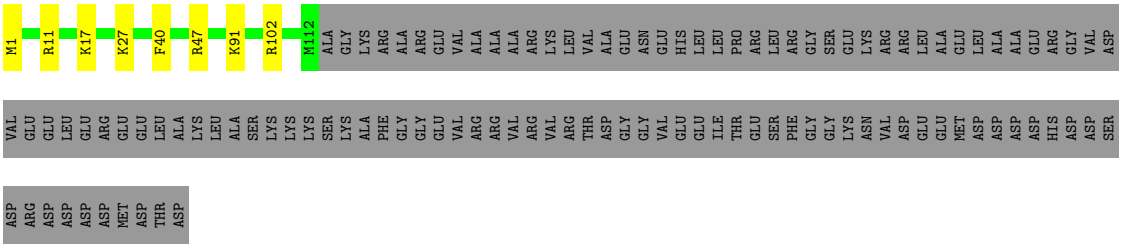
Chain CP:





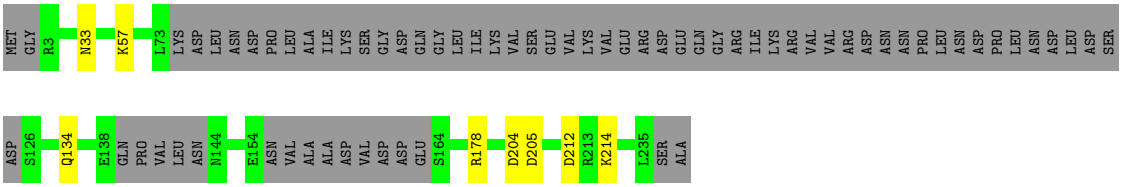
• Molecule 19: Ribosome biogenesis protein RLP24

Chain CQ:



• Molecule 20: Nucleolar protein 16

Chain CR:

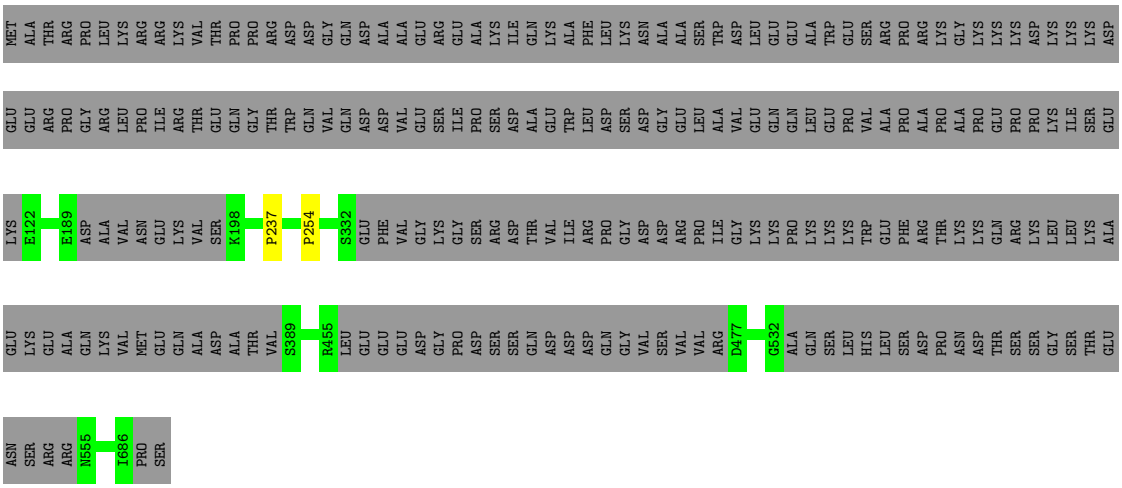


• Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

Chain CS:

• Molecule 22: Nucleolar complex-associated protein 3

Chain CT:

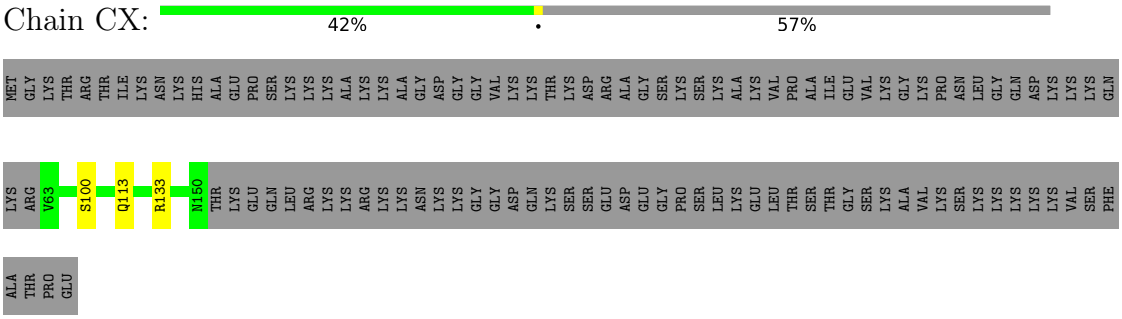


• Molecule 23: rRNA-processing protein EBP2

Chain CU:

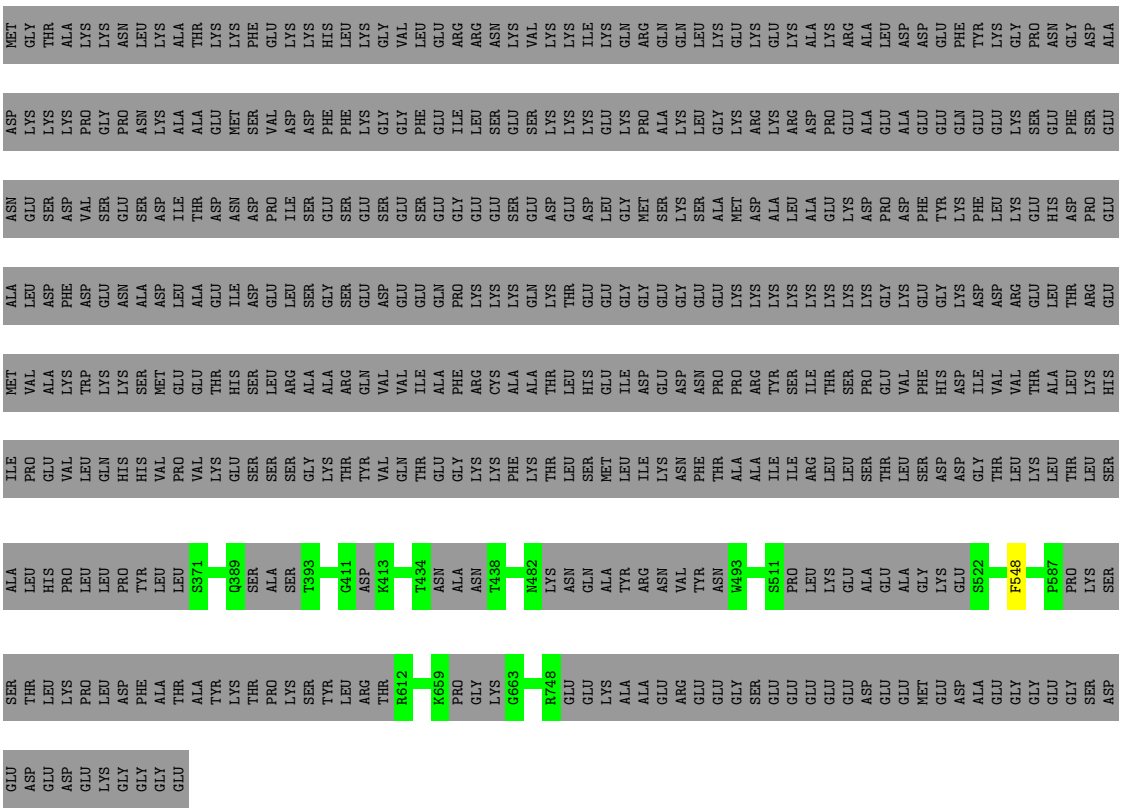
• Molecule 24: 60S ribosomal subunit-like protein

Chain CX:



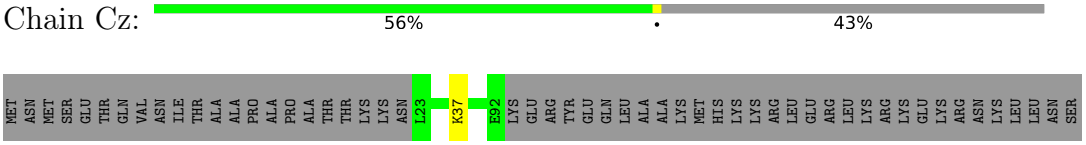
• Molecule 25: Putative NOC2 family protein

Chain CY:



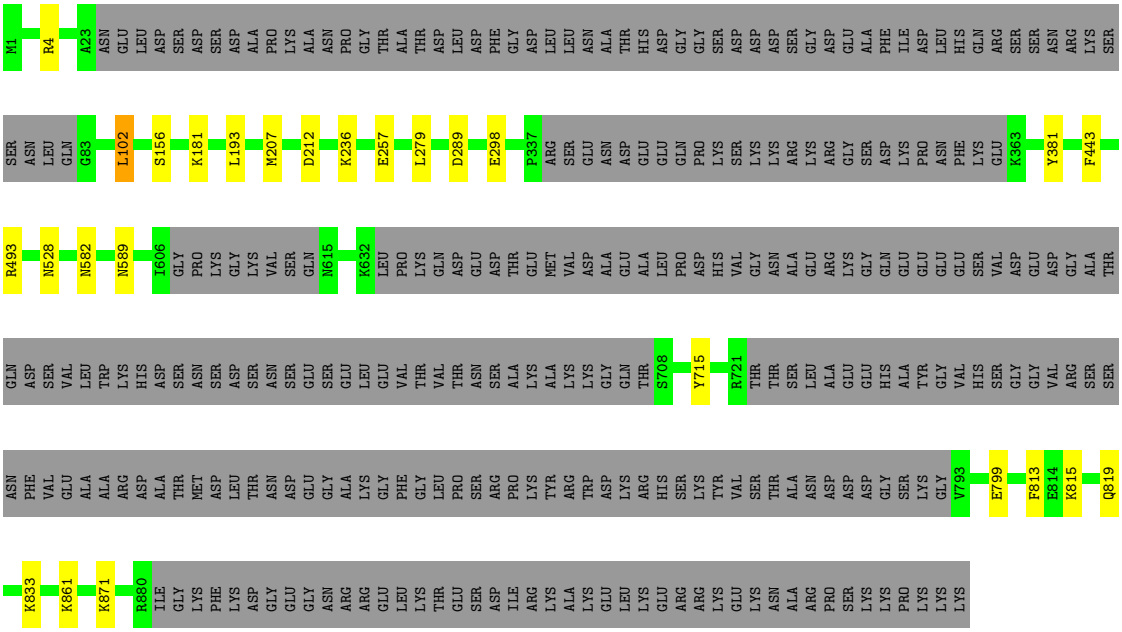
• Molecule 26: rRNA-processing protein

Chain Cz:



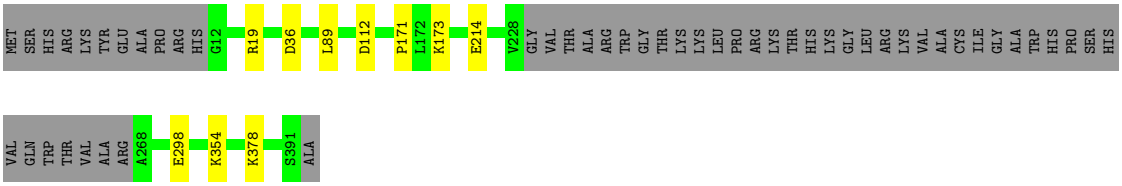
• Molecule 27: ATP-dependent RNA helicase DBP10

Chain Cb:



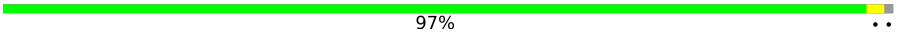
• Molecule 28: 60S ribosomal protein L3-like protein

Chain LB:



• Molecule 29: 60S ribosomal protein L4-like protein

Chain LC:

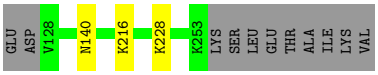


• Molecule 30: 60S ribosomal protein L6

Chain LE:

• Molecule 31: 60S ribosomal protein L8

Chain LG:

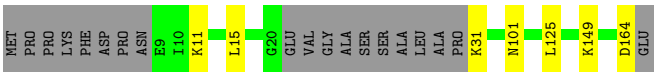


• Molecule 32: 60S ribosomal protein l9-like protein

Chain LH:

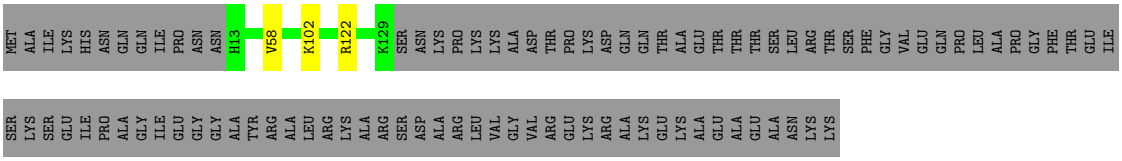
• Molecule 33: 60S ribosomal protein L12-like protein

Chain LK:



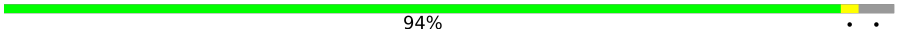
• Molecule 34: 60S ribosomal protein L13

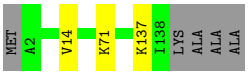
Chain LL:



• Molecule 35: 60S ribosomal protein L14-like protein

Chain LM:



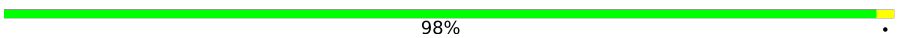


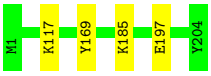
• Molecule 36: Ribosomal protein L15

Chain LN:

• Molecule 37: 60S ribosomal protein L16-like protein

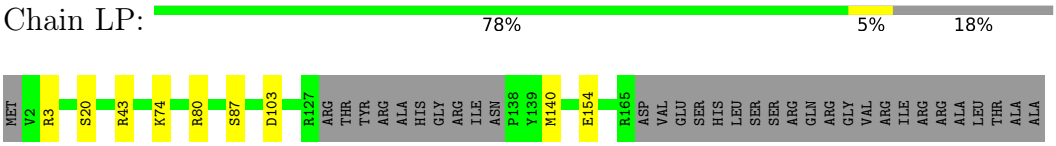
Chain LO:





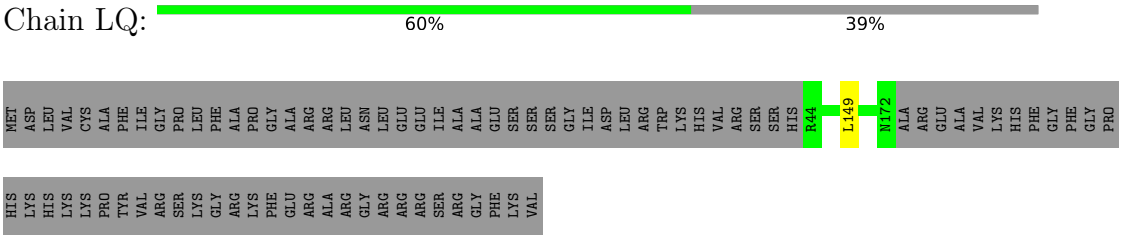
• Molecule 38: 60S ribosomal protein l17-like protein

Chain LP:



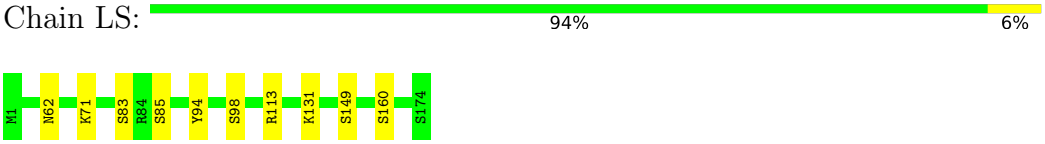
• Molecule 39: Ribosomal protein L18-like protein

Chain LQ:



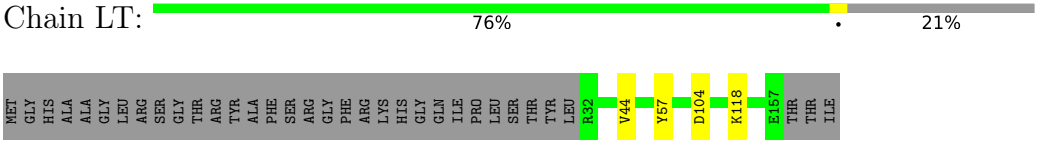
• Molecule 40: 60S ribosomal protein L20

Chain LS:



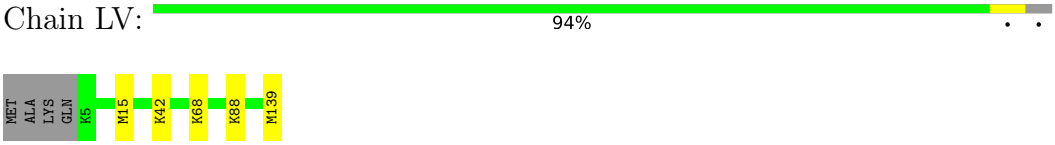
• Molecule 41: 60S ribosomal protein l21-like protein

Chain LT:



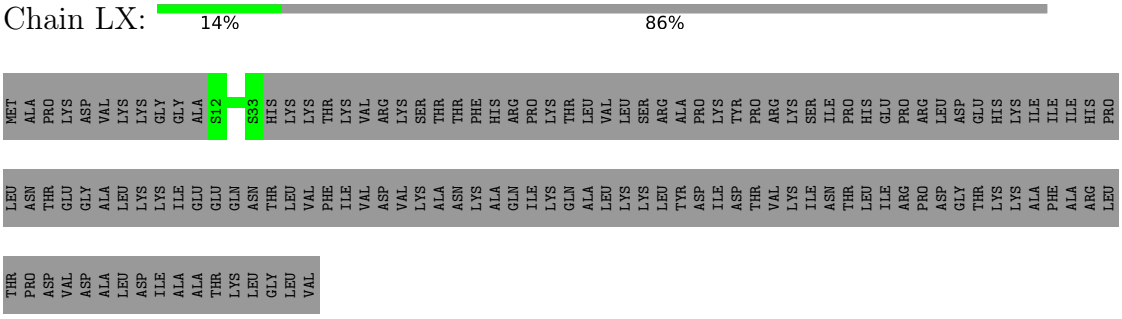
• Molecule 42: 60S ribosomal protein l23-like protein

Chain LV:



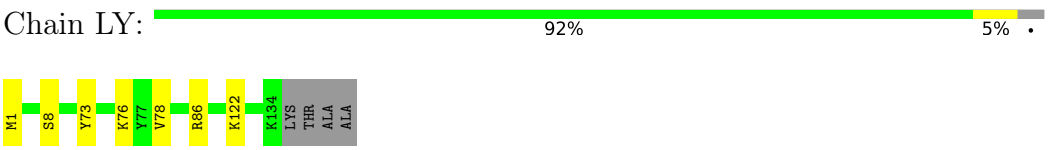
• Molecule 43: 60S ribosomal protein L25-like protein

Chain LX:



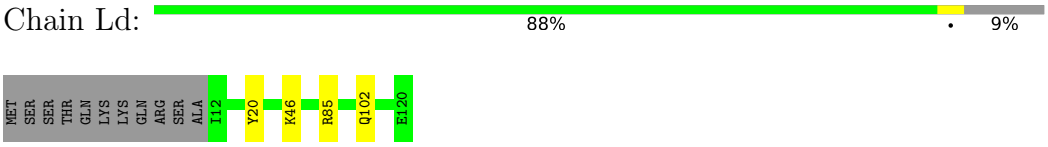
• Molecule 44: 60S ribosomal protein L26-like protein

Chain LY:



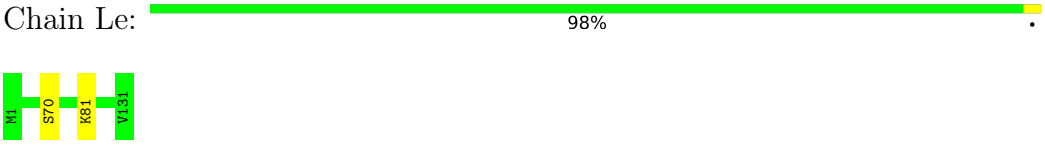
• Molecule 45: Putative 60S ribosomal protein

Chain Ld:



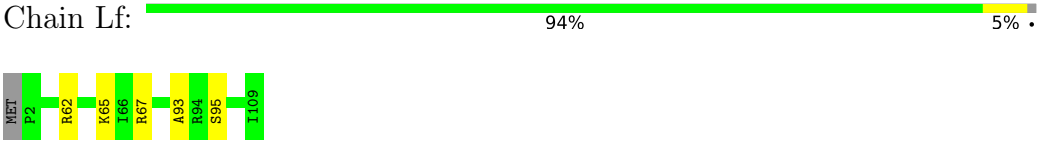
• Molecule 46: 60S ribosomal protein L32-like protein

Chain Le:



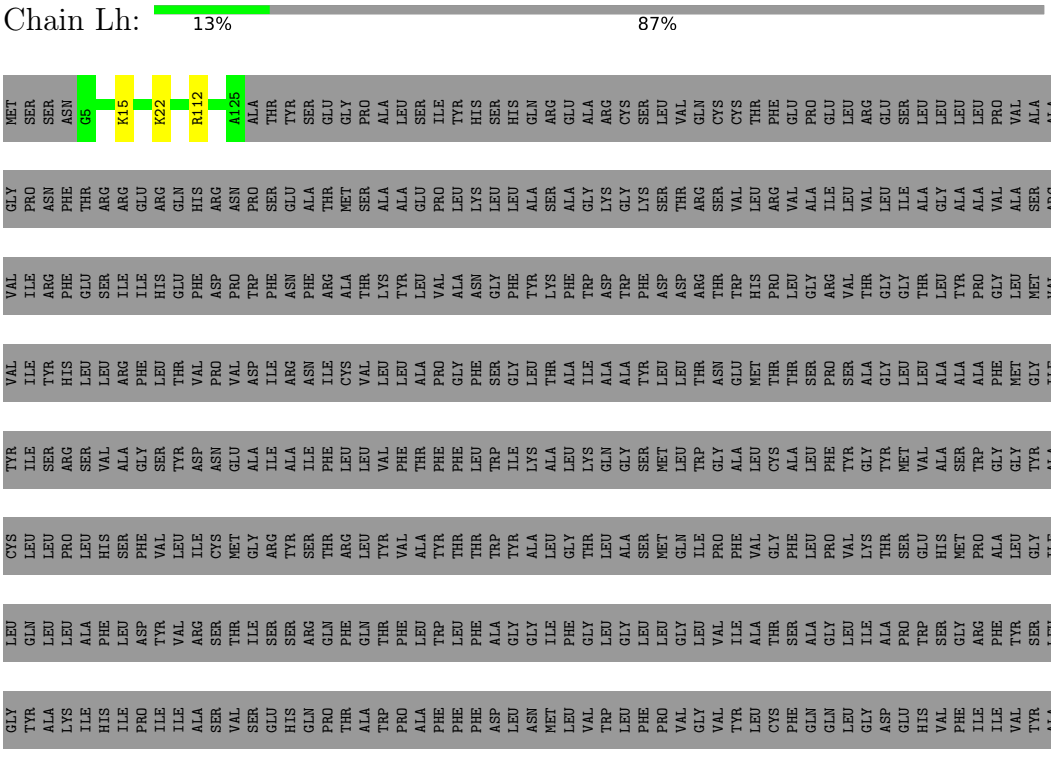
• Molecule 47: 60S ribosomal protein l33-like protein

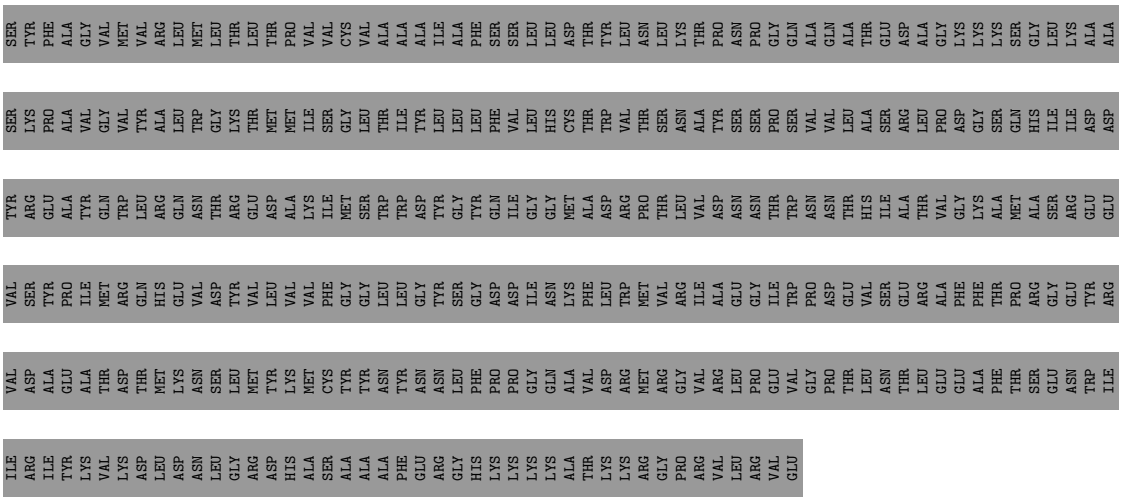
Chain Lf:



• Molecule 48: dolichyl-diphosphooligosaccharide--protein glycotransferase

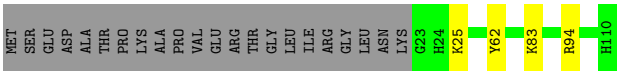
Chain Lh:





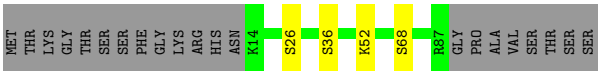
• Molecule 49: 60S ribosomal protein L36

Chain Li:



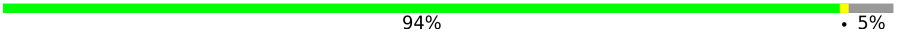
• Molecule 50: Ribosomal protein L37

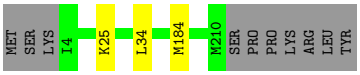
Chain Lj:



• Molecule 51: Ribosomal protein

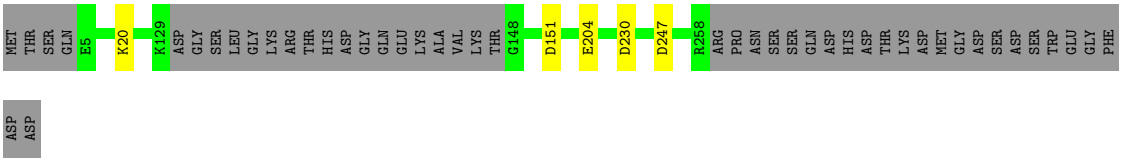
Chain Lq:





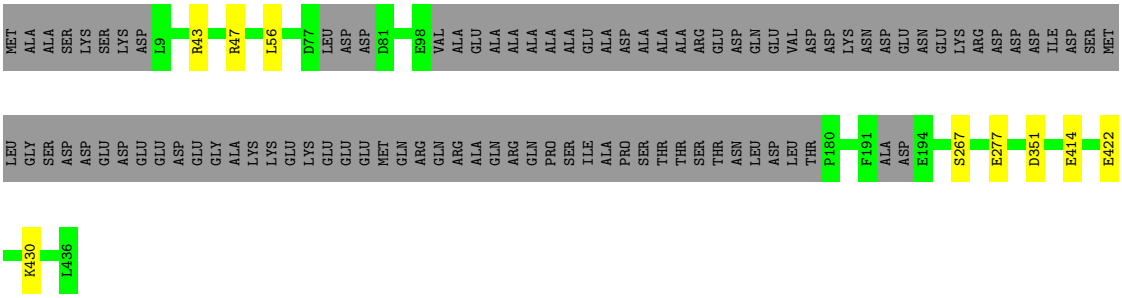
• Molecule 52: Ribosomal RNA-processing protein 1

Chain Cc:



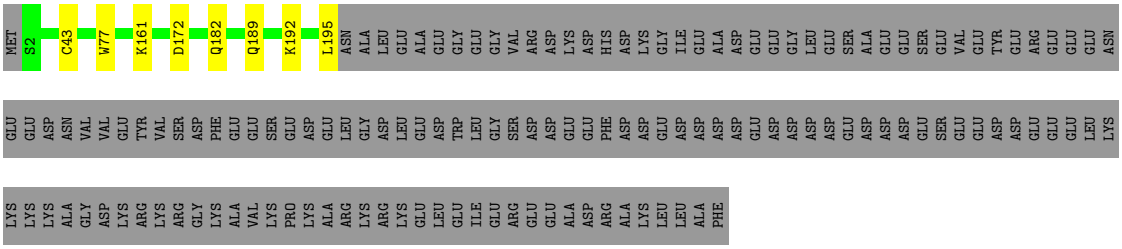
• Molecule 53: Brix domain-containing protein

Chain Cd:



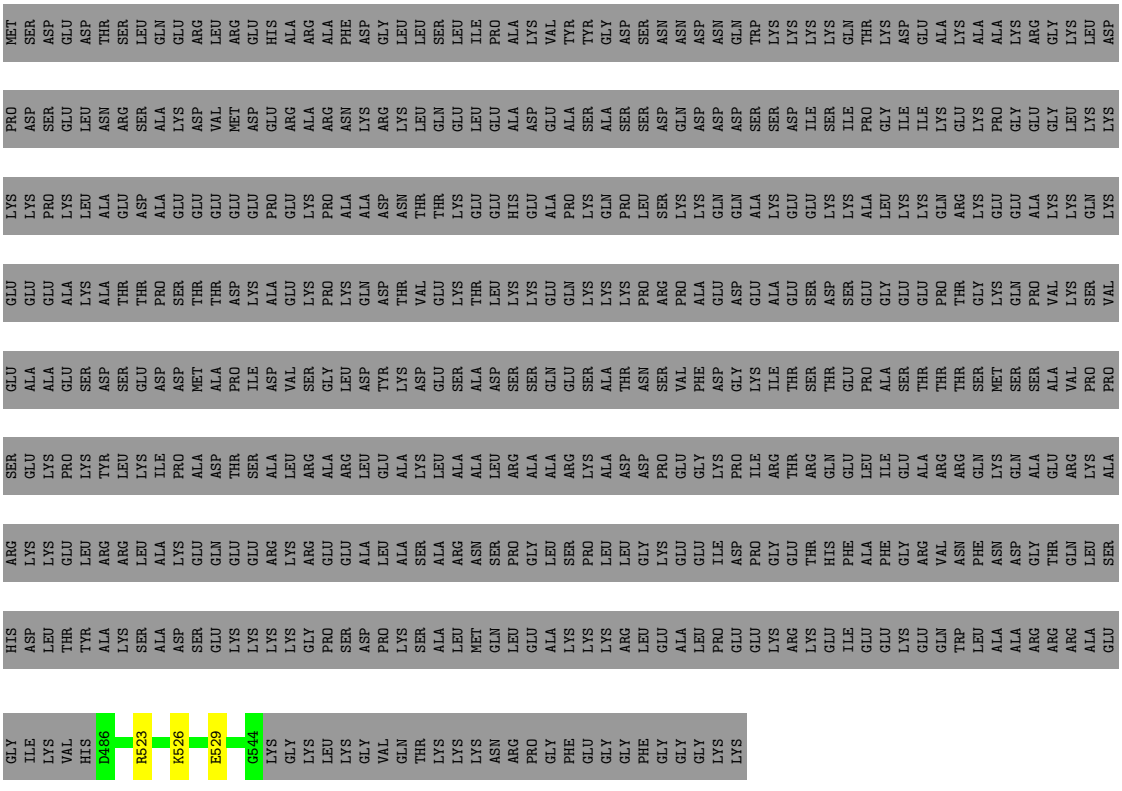
• Molecule 54: Protein MAK16

Chain Ce:



• Molecule 55: 60S ribosome biogenesis protein Rrp14

Chain Cf:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16465	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 ($e^-/Å^2$)	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: GTP, 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	C1	0.43	0/51490	1.00	169/80245 (0.2%)
2	C2	0.39	0/3754	0.90	1/5846 (0.0%)
3	C3	0.39	0/2342	1.07	11/3649 (0.3%)
4	CA	0.30	0/2190	0.61	1/2940 (0.0%)
5	CB	0.36	0/2109	0.72	3/2866 (0.1%)
6	CC	0.29	0/2459	0.56	0/3350
7	CE	0.31	0/3743	0.64	5/5045 (0.1%)
8	CF	0.30	0/1982	0.65	0/2671
9	CG	0.32	0/1422	0.70	2/1920 (0.1%)
10	CH	0.35	0/3927	0.70	7/5307 (0.1%)
11	CI	0.33	0/1225	0.68	1/1645 (0.1%)
12	CJ	0.27	0/3189	0.53	0/4309
13	CK	0.30	0/1885	0.64	2/2529 (0.1%)
14	CL	0.26	0/2178	0.48	0/2983
15	CM	0.32	0/1555	0.67	2/2091 (0.1%)
15	LF	0.29	0/2004	0.56	0/2686
16	CN	0.29	0/1881	0.64	1/2560 (0.0%)
17	CO	0.29	0/470	0.55	0/619
18	CP	0.33	0/2594	0.68	4/3514 (0.1%)
19	CQ	0.32	0/981	0.70	1/1301 (0.1%)
20	CR	0.29	0/1369	0.64	1/1828 (0.1%)
21	CS	0.26	0/1762	0.45	0/2417
22	CT	0.28	0/2264	0.47	0/3149
23	CU	0.33	0/1428	0.66	1/1910 (0.1%)
24	CX	0.27	0/705	0.57	0/938
25	CY	0.31	0/1600	0.47	0/2220
26	Cz	0.29	0/598	0.56	0/785
27	Cb	0.32	0/5150	0.68	4/6936 (0.1%)
28	LB	0.33	0/2760	0.65	2/3701 (0.1%)
29	LC	0.32	0/2809	0.57	0/3787
30	LE	0.30	0/1363	0.55	0/1833
31	LG	0.32	0/1606	0.57	0/2149

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	LH	0.29	0/1516	0.58	1/2038 (0.0%)
33	LK	0.30	0/1124	0.70	2/1507 (0.1%)
34	LL	0.34	0/983	0.65	0/1318
35	LM	0.29	0/1120	0.57	0/1507
36	LN	0.30	0/1595	0.62	0/2132
37	LO	0.31	0/1652	0.56	0/2215
38	LP	0.31	0/1231	0.61	0/1658
39	LQ	0.30	0/1033	0.63	0/1391
40	LS	0.31	0/1468	0.61	0/1975
41	LT	0.28	0/1033	0.68	1/1389 (0.1%)
42	LV	0.32	0/1013	0.57	0/1361
43	LX	0.24	0/148	0.35	0/194
44	LY	0.29	0/1079	0.61	0/1443
45	Ld	0.26	0/904	0.61	0/1209
46	Le	0.29	0/1073	0.56	0/1431
47	Lf	0.33	0/883	0.63	0/1187
48	Lh	0.28	0/1006	0.59	0/1338
49	Li	0.30	0/738	0.64	0/971
50	Lj	0.32	0/606	0.65	0/803
51	Lq	0.25	0/1621	0.55	0/2180
52	Cc	0.31	0/1934	0.57	0/2614
53	Cd	0.31	0/2818	0.61	0/3786
54	Ce	0.30	0/1638	0.56	0/2196
55	Cf	0.27	0/514	0.57	0/669
All	All	0.36	0/145524	0.80	222/208241 (0.1%)

There are no bond length outliers.

The worst 5 of 222 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C1	1050	C	N3-C2-O2	-11.53	113.83	121.90
1	C1	136	C	N3-C2-O2	-10.12	114.82	121.90
1	C1	2852	C	N3-C2-O2	-10.01	114.89	121.90
1	C1	939	C	N3-C2-O2	-9.73	115.09	121.90
28	LB	171	PRO	CA-N-CD	-9.15	98.69	111.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	CA	254/316 (80%)	234 (92%)	19 (8%)	1 (0%)	34	69
5	CB	256/391 (66%)	244 (95%)	10 (4%)	2 (1%)	19	54
6	CC	283/801 (35%)	272 (96%)	11 (4%)	0	100	100
7	CE	459/598 (77%)	445 (97%)	13 (3%)	1 (0%)	47	79
8	CF	243/270 (90%)	234 (96%)	9 (4%)	0	100	100
9	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100	100
10	CH	474/661 (72%)	456 (96%)	18 (4%)	0	100	100
11	CI	144/414 (35%)	136 (94%)	8 (6%)	0	100	100
12	CJ	374/679 (55%)	365 (98%)	9 (2%)	0	100	100
13	CK	226/261 (87%)	216 (96%)	10 (4%)	0	100	100
14	CL	384/558 (69%)	357 (93%)	22 (6%)	5 (1%)	12	42
15	CM	183/249 (74%)	175 (96%)	8 (4%)	0	100	100
15	LF	238/249 (96%)	228 (96%)	9 (4%)	1 (0%)	34	69
16	CN	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	322/751 (43%)	307 (95%)	15 (5%)	0	100	100
19	CQ	110/225 (49%)	106 (96%)	4 (4%)	0	100	100
20	CR	159/237 (67%)	155 (98%)	4 (2%)	0	100	100
21	CS	294/834 (35%)	286 (97%)	6 (2%)	2 (1%)	22	57
22	CT	448/688 (65%)	425 (95%)	21 (5%)	2 (0%)	34	69
23	CU	174/451 (39%)	166 (95%)	8 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	CX	86/203 (42%)	82 (95%)	4 (5%)	0	100	100
25	CY	308/788 (39%)	292 (95%)	15 (5%)	1 (0%)	41	73
26	Cz	68/123 (55%)	67 (98%)	1 (2%)	0	100	100
27	Cb	630/924 (68%)	597 (95%)	33 (5%)	0	100	100
28	LB	337/392 (86%)	320 (95%)	17 (5%)	0	100	100
29	LC	360/365 (99%)	348 (97%)	12 (3%)	0	100	100
30	LE	166/200 (83%)	160 (96%)	6 (4%)	0	100	100
31	LG	192/262 (73%)	188 (98%)	4 (2%)	0	100	100
32	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
33	LK	142/165 (86%)	132 (93%)	10 (7%)	0	100	100
34	LL	115/213 (54%)	109 (95%)	6 (5%)	0	100	100
35	LM	135/142 (95%)	131 (97%)	4 (3%)	0	100	100
36	LN	179/203 (88%)	174 (97%)	5 (3%)	0	100	100
37	LO	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
38	LP	150/187 (80%)	149 (99%)	1 (1%)	0	100	100
39	LQ	127/213 (60%)	123 (97%)	4 (3%)	0	100	100
40	LS	172/174 (99%)	166 (96%)	6 (4%)	0	100	100
41	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	19	54
42	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
43	LX	20/156 (13%)	20 (100%)	0	0	100	100
44	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
45	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
46	Le	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
47	Lf	106/109 (97%)	102 (96%)	3 (3%)	1 (1%)	17	52
48	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
49	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
50	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
51	Lq	205/217 (94%)	186 (91%)	19 (9%)	0	100	100
52	Cc	232/282 (82%)	226 (97%)	6 (3%)	0	100	100
53	Cd	334/436 (77%)	323 (97%)	11 (3%)	0	100	100
54	Ce	192/336 (57%)	185 (96%)	7 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
55	Cf	57/570 (10%)	57 (100%)	0	0	100 100
All	All	11105/18067 (62%)	10656 (96%)	432 (4%)	17 (0%)	50 79

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CA	236	PRO
5	CB	103	ASP
14	CL	414	VAL
21	CS	67	MET
22	CT	254	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	CA	231/276 (84%)	218 (94%)	13 (6%)	21 52
5	CB	222/329 (68%)	202 (91%)	20 (9%)	9 34
6	CC	266/710 (38%)	252 (95%)	14 (5%)	22 54
7	CE	398/517 (77%)	376 (94%)	22 (6%)	21 53
8	CF	214/236 (91%)	202 (94%)	12 (6%)	21 52
9	CG	150/155 (97%)	143 (95%)	7 (5%)	26 59
10	CH	424/575 (74%)	405 (96%)	19 (4%)	27 60
11	CI	121/336 (36%)	116 (96%)	5 (4%)	30 64
12	CJ	332/579 (57%)	324 (98%)	8 (2%)	49 76
13	CK	198/225 (88%)	188 (95%)	10 (5%)	24 56
14	CL	65/458 (14%)	62 (95%)	3 (5%)	27 59
15	CM	161/215 (75%)	153 (95%)	8 (5%)	24 57
15	LF	206/215 (96%)	200 (97%)	6 (3%)	42 72
16	CN	206/206 (100%)	199 (97%)	7 (3%)	37 69
17	CO	48/99 (48%)	47 (98%)	1 (2%)	53 79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	CP	273/632 (43%)	251 (92%)	22 (8%)	11	39
19	CQ	100/192 (52%)	93 (93%)	7 (7%)	15	45
20	CR	144/206 (70%)	137 (95%)	7 (5%)	25	57
21	CS	73/716 (10%)	72 (99%)	1 (1%)	67	86
23	CU	149/376 (40%)	146 (98%)	3 (2%)	55	80
24	CX	76/172 (44%)	73 (96%)	3 (4%)	32	65
26	Cz	60/107 (56%)	59 (98%)	1 (2%)	60	83
27	Cb	540/779 (69%)	517 (96%)	23 (4%)	29	62
28	LB	290/331 (88%)	282 (97%)	8 (3%)	43	73
29	LC	283/285 (99%)	275 (97%)	8 (3%)	43	73
30	LE	143/166 (86%)	139 (97%)	4 (3%)	43	73
31	LG	168/222 (76%)	163 (97%)	5 (3%)	41	71
32	LH	167/169 (99%)	155 (93%)	12 (7%)	14	44
33	LK	121/136 (89%)	116 (96%)	5 (4%)	30	64
34	LL	99/176 (56%)	96 (97%)	3 (3%)	41	71
35	LM	115/117 (98%)	112 (97%)	3 (3%)	46	74
36	LN	164/180 (91%)	157 (96%)	7 (4%)	29	62
37	LO	163/163 (100%)	159 (98%)	4 (2%)	47	75
38	LP	125/152 (82%)	116 (93%)	9 (7%)	14	44
39	LQ	110/178 (62%)	109 (99%)	1 (1%)	78	91
40	LS	154/154 (100%)	144 (94%)	10 (6%)	17	47
41	LT	109/135 (81%)	107 (98%)	2 (2%)	59	82
42	LV	99/102 (97%)	94 (95%)	5 (5%)	24	56
43	LX	12/129 (9%)	12 (100%)	0	100	100
44	LY	117/119 (98%)	110 (94%)	7 (6%)	19	49
45	Ld	95/105 (90%)	91 (96%)	4 (4%)	30	62
46	Le	114/114 (100%)	112 (98%)	2 (2%)	59	82
47	Lf	89/90 (99%)	85 (96%)	4 (4%)	27	60
48	Lh	108/781 (14%)	105 (97%)	3 (3%)	43	73
49	Li	75/93 (81%)	71 (95%)	4 (5%)	22	54
50	Lj	61/78 (78%)	57 (93%)	4 (7%)	16	47

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
51	Lq	179/189 (95%)	176 (98%)	3 (2%)	60 83
52	Cc	204/244 (84%)	199 (98%)	5 (2%)	47 75
53	Cd	291/367 (79%)	282 (97%)	9 (3%)	40 70
54	Ce	173/297 (58%)	165 (95%)	8 (5%)	27 59
55	Cf	53/482 (11%)	50 (94%)	3 (6%)	20 52
All	All	8538/14065 (61%)	8174 (96%)	364 (4%)	33 62

5 of 364 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	LC	360	GLU
38	LP	87	SER
15	LF	100	LYS
33	LK	31	LYS
40	LS	160	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
48	Lh	37	GLN
54	Ce	185	ASN
19	CQ	58	ASN
20	CR	133	GLN
20	CR	148	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2134/3341 (63%)	479 (22%)	15 (0%)
2	C2	157/256 (61%)	30 (19%)	1 (0%)
3	C3	96/161 (59%)	34 (35%)	0
All	All	2387/3758 (63%)	543 (22%)	16 (0%)

5 of 543 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	A
1	C1	26	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C1	40	A
1	C1	43	A
1	C1	49	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3297	U
1	C1	3296	G
1	C1	3078	U
1	C1	3263	A
1	C1	2929	A

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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	$\#\|Z\| > 2$
56	GTP	CH	701	-	26,34,34	1.16	2 (7%)	32,54,54	1.60	7 (21%)

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
56	GTP	CH	701	-	-	6/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	CH	701	GTP	C5-C6	-4.17	1.38	1.47
56	CH	701	GTP	C2-N3	2.11	1.38	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	CH	701	GTP	PB-O3B-PG	-3.73	120.02	132.83
56	CH	701	GTP	PA-O3A-PB	-3.20	121.86	132.83
56	CH	701	GTP	C5-C6-N1	3.15	119.51	113.95
56	CH	701	GTP	C3'-C2'-C1'	2.97	105.46	100.98
56	CH	701	GTP	C8-N7-C5	2.92	108.55	102.99

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

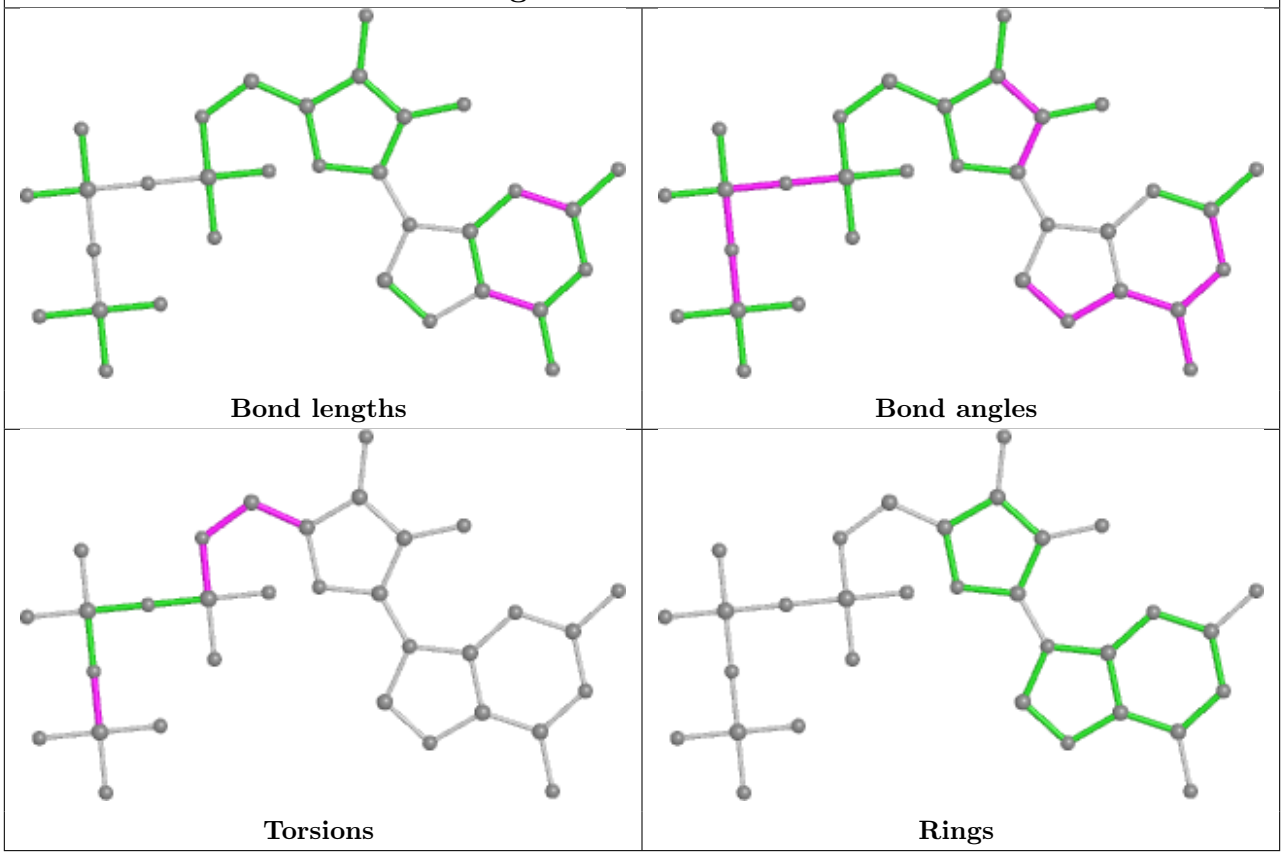
Mol	Chain	Res	Type	Atoms
56	CH	701	GTP	PB-O3B-PG-O2G
56	CH	701	GTP	PB-O3B-PG-O3G
56	CH	701	GTP	C5'-O5'-PA-O3A
56	CH	701	GTP	C4'-C5'-O5'-PA
56	CH	701	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP CH 701



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.