



wwPDB EM Validation Summary Report ⓘ

Dec 14, 2022 – 03:33 AM EST

PDB ID : 4V47
Title : Real space refined coordinates of the 30S and 50S subunits fitted into the low resolution cryo-EM map of the EF-G.GTP state of E. coli 70S ribosome
Authors : Gao, H.; Sengupta, J.; Valle, M.; Korostelev, A.; Eswar, N.; Stagg, S.M.; Van Roey, P.; Agrawal, R.K.; Harvey, S.T.; Sali, A.; Chapman, M.S.; Frank, J.
Deposited on : 2003-05-06
Resolution : 12.30 Å (reported)
Based on initial models : 1IBL, 1LNR, 1JJ2, 1FJG, 1FFK, 1GIY

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB 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:

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

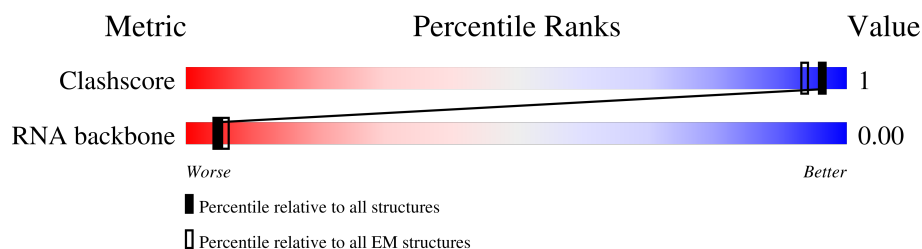
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY










The reported resolution of this entry is 12.30 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.



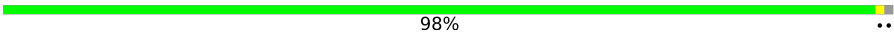

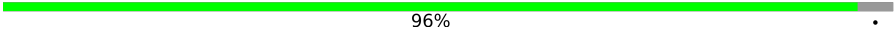

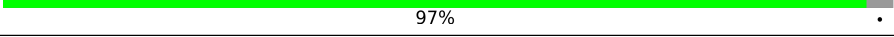
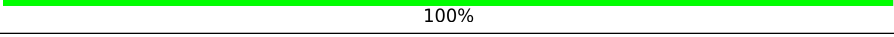

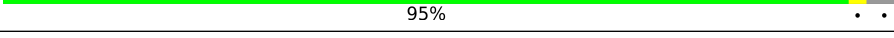
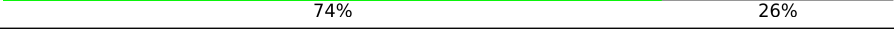
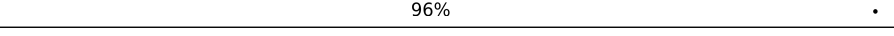
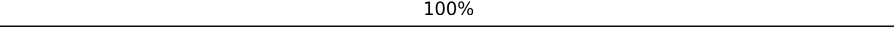
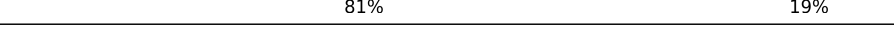
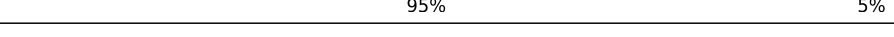
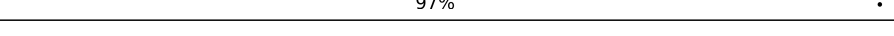

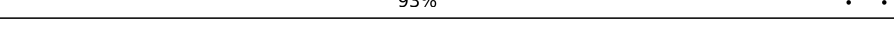
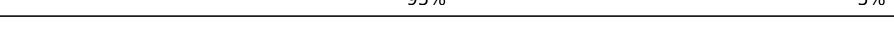
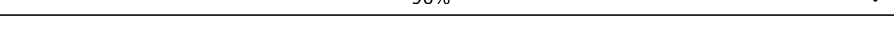
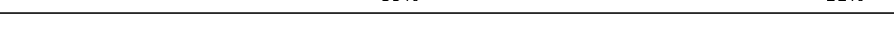






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain	
1	A0	2904		
2	A9	120		
3	AA	272		
4	AB	209		
5	AC	201		
6	AD	178		.
7	AE	176		5%
8	AF	149		
9	AG	141		.
10	AH	142		.

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Mol	Chain	Length	Quality of chain
11	AI	123	
12	AJ	144	
13	AK	136	
14	AL	127	
15	AM	117	
16	AN	114	
17	AO	117	
18	AQ	110	
19	AR	100	
20	AS	103	
21	AT	94	
22	AU	84	
23	AW	63	
24	AX	58	
25	AZ	56	
26	A1	54	
27	A4	38	
28	BA	1542	
29	BC	232	
30	BD	205	
31	BE	166	
32	BF	135	
33	BG	178	
34	BH	129	
35	BI	129	

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Mol	Chain	Length	Quality of chain
36	BJ	103	 93% 7%
37	BK	128	 79% 21%
38	BL	123	 79% 21%
39	BM	117	 98% .
40	BN	100	 32% 68%
41	BO	88	 98% .
42	BP	82	 95% 5%
43	BQ	83	 95% 5%
44	BR	74	 69% 31%
45	BS	91	 71% 29%
46	BT	86	 97% .

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 8647 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A0	2536	Total	P	0	2536
			2536	2536		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
2	A9	108	Total	P	0	108
			108	108		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	AA	227	Total	C	0	227
			227	227		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	AB	156	Total	C	0	156
			156	156		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	AC	142	Total	C	0	142
			142	142		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	AD	177	Total	C	0	177
			177	177		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	AE	167	Total	C	0	167
			167	167		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	AF	76	Total	C	0	76
			76	76		

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	AG	139	Total	C	0	139
			139	139		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms		AltConf	Trace
10	AH	142	Total	C	0	142
			142	142		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	AI	122	Total	C	0	122
			122	122		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	AJ	70	Total	C	0	70
			70	70		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	AK	131	Total	C	0	131
			131	131		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	AL	99	Total	C	0	99
			99	99		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	AM	113	Total	C	0	113
			113	113		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms		AltConf	Trace
16	AN	114	Total	C	0	114
			114	114		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms		AltConf	Trace
17	AO	68	Total	C	0	68
			68	68		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms		AltConf	Trace
18	AQ	106	Total	C	0	106
			106	106		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms		AltConf	Trace
19	AR	74	Total	C	0	74
			74	74		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms		AltConf	Trace
20	AS	99	Total	C	0	99
			99	99		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms	AltConf	Trace
21	AT	94	Total C 94 94	0	94

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms	AltConf	Trace
22	AU	68	Total C 68 68	0	68

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms	AltConf	Trace
23	AW	60	Total C 60 60	0	60

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms	AltConf	Trace
24	AX	56	Total C 56 56	0	56

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms	AltConf	Trace
25	AZ	29	Total C 29 29	0	29

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms	AltConf	Trace
26	A1	52	Total C 52 52	0	52

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms	AltConf	Trace
27	A4	36	Total C 36 36	0	36

- Molecule 28 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
28	BA	1487	Total	P	0	1487
			1487	1487		

- Molecule 29 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms		AltConf	Trace
29	BC	206	Total	C	0	206
			206	206		

- Molecule 30 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms		AltConf	Trace
30	BD	204	Total	C	0	204
			204	204		

- Molecule 31 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms		AltConf	Trace
31	BE	148	Total	C	0	148
			148	148		

- Molecule 32 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms		AltConf	Trace
32	BF	95	Total	C	0	95
			95	95		

- Molecule 33 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms		AltConf	Trace
33	BG	137	Total	C	0	137
			137	137		

- Molecule 34 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms		AltConf	Trace
34	BH	127	Total	C	0	127
			127	127		

- Molecule 35 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms		AltConf	Trace
35	BI	99	Total	C	0	99
			99	99		

- Molecule 36 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms		AltConf	Trace
36	BJ	96	Total	C	0	96
			96	96		

- Molecule 37 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms		AltConf	Trace
37	BK	101	Total	C	0	101
			101	101		

- Molecule 38 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms		AltConf	Trace
38	BL	97	Total	C	0	97
			97	97		

- Molecule 39 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms		AltConf	Trace
39	BM	115	Total	C	0	115
			115	115		

- Molecule 40 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms		AltConf	Trace
40	BN	32	Total	C	0	32
			32	32		

- Molecule 41 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms		AltConf	Trace
41	BO	86	Total	C	0	86
			86	86		

- Molecule 42 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms		AltConf	Trace
42	BP	78	Total	C	0	78
			78	78		

- Molecule 43 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms		AltConf	Trace
43	BQ	79	Total	C	0	79
			79	79		

- Molecule 44 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms		AltConf	Trace
44	BR	51	Total	C	0	51
			51	51		

- Molecule 45 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms		AltConf	Trace
45	BS	65	Total	C	0	65
			65	65		

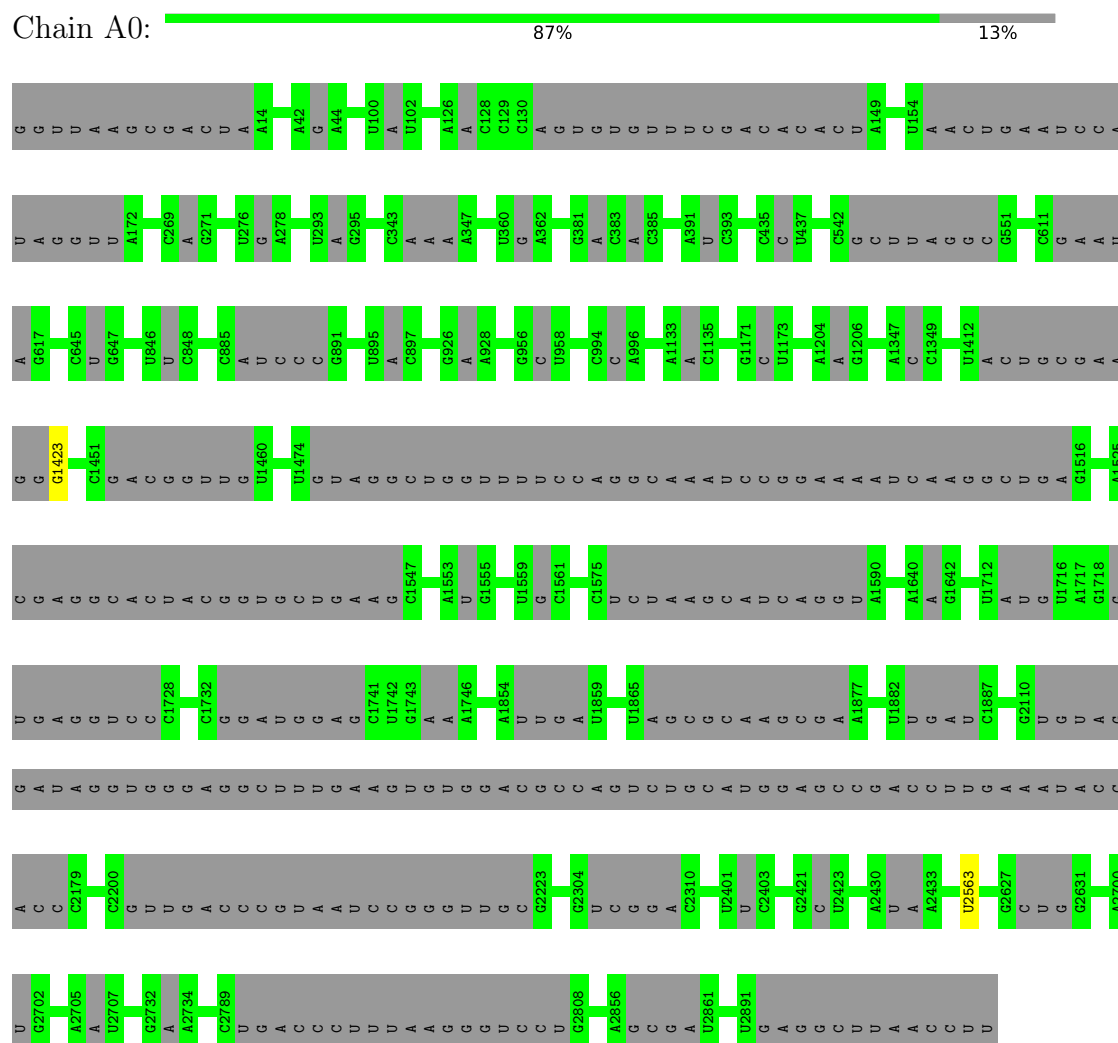
- Molecule 46 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms		AltConf	Trace
46	BT	83	Total	C	0	83
			83	83		

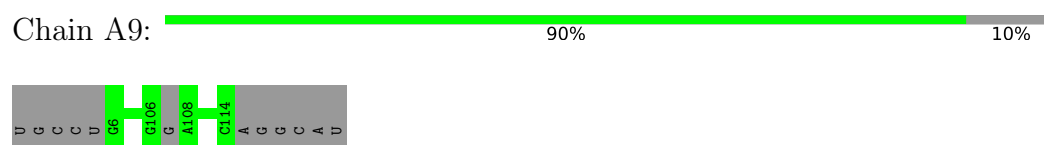
3 Residue-property plots [i](#)

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: 23S ribosomal RNA



- Molecule 2: 5S ribosomal RNA



- Molecule 3: 50S ribosomal protein L2

ALA	VAL	VAL	LYS	CYS	LYS	PRO	THR	SER	PRO	GLY	ARG	ARG	HIS	VAL	VAL	LYS	LYS	VAL	ASN	PRO	GLU	LEU	HIS	LYS	GLY	LYS	PRO	PHE	PRO	ALA	PRO	LEU	LEU	GLU	LYS	ASN	SER	K38	G150	P264	PHE	TLE	VAL	ARG	ARG	ARG	SER	YS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	----

- Chain AB: 75% 25%

#1	K114	GLY	LYS	GLY	PHE	ALA	GLY	THR	VAL	LYS	ARG	TRP	ASN	PHE	ARG	THR	GLN	ASP	ALA	THR	HIS	GLY	ASN	SER	LEU	SER	HIS	ARG	VAL	PRO	GLY	SER	ILE	GLY	GLN	ASN	GLN	THR	PRO	GLY	LYS	VAL	PHE	LYS	GLY	LYS	LYS	MET	ALA	GLY	GLN	MET	GLY	ASN	E168	K208
----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------

- Chain AC:  71% 29%

#1	R40
GLN	THR
GLY	ARG
ALA	ALA
GLN	LYS
THR	ARG
ARG	ALA
GLU	VAL
THR	GLY
GLY	SER
SER	GLY
LYS	LYS
LYS	PRO
PRO	TRP
TRP	ARG
ARG	GLN
LYS	LYS
GLY	THR
THR	GLY
ARG	ALA
ALA	ARG
SER	SER
GLY	GLY
SER	ILE
ILE	LYS
LYS	SER
SER	PRO
PRO	TRP
TRP	ARG
ARG	GLY
GLY	VAL
VAL	THR
THR	PHE
PHE	ALA
ALA	ALA
ALA	ARG
ARG	PRO
PRO	GLN
GLN	ASP
ASP	HIS
HIS	SER
SER	Gln
Gln	LYS
LYS	Val
Val	

E198
MET
LEU
ALA

- Chain AD: 99%

ALA K2 K178

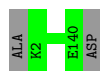
- Chain AE: 95% 5%

SER			
ARG			
VAL			
ALA			
K5			
K171			
GLU			
ALA			
LYS			
LYS			
LYS			

- Chain AF: 

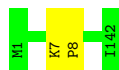
VAL	HIS	SER	GLU	VAL	PHE	ALA	LYS	VAL	ILE	VAL	ASN	GLY	VAL	LEU	ARG	THR	THR	GLY	GLU	HIS	GLU	VAL	SER	PHE																																				
MI	E76	THR	VAL	THR	ALA	ALA	SER	LYS	ALA	GLY	ASP	GLY	GLU	GLY	LEU	PHE	GLY	SER	ILE	GLY	THR	ARG	ASP	ILE	ALA	ALA	ASP	ALA	VAL	THR	ALA	ALA	GLY	VAL	GLU	VAL	VAL	LYS	SER	GLU	VAL	VAL	ASN	GLY	VAL	LEU	ARG	PRO	LEU	VAL	GLU	THR	THR	GLY	GLU	HIS	GLU	VAL	SER	PHE

- Chain AG:  99%



- Molecule 10: 50S ribosomal protein L13

Chain AH: 99%



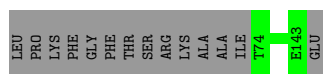
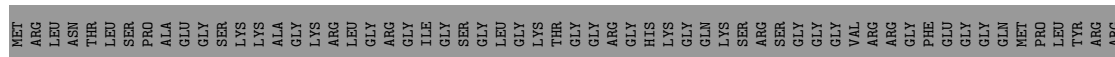
- Molecule 11: 50S ribosomal protein L14

Chain AI: 98%



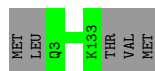
- Molecule 12: 50S ribosomal protein L15

Chain AJ: 49% 51%



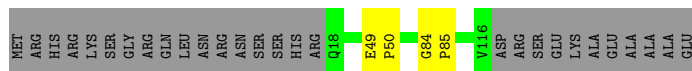
- Molecule 13: 50S ribosomal protein L16

Chain AK: 96%



- Molecule 14: 50S ribosomal protein L17

Chain AL: 75% 22%



- Molecule 15: 50S ribosomal protein L18

Chain AM: 97%



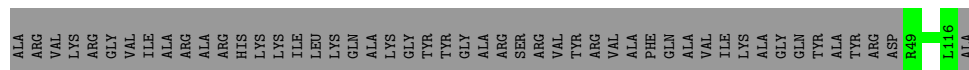
- Molecule 16: 50S ribosomal protein L19

Chain AN:  100%

There are no outlier residues recorded for this chain.

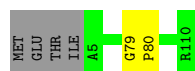
- Molecule 17: 50S ribosomal protein L20

Chain AO:  58% 42%



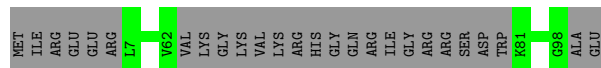
- Molecule 18: 50S ribosomal protein L22

Chain AQ:  95%



- Molecule 19: 50S ribosomal protein L23

Chain AR:  74% 26%



- Molecule 20: 50S ribosomal protein L24

Chain AS:  96%




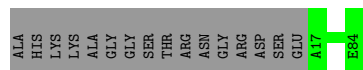
- Molecule 21: 50S ribosomal protein L25

Chain AT:  100%

There are no outlier residues recorded for this chain.

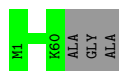
- Molecule 22: 50S ribosomal protein L27

Chain AU:  81% 19%



- Molecule 23: 50S ribosomal protein L29

Chain AW:  95% 5%



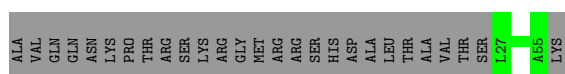
- Molecule 24: 50S ribosomal protein L30

Chain AX: 97%



- Molecule 25: 50S ribosomal protein L32

Chain AZ: 52% 48%



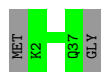
- Molecule 26: 50S ribosomal protein L33

Chain A1: 93%



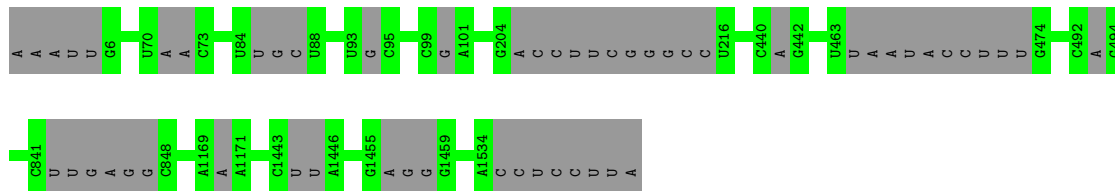
- Molecule 27: 50S ribosomal protein L36

Chain A4: 95% 5%



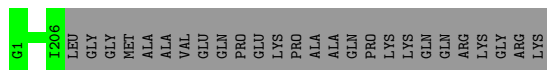
- Molecule 28: 16S RIBOSOMAL RNA

Chain BA: 96%



- Molecule 29: 30S RIBOSOMAL PROTEIN S3

Chain BC: 89% 11%



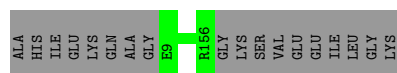
- Molecule 30: 30S RIBOSOMAL PROTEIN S4

Chain BD:  100%



- Molecule 31: 30S RIBOSOMAL PROTEIN S5

Chain BE:  89% 11%




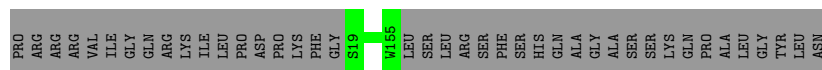
- Molecule 32: 30S RIBOSOMAL PROTEIN S6

Chain BF:  70% 30%



- Molecule 33: 30S RIBOSOMAL PROTEIN S7

Chain BG:  77% 23%




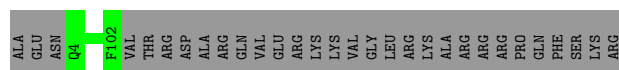
- Molecule 34: 30S RIBOSOMAL PROTEIN S8

Chain BH:  98%



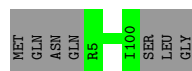
- Molecule 35: 30S RIBOSOMAL PROTEIN S9

Chain BI:  77% 23%




- Molecule 36: 30S RIBOSOMAL PROTEIN S10

Chain BJ:  93% 7%



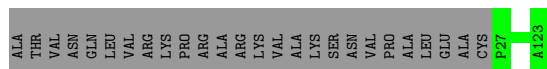
- Molecule 37: 30S RIBOSOMAL PROTEIN S11

Chain BK:  79% 21%



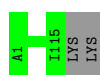
• Molecule 38: 30S RIBOSOMAL PROTEIN S12

Chain BL: 79% 21%



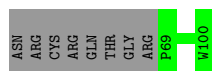
• Molecule 39: 30S RIBOSOMAL PROTEIN S13

Chain BM: 98% .



• Molecule 40: 30S RIBOSOMAL PROTEIN S14

Chain BN: 32% 68%



• Molecule 41: 30S RIBOSOMAL PROTEIN S15

Chain BO: 98% .



• Molecule 42: 30S RIBOSOMAL PROTEIN S16

Chain BP: 95% 5%



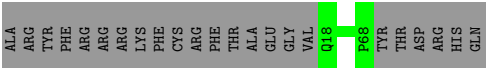
• Molecule 43: 30S RIBOSOMAL PROTEIN S17

Chain BQ: 95% 5%

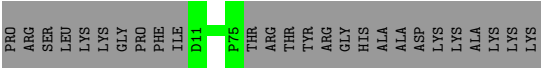


• Molecule 44: 30S RIBOSOMAL PROTEIN S18

Chain BR: 69% 31%



● Molecule 45: 30S RIBOSOMAL PROTEIN S19



● Molecule 46: 30S RIBOSOMAL PROTEIN S20



4 Data and refinement statistics

Xtrriage (Phenix) and EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	1.00Å 1.00Å 1.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 12.30	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-12.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8647	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A0	2536	0	0	2	0
2	A9	108	0	0	0	0
3	AA	227	0	0	1	0
4	AB	156	0	0	0	0
5	AC	142	0	0	0	0
6	AD	177	0	0	0	0
7	AE	167	0	0	0	0
8	AF	76	0	0	0	0
9	AG	139	0	0	0	0
10	AH	142	0	0	1	0
11	AI	122	0	0	1	0
12	AJ	70	0	0	0	0
13	AK	131	0	0	0	0
14	AL	99	0	0	2	0
15	AM	113	0	0	0	0
16	AN	114	0	0	0	0
17	AO	68	0	0	0	0
18	AQ	106	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	AR	74	0	0	0	0
20	AS	99	0	0	0	0
21	AT	94	0	0	0	0
22	AU	68	0	0	0	0
23	AW	60	0	0	0	0
24	AX	56	0	0	0	0
25	AZ	29	0	0	0	0
26	A1	52	0	0	1	0
27	A4	36	0	0	0	0
28	BA	1487	0	0	0	0
29	BC	206	0	0	0	0
30	BD	204	0	0	0	0
31	BE	148	0	0	0	0
32	BF	95	0	0	0	0
33	BG	137	0	0	0	0
34	BH	127	0	0	0	0
35	BI	99	0	0	0	0
36	BJ	96	0	0	0	0
37	BK	101	0	0	0	0
38	BL	97	0	0	0	0
39	BM	115	0	0	0	0
40	BN	32	0	0	0	0
41	BO	86	0	0	0	0
42	BP	78	0	0	0	0
43	BQ	79	0	0	0	0
44	BR	51	0	0	0	0
45	BS	65	0	0	0	0
46	BT	83	0	0	0	0
All	All	8647	0	0	7	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 7 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A0:1423:G:P	3:AA:150:GLY:CA	2.65	0.83
1:A0:2563:U:P	11:AI:25:LEU:CA	2.85	0.64
26:A1:29:LYS:CA	26:A1:30:PRO:CA	2.94	0.45
10:AH:7:LYS:CA	10:AH:8:PRO:CA	2.94	0.45
14:AL:84:GLY:CA	14:AL:85:PRO:CA	2.96	0.44

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A0	0/2904	-	-
2	A9	0/120	-	-
28	BA	0/1542	-	-
All	All	0/4566	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.