



wwPDB EM Validation Summary Report ⓘ

Feb 22, 2024 – 11:08 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 : 1GIY, 1IBL, 1FFK, 1FJG, 1LNR, 1JJ2

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:

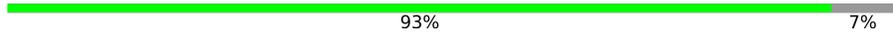
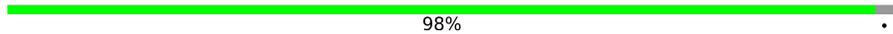
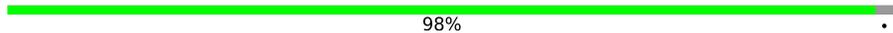
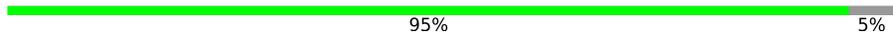
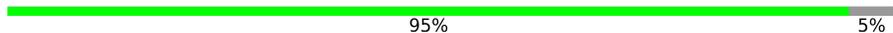
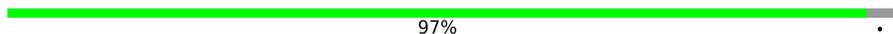
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

Continued from previous page...

Mol	Chain	Length	Quality of chain
11	AI	123	98%
12	AJ	144	49% 51%
13	AK	136	96%
14	AL	127	75% 22%
15	AM	117	97%
16	AN	114	100%
17	AO	117	58% 42%
18	AQ	110	95%
19	AR	100	74% 26%
20	AS	103	96%
21	AT	94	100%
22	AU	84	81% 19%
23	AW	63	95% 5%
24	AX	58	97%
25	AZ	56	52% 48%
26	A1	54	93%
27	A4	38	95% 5%
28	BA	1542	96%
29	BC	232	89% 11%
30	BD	205	100%
31	BE	166	89% 11%
32	BF	135	70% 30%
33	BG	178	77% 23%
34	BH	129	98%
35	BI	129	77% 23%

Continued on next page...

Continued from previous page...

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 167 167	0	167

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



- Molecule 10: 50S ribosomal protein L13

Chain AH: 99%



- Molecule 11: 50S ribosomal protein L14

Chain AI: 98%



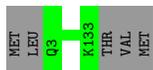
- Molecule 12: 50S ribosomal protein L15

Chain AJ: 49%



- Molecule 13: 50S ribosomal protein L16

Chain AK: 96%



- Molecule 14: 50S ribosomal protein L17

Chain AL: 75%



- 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%

ALA ARG VAL LYS ARG GLY VAL ILE ALA ARG ALA ARG HIS LYS ILE LEU LYS GLN ALA GLY TYR TYR GLY ALA ARG SER ARG VAL TYR ARG VAL PHE GLN ALA VAL ILE LYS ALA GLY TYR ALA TYR ARG ASP R49 L116 ALA

- Molecule 18: 50S ribosomal protein L22

Chain AQ:  95%

MET GLU THR ILE A5 G78 P80 R110

- Molecule 19: 50S ribosomal protein L23

Chain AR:  74% 26%

MET ILE ARG GLU ARG L7 Y62 VAL LYS GLY LYS VAL LYS ARG HIS GLY GLN ARG ILE GLY ARG ARG SER ASP TRP R81 G98 ALA GLU

- Molecule 20: 50S ribosomal protein L24

Chain AS:  96%

ALA ALA K3 T101 ILE LYS

- 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%

ALA HIS LYS LYS ALA GLY GLY SER THR ARG ASN GLY ARG ASP SER GLU A17 E64

- Molecule 23: 50S ribosomal protein L29

Chain AW:  95% 5%



- Molecule 24: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L32



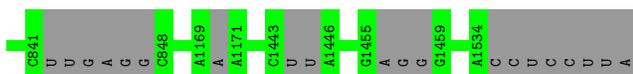
- Molecule 26: 50S ribosomal protein L33



- Molecule 27: 50S ribosomal protein L36



- Molecule 28: 16S RIBOSOMAL RNA



- Molecule 29: 30S RIBOSOMAL PROTEIN S3



- 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%

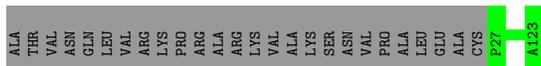
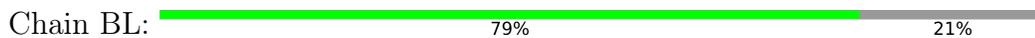


- Molecule 37: 30S RIBOSOMAL PROTEIN S11

Chain BK:  79% 21%



- Molecule 38: 30S RIBOSOMAL PROTEIN S12



- Molecule 39: 30S RIBOSOMAL PROTEIN S13



- Molecule 40: 30S RIBOSOMAL PROTEIN S14



- Molecule 41: 30S RIBOSOMAL PROTEIN S15



- Molecule 42: 30S RIBOSOMAL PROTEIN S16



- Molecule 43: 30S RIBOSOMAL PROTEIN S17



- Molecule 44: 30S RIBOSOMAL PROTEIN S18



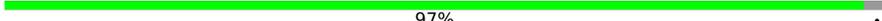
ALA	ARG	TYR	PHE	ARG	ARG	ARG	LYS	GLY	PRO	PHE	CYS	ARG	PHE	THR	ALA	GLU	GLY	VAL	Q18	F68	TYR	THR	ASP	ARG	HIS	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 45: 30S RIBOSOMAL PROTEIN S19

Chain BS:  71% 29%

PRO	ARG	SER	LEU	LYS	GLY	PRO	PHE	ILE	D11	P75	THR	ARG	THR	TYR	ARG	GLY	HIS	ALA	ALA	ASP	LYS	LYS	ALA	LYS	LYS	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 46: 30S RIBOSOMAL PROTEIN S20

Chain BT:  97%

ALA	ASN	ILE	R4	A86
-----	-----	-----	----	-----

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

Continued on next page...

Continued from previous page...

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.