



wwPDB EM Validation Summary Report ⓘ

Oct 22, 2024 – 12:49 AM JST

PDB ID : 8I9T
EMDB ID : EMD-35283
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Dbp10-1
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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

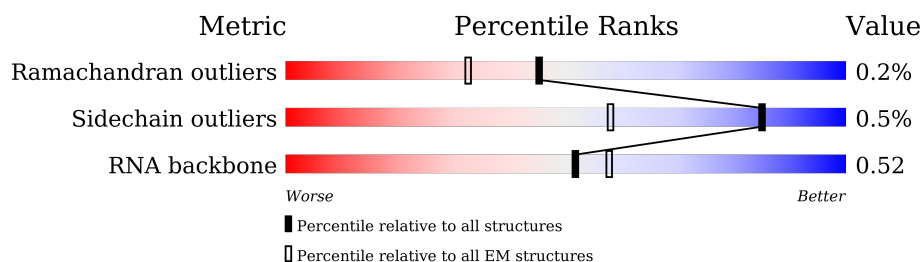
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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









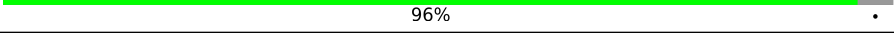
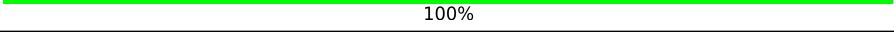
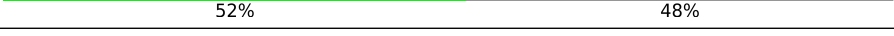

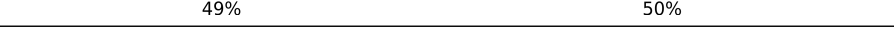
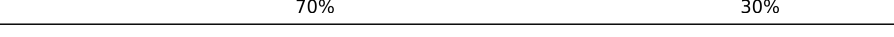

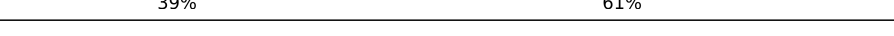


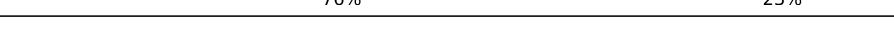

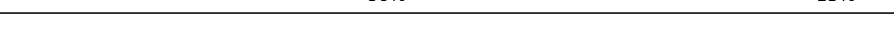






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	C1	3341	
2	C2	256	
3	C3	161	
4	CA	316	
5	CB	391	
6	CC	801	
7	CE	598	
8	CF	270	
9	CG	184	

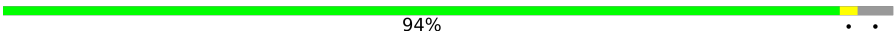

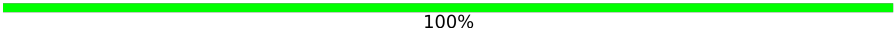


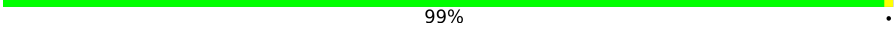

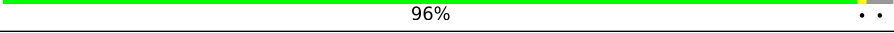

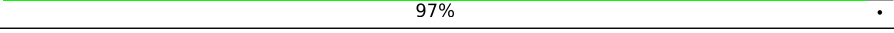
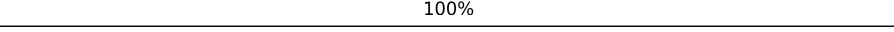
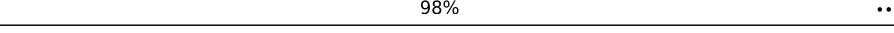
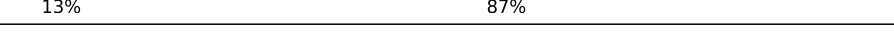
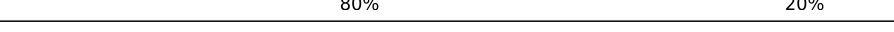

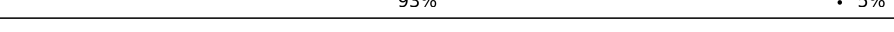



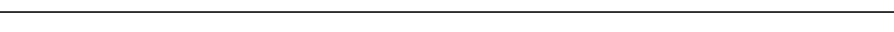

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Mol	Chain	Length	Quality of chain
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	726	
22	CU	451	
23	CX	203	
24	Cz	123	
25	Cb	732	
26	Ch	354	
27	LB	392	
28	LC	365	
29	LE	200	
30	LG	262	
31	LH	192	
32	LK	165	
33	LL	213	

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Mol	Chain	Length	Quality of chain
34	LM	142	 94% . .
35	LN	203	 90% 10%
36	LO	204	 100%
37	LP	187	 82% 18%
38	LQ	213	 61% 39%
39	LS	174	 99% .
40	LT	160	 78% . 21%
41	LV	139	 96% . .
42	LX	156	 14% 86%
43	LY	138	 97% .
44	Le	131	 100%
45	Lf	109	 98% . .
46	Lh	935	 13% 87%
47	Li	110	 80% 20%
48	Lj	95	 78% 22%
49	Lq	217	 93% . 5%
50	Cc	282	 83% 16%
51	Cd	436	 76% . 22%
52	Ce	336	 57% 42%
53	Cf	570	 16% . 83%
54	Cg	478	 49% 51%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 133790 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	2132	Total	C	N	O	P	0	0
			45600	20357	8256	14855	2132		

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

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

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

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

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

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

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

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

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

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

- 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

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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	222	Total	C	N	O	S	0	0
			1778	1113	349	312	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	90	Total	C	N	O	S	0	0
			734	463	124	145	2		

- Molecule 22 is a protein called rRNA-processing protein EBP2.

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

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

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

- Molecule 24 is a protein called rRNA-processing protein.

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

- Molecule 25 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cb	560	Total	C	N	O	S	0	0
			4397	2797	791	800	9		

- Molecule 26 is a protein called Ribosomal RNA-processing protein 15.

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

- Molecule 27 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 28 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L6.

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

- Molecule 30 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LG	195	Total	C	N	O	S	0	0
			1574	1015	285	269	5		

- Molecule 31 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	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 32 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 33 is a protein called 60S ribosomal protein L13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 35 is a protein called Ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 37 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 38 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 39 is a protein called 60S ribosomal protein L20.

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

- Molecule 40 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 41 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 42 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 43 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 45 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 46 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 47 is a protein called 60S ribosomal protein L36.

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

- Molecule 48 is a protein called Ribosomal protein L37.

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

- Molecule 49 is a protein called Ribosomal protein.

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

- Molecule 50 is a protein called Ribosomal RNA-processing protein 1.

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

- Molecule 51 is a protein called Brix domain-containing protein.

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

- Molecule 52 is a protein called Protein MAK16.

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

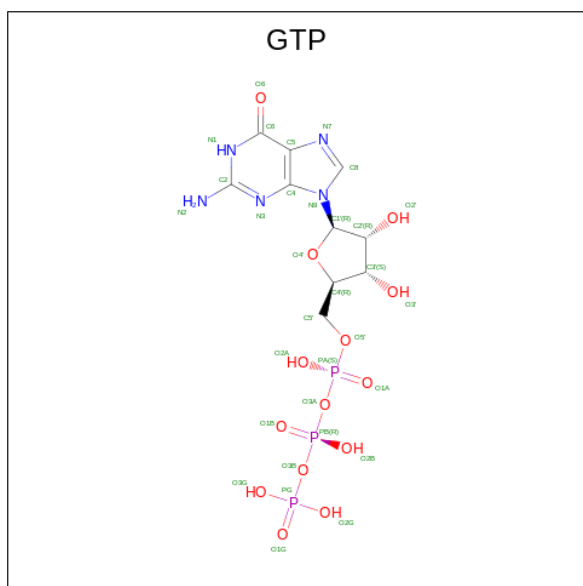
- Molecule 53 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Cf	98	Total	C	N	O	S	0	0
			845	517	173	154	1		

- Molecule 54 is a protein called Brix domain-containing protein.

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

- Molecule 55 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{14}\text{P}_3$).

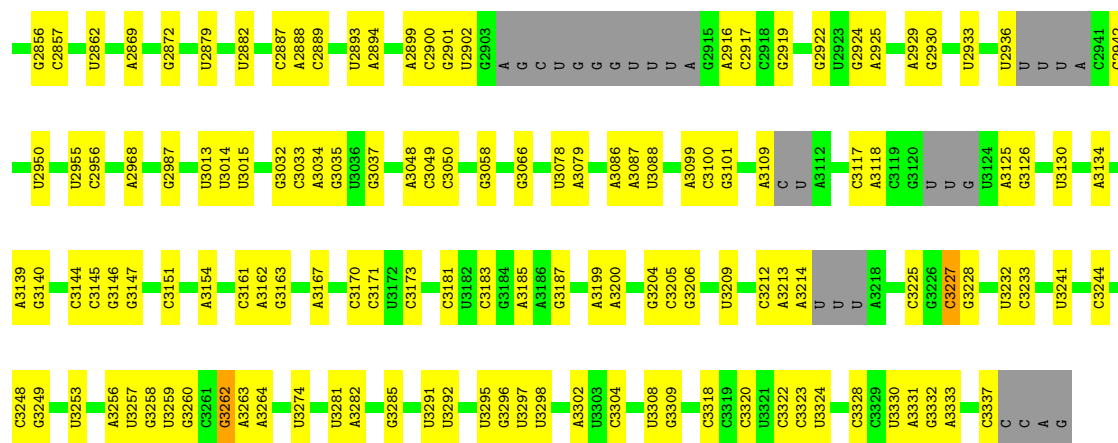


Mol	Chain	Residues	Atoms					AltConf
55	CH	1	Total 32	C 10	N 5	O 14	P 3	0

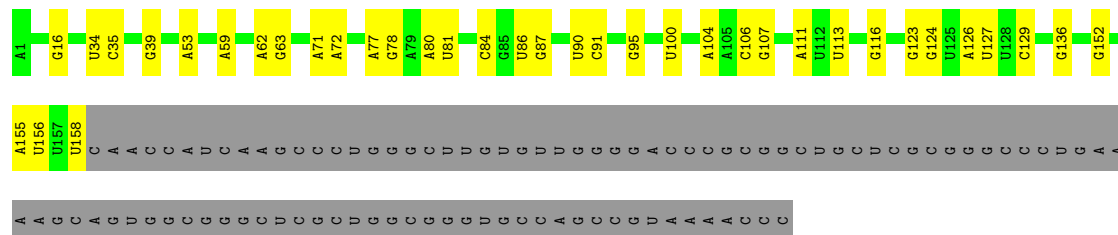
- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

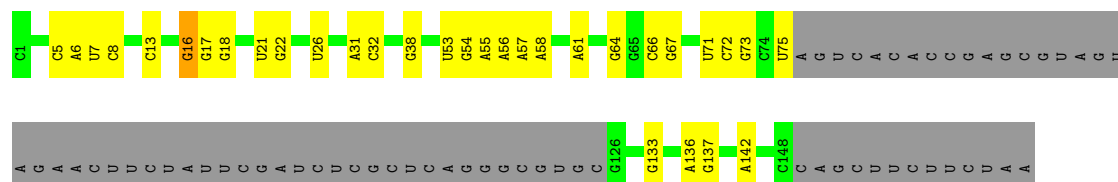




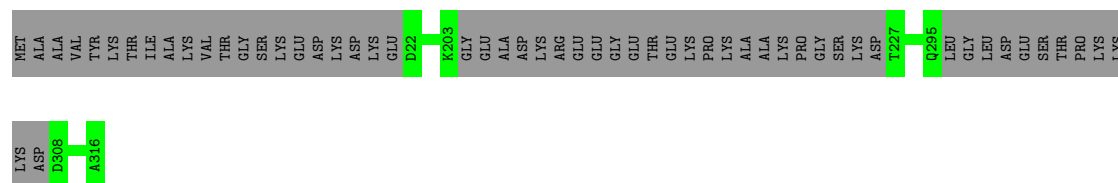
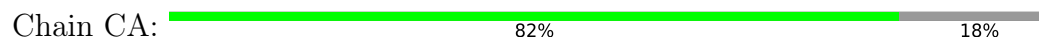
• Molecule 2: RNA (256-MER)



• Molecule 3: RNA (161-MER)

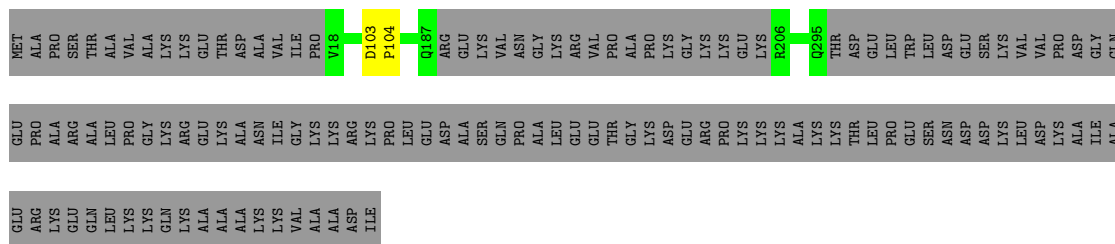


• Molecule 4: Brix domain-containing protein

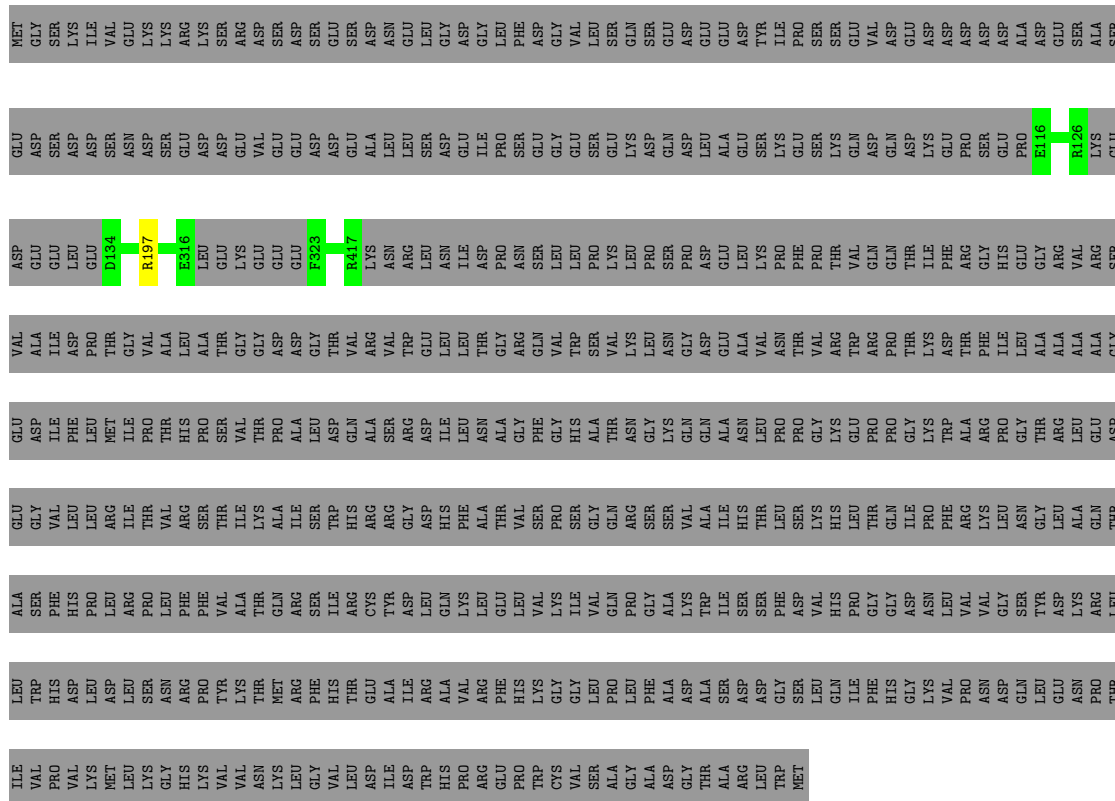


• Molecule 5: Ribosome biogenesis protein C8F11.04

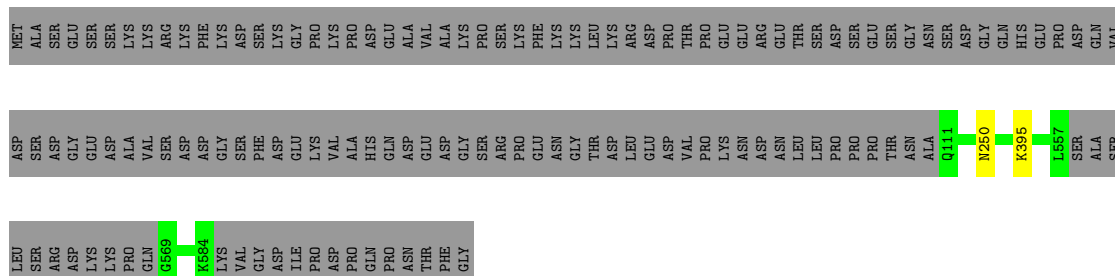
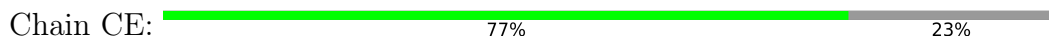




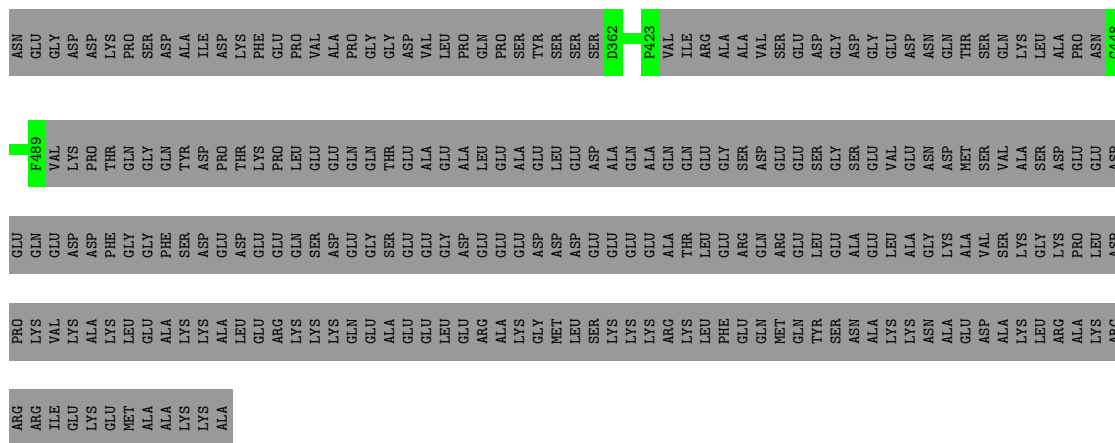
- Molecule 6: Ribosome biogenesis protein ERB1



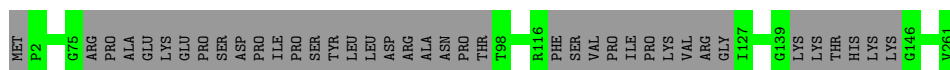
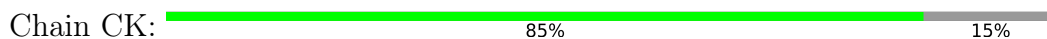
- Molecule 7: RNA helicase



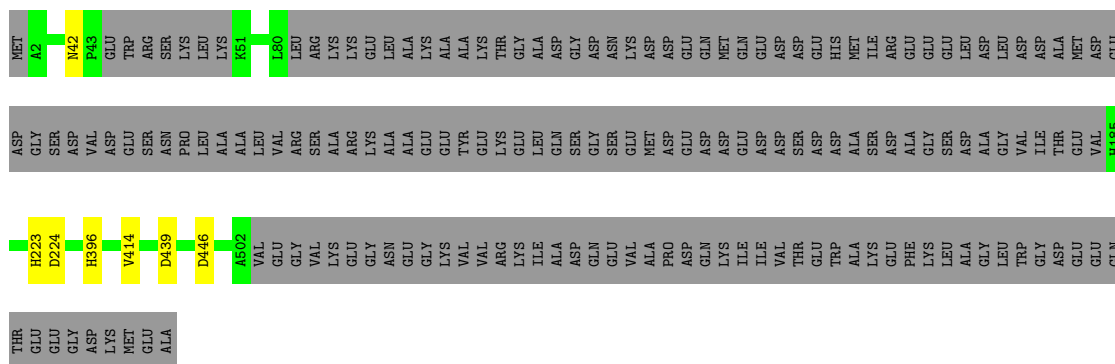
- Molecule 8: Ribosome assembly factor mrt4



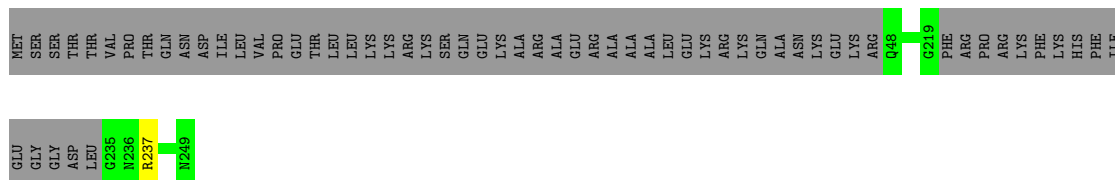
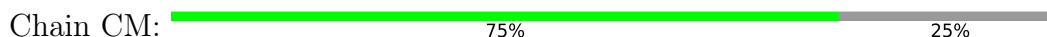
- Molecule 13: Ribosome biogenesis protein NSA2 homolog



- Molecule 14: Putative GTP binding protein



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

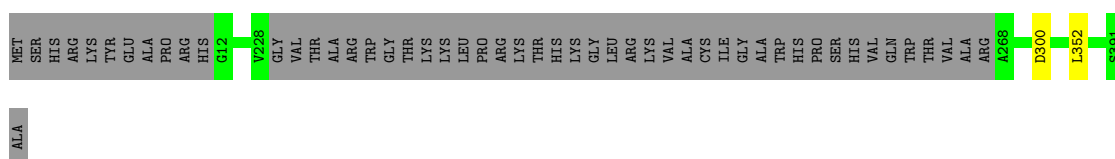


- Molecule 15: 60S ribosomal protein l7-like protein



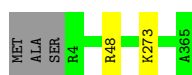
- Molecule 27: 60S ribosomal protein L3-like protein

Chain LB: 86% 13%




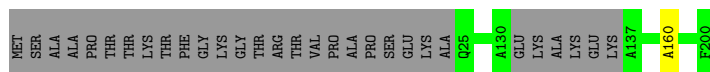
- Molecule 28: 60S ribosomal protein L4-like protein

Chain LC: 99%

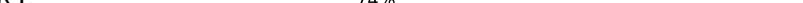


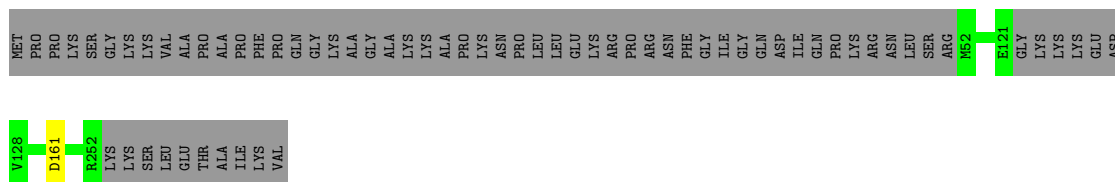
- Molecule 29: 60S ribosomal protein L6

Chain LE:  84% 15%



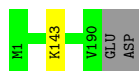
- Molecule 30: 60S ribosomal protein L8

Chain LG: 



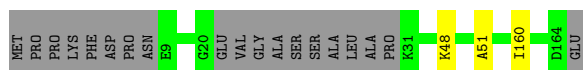
- Molecule 31: 60S ribosomal protein 19-like protein

Chain LH:  98%



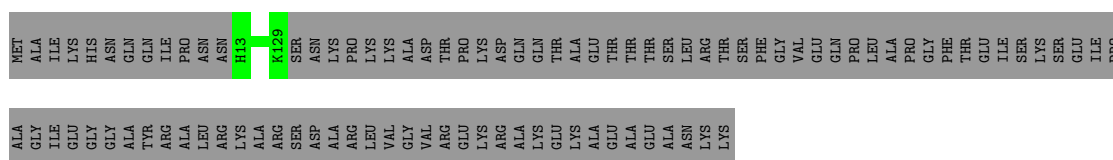
- Molecule 32: 60S ribosomal protein L12-like protein

Chain LK: 87% 12%



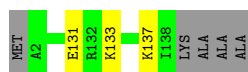
- Molecule 33: 60S ribosomal protein L13

Chain LL: 55% 45%



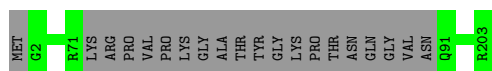
- Molecule 34: 60S ribosomal protein L14-like protein

Chain LM: 94%



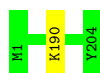
- Molecule 35: Ribosomal protein L15

Chain LN: 90% 10%



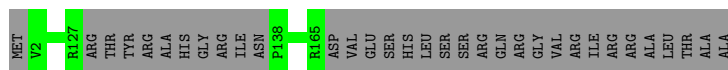
- Molecule 36: 60S ribosomal protein L16-like protein

Chain LO: 100%



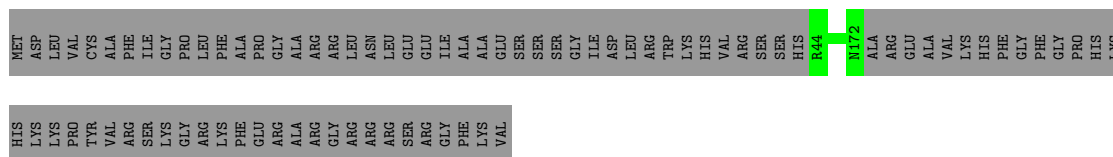
- Molecule 37: 60S ribosomal protein L17-like protein

Chain LP: 82% 18%



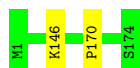
- Molecule 38: Ribosomal protein L18-like protein

Chain LQ:  61% 39%




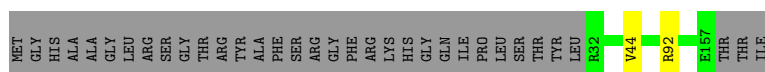
- Molecule 39: 60S ribosomal protein L20

Chain LS:  99% .



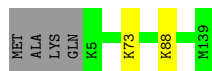
- Molecule 40: 60S ribosomal protein l21-like protein

Chain LT:  78% 21%



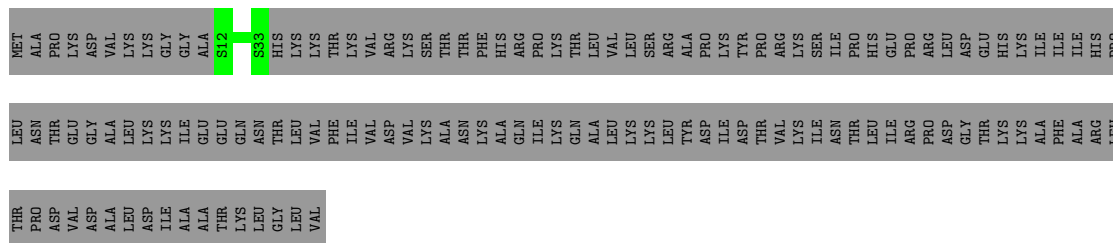
- Molecule 41: 60S ribosomal protein l23-like protein

Chain LV:  96% . .



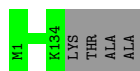
- Molecule 42: 60S ribosomal protein L25-like protein

Chain LX:  14% 86%



- Molecule 43: 60S ribosomal protein L26-like protein

Chain LY:  97% .




- Molecule 44: 60S ribosomal protein L32-like protein

- Molecule 45: 60S ribosomal protein l33-like protein

- Molecule 46: dolichyl-diphosphooligosaccharide--protein glycotransferase


- Molecule 47: 60S ribosomal protein L36

MET	SER	GLU	ASP	ALA	THR	PRO	LYS	ALA	PRO	VAL	GLU	ARG	THR	GLY	LEU	ILE	ARG	GLY	LEU	ASN	LYS	G23	H110
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------

- Chain Lj:  78% 22%

MET	THR	LYS	GLY	THR	SER	SER	PHE	GLY	LYS	ARG	HIS	ASN	K14	R87	GLY	PRO	ALA	VAL	SER	THR	SER	SER
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- Chain Lq: 93% • 5%

- Chain Cc:  83% 16%

MET	THR	SER	SER	GLN	ES	K125	K129	ASP	GLY	SER	SER	LEU	GLY	LYS	ARG	THR	THR	HIS	ASP	GLY	GLN	GLU	LYS	ALA	VAL	VAL	LYS	THR	THR	GL48	R258	ARG	PRO	ASN	SER	SER	SER	GLN	ASP	ASP	HIS	ASP	THR	THR	LYS	ASP	ASP	MET	GLY	ASP	SER	SER	ASP	ASP	THR	TRP	GLU	GLY	PHE	ASP	ASP
-----	-----	-----	-----	-----	----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain Cd: 76% 22%

NET	ALA	ALA	SER	LYS	LYS	ASP	L9	D77	LEU	ASP	ASP	D81	R94	E96	VAL	ALA	GLU	ALA	ALA	ALA	ALA	ALA	GLU	ASP	ALA	ALA	ALA	ALA	ARG	GLU	ASP	LYS	ASN	ASP	GLU	ASN	GLU	LYS	ARG	ASP	ASP	TLE	ASP	SER	MET	LEU	GLY	SER	ASP	ASP
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[illegible]

T398 K406 L436

- Chain Ce:  57% 42%

MET	S2	L190	L195	ASN	ALA	LEU	GLU	ALA	GLU	GLY	GLU	GLY	VAL	ARG	ASP	LYS	ASP	HIS	ASP	LYS	GLY	ILE	GLU	ALA	ASP	GLU	GLU	LEU	GLU	SER	ALA	GLU	GLU	SER	GLU	VAL	GLU	GLU	TYR	GLU	ARG	GLU	GLU	GLU	GLU	ASN	GLU	ASP	ASN	VAL	VAL	GLU	TYR	VAL	SER	ASP	PRO
-----	----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	GLU	SER	GLU	ASP	GLU	LEU	GLY	ASP	LEU	GLU	ASP	ASP	TRP	LEU	GLY	SER	ASP	ASP	GLU	GLU	PHE	ASP	ASP	ASP	GLU	ASP	ASP	GLU	ASP	ASP	GLU	GLY	GLU	GLU	GLU	GLU	LEU	LYS	LYS	LYS	ALA	ASP	LYS	ARG	LYS	ARG	GLY	LYS
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WORLD WIDE
PDB
PROTEIN DATA BANK

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52677	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, GTP

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	0.22	0/51017	0.83	33/79513 (0.0%)
2	C2	0.20	0/3754	0.78	0/5846
3	C3	0.22	0/2342	0.85	2/3649 (0.1%)
4	CA	0.28	0/2190	0.58	0/2940
5	CB	0.27	0/2109	0.57	0/2866
6	CC	0.26	0/2459	0.50	0/3350
7	CE	0.27	0/3743	0.55	1/5045 (0.0%)
8	CF	0.26	0/1982	0.56	1/2671 (0.0%)
9	CG	0.26	0/1422	0.56	0/1920
10	CH	0.29	0/3927	0.58	0/5307
11	CI	0.28	0/1225	0.61	0/1645
12	CJ	0.26	0/3189	0.53	0/4309
13	CK	0.27	0/1804	0.57	0/2417
14	CL	0.25	0/2178	0.49	0/2983
15	CM	0.26	0/1555	0.52	0/2091
15	LF	0.27	0/2004	0.52	0/2686
16	CN	0.25	0/1881	0.56	0/2560
17	CO	0.25	0/470	0.54	0/619
18	CP	0.28	0/2594	0.54	0/3514
19	CQ	0.28	0/981	0.64	0/1301
20	CR	0.25	0/1369	0.56	0/1828
21	CS	0.23	0/746	0.42	0/997
22	CU	0.27	0/1428	0.58	1/1910 (0.1%)
23	CX	0.28	0/705	0.53	0/938
24	Cz	0.28	0/598	0.58	0/785
25	Cb	0.26	0/4474	0.53	0/6037
26	Ch	0.30	0/563	0.69	1/746 (0.1%)
27	LB	0.27	0/2760	0.58	2/3701 (0.1%)
28	LC	0.26	0/2809	0.53	1/3787 (0.0%)
29	LE	0.27	0/1363	0.52	0/1833
30	LG	0.27	0/1597	0.55	0/2138
31	LH	0.26	0/1516	0.54	0/2038

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LK	0.26	0/1124	0.57	0/1507
33	LL	0.24	0/983	0.62	0/1318
34	LM	0.28	0/1120	0.58	0/1507
35	LN	0.25	0/1595	0.59	0/2132
36	LO	0.27	0/1652	0.57	0/2215
37	LP	0.26	0/1231	0.59	0/1658
38	LQ	0.25	0/1033	0.59	0/1391
39	LS	0.26	0/1468	0.56	1/1975 (0.1%)
40	LT	0.24	0/1033	0.54	0/1389
41	LV	0.27	0/1013	0.52	0/1361
42	LX	0.23	0/148	0.38	0/194
43	LY	0.26	0/1079	0.57	0/1443
44	Le	0.24	0/1073	0.53	0/1431
45	Lf	0.26	0/883	0.55	0/1187
46	Lh	0.25	0/1006	0.57	0/1338
47	Li	0.27	0/738	0.63	0/971
48	Lj	0.25	0/606	0.60	0/803
49	Lq	0.25	0/1621	0.56	0/2180
50	Cc	0.25	0/1934	0.55	0/2614
51	Cd	0.30	0/2818	0.62	0/3786
52	Ce	0.28	0/1638	0.57	0/2196
53	Cf	0.33	0/851	0.74	2/1118 (0.2%)
54	Cg	0.26	0/1887	0.57	0/2544
All	All	0.25	0/141288	0.69	45/202228 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	CB	0	1
14	CL	0	1
30	LG	0	1
49	Lq	0	1
51	Cd	0	1
53	Cf	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1084	U	OP1-P-O3'	-10.82	81.39	105.20
1	C1	1050	C	N3-C2-O2	-10.36	114.65	121.90
1	C1	1084	U	OP2-P-O3'	-9.41	84.49	105.20
1	C1	3241	U	N3-C2-O2	-8.18	116.48	122.20
1	C1	1085	A	OP1-P-OP2	8.16	131.85	119.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	CB	103	ASP	Peptide
14	CL	223	HIS	Peptide
51	Cd	360	TYR	Peptide
30	LG	161	ASP	Peptide
49	Lq	60	ARG	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	CA	254/316 (80%)	230 (91%)	24 (9%)	0	100	100
5	CB	256/391 (66%)	237 (93%)	18 (7%)	1 (0%)	30	63
6	CC	283/801 (35%)	271 (96%)	12 (4%)	0	100	100
7	CE	459/598 (77%)	435 (95%)	24 (5%)	0	100	100
8	CF	243/270 (90%)	230 (95%)	12 (5%)	1 (0%)	30	63
9	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100	100
10	CH	474/661 (72%)	446 (94%)	26 (6%)	2 (0%)	30	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	CI	144/414 (35%)	133 (92%)	10 (7%)	1 (1%)	19	53
12	CJ	374/679 (55%)	363 (97%)	11 (3%)	0	100	100
13	CK	214/261 (82%)	208 (97%)	6 (3%)	0	100	100
14	CL	384/558 (69%)	347 (90%)	31 (8%)	6 (2%)	8	38
15	CM	183/249 (74%)	175 (96%)	8 (4%)	0	100	100
15	LF	238/249 (96%)	232 (98%)	5 (2%)	1 (0%)	30	63
16	CN	244/246 (99%)	234 (96%)	10 (4%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	322/751 (43%)	308 (96%)	14 (4%)	0	100	100
19	CQ	110/225 (49%)	103 (94%)	6 (6%)	1 (1%)	14	48
20	CR	159/237 (67%)	155 (98%)	4 (2%)	0	100	100
21	CS	86/726 (12%)	84 (98%)	2 (2%)	0	100	100
22	CU	174/451 (39%)	168 (97%)	6 (3%)	0	100	100
23	CX	86/203 (42%)	83 (96%)	3 (4%)	0	100	100
24	Cz	68/123 (55%)	68 (100%)	0	0	100	100
25	Cb	550/732 (75%)	527 (96%)	23 (4%)	0	100	100
26	Ch	69/354 (20%)	65 (94%)	4 (6%)	0	100	100
27	LB	337/392 (86%)	322 (96%)	15 (4%)	0	100	100
28	LC	360/365 (99%)	346 (96%)	14 (4%)	0	100	100
29	LE	166/200 (83%)	159 (96%)	6 (4%)	1 (1%)	22	55
30	LG	191/262 (73%)	179 (94%)	12 (6%)	0	100	100
31	LH	188/192 (98%)	180 (96%)	8 (4%)	0	100	100
32	LK	142/165 (86%)	131 (92%)	9 (6%)	2 (1%)	9	40
33	LL	115/213 (54%)	110 (96%)	5 (4%)	0	100	100
34	LM	135/142 (95%)	130 (96%)	5 (4%)	0	100	100
35	LN	179/203 (88%)	173 (97%)	6 (3%)	0	100	100
36	LO	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
37	LP	150/187 (80%)	143 (95%)	7 (5%)	0	100	100
38	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
39	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
40	LT	124/160 (78%)	116 (94%)	7 (6%)	1 (1%)	16	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LV	133/139 (96%)	128 (96%)	5 (4%)	0	100	100
42	LX	20/156 (13%)	20 (100%)	0	0	100	100
43	LY	132/138 (96%)	125 (95%)	7 (5%)	0	100	100
44	Le	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
45	Lf	106/109 (97%)	103 (97%)	2 (2%)	1 (1%)	14	48
46	Lh	119/935 (13%)	113 (95%)	6 (5%)	0	100	100
47	Li	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
48	Lj	72/95 (76%)	69 (96%)	3 (4%)	0	100	100
49	Lq	205/217 (94%)	181 (88%)	23 (11%)	1 (0%)	25	59
50	Cc	232/282 (82%)	223 (96%)	9 (4%)	0	100	100
51	Cd	334/436 (77%)	314 (94%)	20 (6%)	0	100	100
52	Ce	192/336 (57%)	187 (97%)	4 (2%)	1 (0%)	25	59
53	Cf	96/570 (17%)	93 (97%)	3 (3%)	0	100	100
54	Cg	229/478 (48%)	218 (95%)	11 (5%)	0	100	100
All	All	10278/17003 (60%)	9776 (95%)	482 (5%)	20 (0%)	45	73

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	CB	104	PRO
11	CI	268	VAL
14	CL	224	ASP
14	CL	414	VAL
8	CF	238	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	CA	231/276 (84%)	231 (100%)	0	100	100
5	CB	222/329 (68%)	222 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	CC	266/710 (38%)	265 (100%)	1 (0%)	89	95
7	CE	398/517 (77%)	397 (100%)	1 (0%)	91	96
8	CF	214/236 (91%)	214 (100%)	0	100	100
9	CG	150/155 (97%)	148 (99%)	2 (1%)	65	81
10	CH	424/575 (74%)	421 (99%)	3 (1%)	81	90
11	CI	121/336 (36%)	121 (100%)	0	100	100
12	CJ	332/579 (57%)	330 (99%)	2 (1%)	84	92
13	CK	189/225 (84%)	189 (100%)	0	100	100
14	CL	65/458 (14%)	65 (100%)	0	100	100
15	CM	161/215 (75%)	160 (99%)	1 (1%)	84	92
15	LF	206/215 (96%)	206 (100%)	0	100	100
16	CN	206/206 (100%)	206 (100%)	0	100	100
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	273/632 (43%)	273 (100%)	0	100	100
19	CQ	100/192 (52%)	100 (100%)	0	100	100
20	CR	144/206 (70%)	144 (100%)	0	100	100
21	CS	74/618 (12%)	74 (100%)	0	100	100
22	CU	149/376 (40%)	148 (99%)	1 (1%)	81	90
23	CX	76/172 (44%)	75 (99%)	1 (1%)	65	81
24	Cz	60/107 (56%)	60 (100%)	0	100	100
25	Cb	470/619 (76%)	469 (100%)	1 (0%)	92	96
26	Ch	58/291 (20%)	57 (98%)	1 (2%)	56	75
27	LB	290/331 (88%)	290 (100%)	0	100	100
28	LC	283/285 (99%)	282 (100%)	1 (0%)	89	95
29	LE	143/166 (86%)	143 (100%)	0	100	100
30	LG	167/222 (75%)	167 (100%)	0	100	100
31	LH	167/169 (99%)	166 (99%)	1 (1%)	84	92
32	LK	121/136 (89%)	120 (99%)	1 (1%)	79	88
33	LL	99/176 (56%)	99 (100%)	0	100	100
34	LM	115/117 (98%)	112 (97%)	3 (3%)	41	65
35	LN	164/180 (91%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LO	163/163 (100%)	162 (99%)	1 (1%)	84	92
37	LP	125/152 (82%)	125 (100%)	0	100	100
38	LQ	110/178 (62%)	110 (100%)	0	100	100
39	LS	154/154 (100%)	153 (99%)	1 (1%)	84	92
40	LT	109/135 (81%)	108 (99%)	1 (1%)	75	87
41	LV	99/102 (97%)	97 (98%)	2 (2%)	50	72
42	LX	12/129 (9%)	12 (100%)	0	100	100
43	LY	117/119 (98%)	117 (100%)	0	100	100
44	Le	114/114 (100%)	114 (100%)	0	100	100
45	Lf	89/90 (99%)	89 (100%)	0	100	100
46	Lh	108/781 (14%)	107 (99%)	1 (1%)	75	87
47	Li	75/93 (81%)	75 (100%)	0	100	100
48	Lj	61/78 (78%)	61 (100%)	0	100	100
49	Lq	179/189 (95%)	176 (98%)	3 (2%)	56	75
50	Cc	204/244 (84%)	203 (100%)	1 (0%)	86	93
51	Cd	291/367 (79%)	282 (97%)	9 (3%)	35	62
52	Ce	173/297 (58%)	173 (100%)	0	100	100
53	Cf	88/482 (18%)	86 (98%)	2 (2%)	45	68
54	Cg	210/417 (50%)	210 (100%)	0	100	100
All	All	8667/14410 (60%)	8626 (100%)	41 (0%)	85	93

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	Lq	133	LYS
51	Cd	285	LEU
50	Cc	125	LYS
51	Cd	267	SER
51	Cd	398	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
27	LB	274	HIS

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Mol	Chain	Res	Type
49	Lq	27	ASN
27	LB	319	ASN
30	LG	140	ASN
54	Cg	216	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2116/3341 (63%)	485 (22%)	20 (0%)
2	C2	157/256 (61%)	36 (22%)	1 (0%)
3	C3	96/161 (59%)	32 (33%)	2 (2%)
All	All	2369/3758 (63%)	553 (23%)	23 (0%)

5 of 553 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	A
1	C1	20	A
1	C1	26	A
1	C1	40	A
1	C1	43	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3204	G
1	C1	3281	U
1	C1	3257	U
1	C1	3296	G
1	C1	1223	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 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
55	GTP	CH	701	-	26,34,34	1.12	2 (7%)	32,54,54	1.49	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
55	GTP	CH	701	-	-	5/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	CH	701	GTP	C5-C6	-3.94	1.39	1.47
55	CH	701	GTP	C2-N3	2.19	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	CH	701	GTP	C5-C6-N1	3.17	119.55	113.95
55	CH	701	GTP	PA-O3A-PB	-3.09	122.24	132.83
55	CH	701	GTP	C8-N7-C5	2.96	108.62	102.99
55	CH	701	GTP	C3'-C2'-C1'	2.91	105.36	100.98
55	CH	701	GTP	C2-N1-C6	-2.82	119.91	125.10

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	CH	701	GTP	C5'-O5'-PA-O3A

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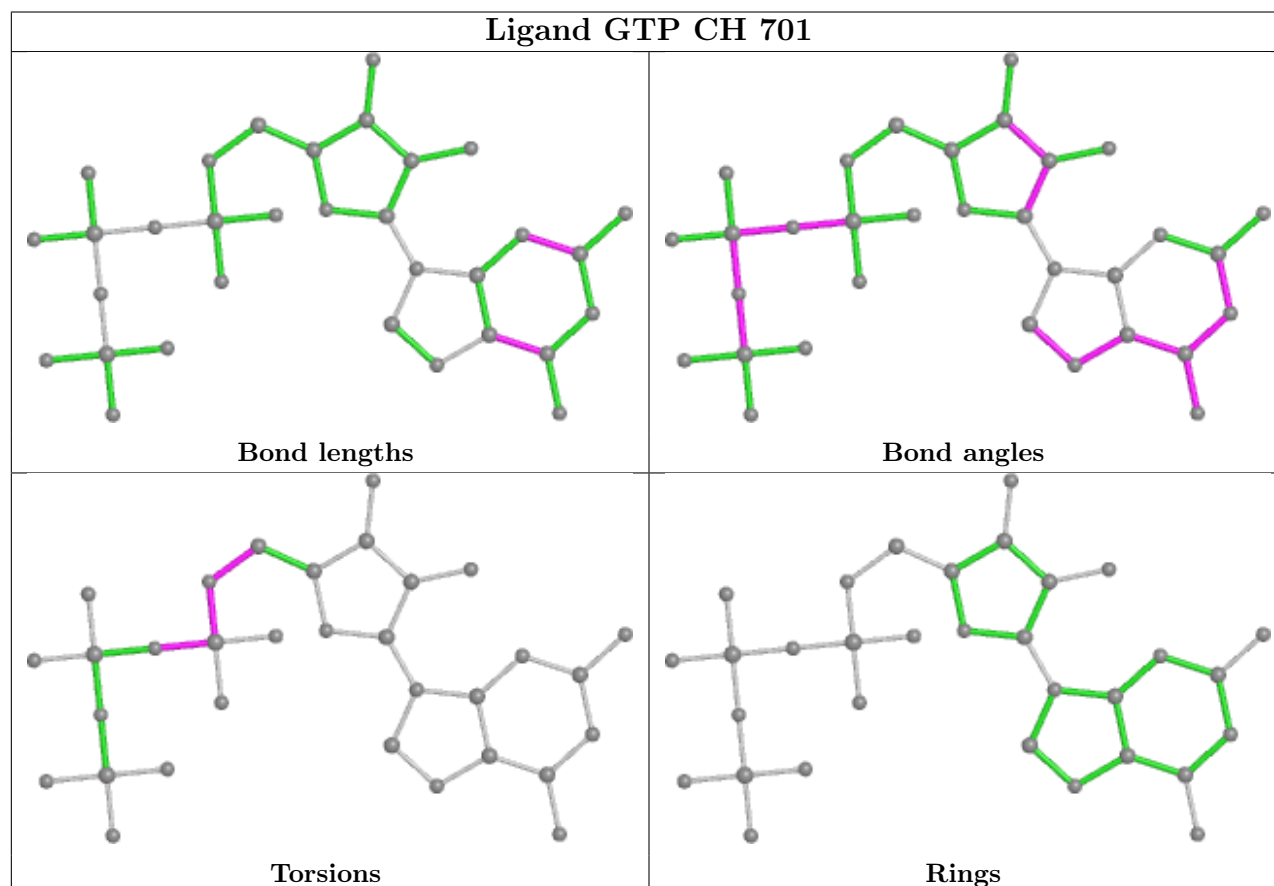
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Mol	Chain	Res	Type	Atoms
55	CH	701	GTP	PB-O3A-PA-O2A
55	CH	701	GTP	C5'-O5'-PA-O2A
55	CH	701	GTP	C4'-C5'-O5'-PA
55	CH	701	GTP	PB-O3A-PA-O1A

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 than 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.



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.