



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:12 PM BST

PDB ID : 4V48
Title : Real space refined coordinates of the 30S and 50S subunits fitted into the low resolution cryo-EM map of the initiation-like 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 : 11.50 Å(reported)
Based on PDB ID : 1IBL, 1FJG, 1FFK, 1JJ2, 1LNR, 1GIY

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

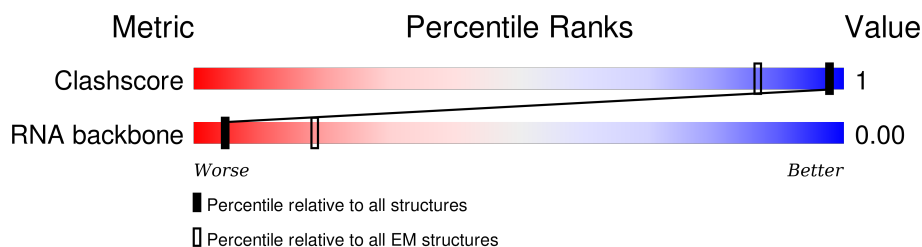
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.50 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.






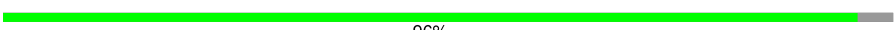






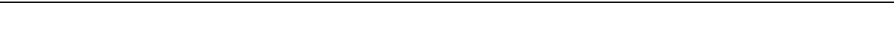

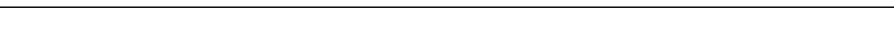
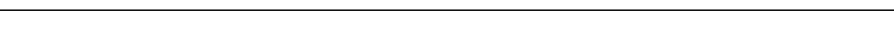
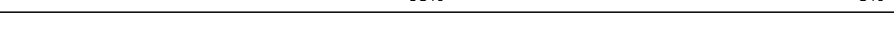
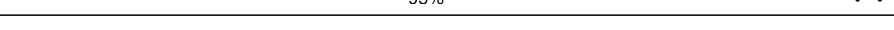

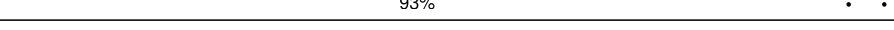
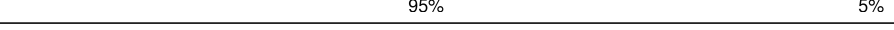
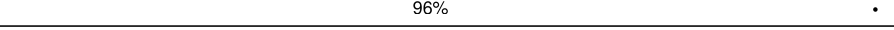
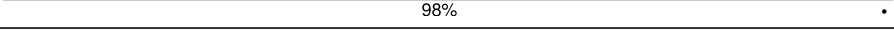

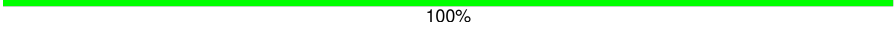


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	87%	13%
2	A9	120	90%	10%
3	A6	76	100%	
4	AA	272	83%	17%
5	AB	209	75%	25%
6	AC	201	71%	29%
7	AD	178	99%	.
8	AE	176	95%	5%
9	AF	149	100%	
10	AG	141	99%	.

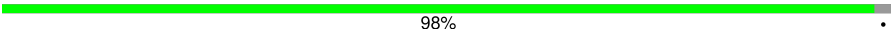







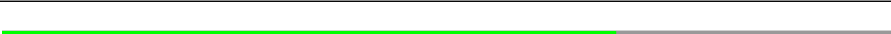


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Mol	Chain	Length	Quality of chain
11	AH	142	 99%
12	AI	123	 99%
13	AJ	144	 49% 51%
14	AK	136	 96%
15	AL	127	 75% 22%
16	AM	117	 97%
17	AN	114	 100%
18	AO	117	 58% 42%
19	AQ	110	 95%
20	AR	100	 74% 26%
21	AS	103	 96%
22	AT	94	 100%
23	AU	84	 81% 19%
24	AW	63	 95% 5%
25	AX	58	 95%
26	AZ	56	 52% 48%
27	A1	54	 93%
28	A4	38	 95% 5%
29	BA	1543	 96%
30	BB	240	 98%
31	BC	232	 89% 11%
32	BD	205	 100%
33	BE	166	 89% 11%
34	BF	135	 70% 30%
35	BG	178	 77% 23%

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Mol	Chain	Length	Quality of chain
36	BH	129	 98% .
37	BI	129	 77% 23%
38	BJ	103	 93% 7%
39	BK	128	 79% 21%
40	BL	123	 79% 21%
41	BM	117	 98% .
42	BN	100	 32% 68%
43	BO	88	 98% .
44	BP	82	 95% 5%
45	BQ	83	 95% 5%
46	BR	74	 69% 31%
47	BS	91	 71% 29%
48	BT	86	 97% .

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 9032 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 RNA chain called tRNA-PHE.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	A6	76	Total	P	0	76
			76	76		

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	AF	149	Total	C	0	149
			149	149		

- Molecule 10 is a protein called 50S ribosomal protein L11.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.

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

- Molecule 20 is a protein called 50S ribosomal protein L23.

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

- Molecule 21 is a protein called 50S ribosomal protein L24.

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

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L36.

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

- Molecule 29 is a RNA chain called 16S RIBOSOMAL RNA.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	1246	C	-	INSERTION	EMBL V00348

- Molecule 30 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms	AltConf	Trace
30	BB	236	Total C 236 236	0	236

- Molecule 31 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 32 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 33 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 34 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 35 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 36 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 37 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 38 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 39 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 40 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 41 is a protein called 30S RIBOSOMAL PROTEIN S13.

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

- Molecule 42 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 43 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 44 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

- Molecule 45 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 46 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 47 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

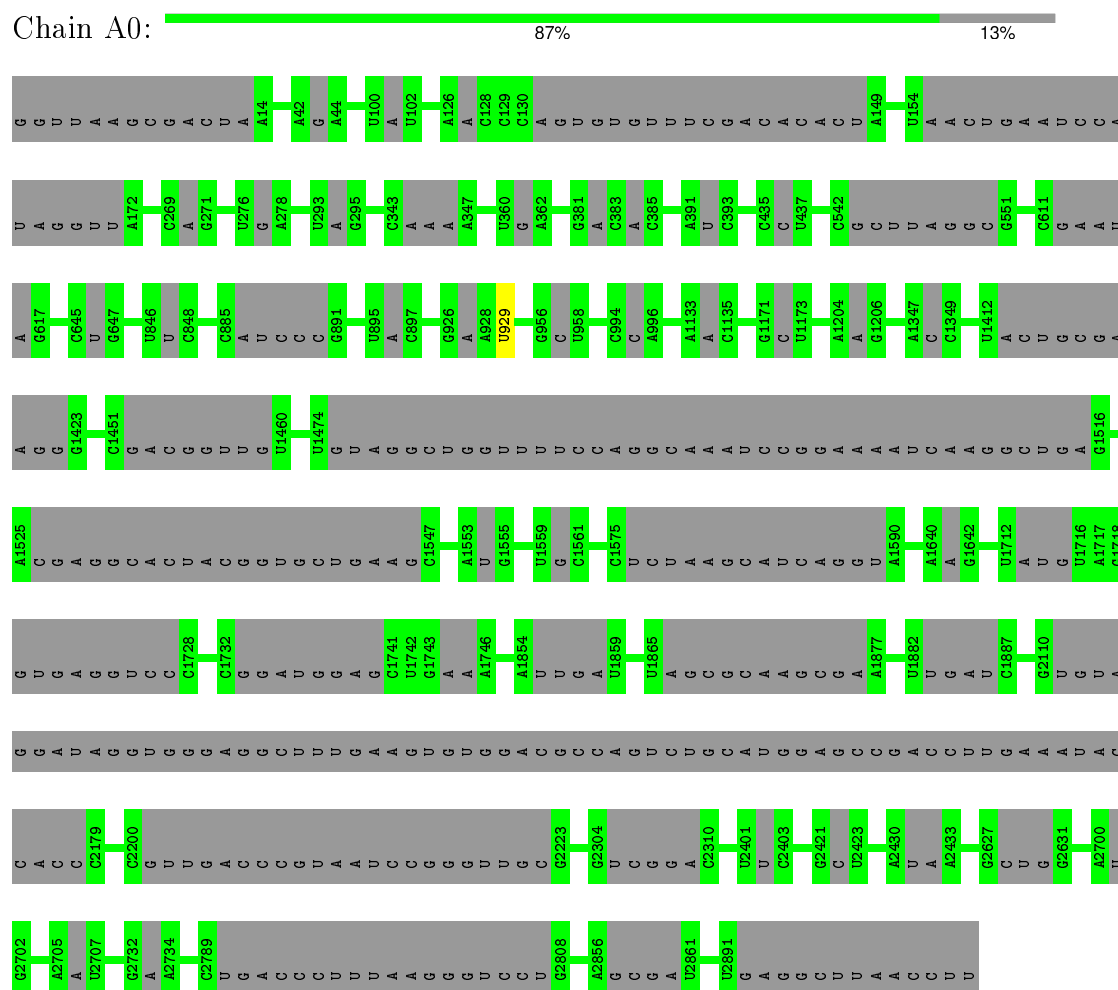
- Molecule 48 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

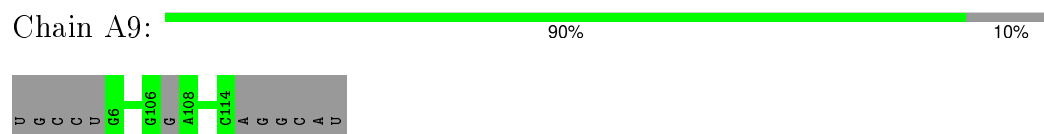
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

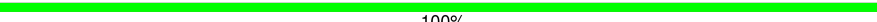
- Molecule 1: 23S ribosomal RNA



- Molecule 2: 5S ribosomal RNA


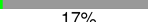


- Molecule 3: tRNA-PHE

Chain A6:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 50S ribosomal protein L2

Chain AA:  83%  17%

ALA VAL VAL GLN LYS LYS CYS VAL PRO THR SER PRO THR VAL ARG ARG HIS VAL VAL ASN PRO GLU LEU HIS LYS GLY LYS PRO PHE PHE ALA PRO LEU LEU GLU LYS ASN SER K38 K264 PHE ILE VAL ARG ARG SER LYS

- Molecule 5: 50S ribosomal protein L3

Chain AB:  75%  25%

K1 K114 GLN LYS LYS PHE PHE ALA 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 SER ILE GLY GLN ASN GIN THR PRO GLY LYS VAL PHE GLY LYS LYS MET ALA GLY GIN MET GLY ASN E168 K209

- Molecule 6: 50S ribosomal protein L4

Chain AC:  71%  29%

K1 K40 GLN THR ARG ARG ALA GLN LYS THR ARG ALA GLU VAL THR GLY SER GLY LYS LYS PRO TRP ARG GLN LYS GLY THR GLY ARG ALA ARG SER SER ILE LYS SER PRO ILE TRP ARG SER GLY VAL THR PHE ALA ALA ARG PRO GIN ASP HIS SER GIN LYS VAL E198 MET LEU ALA

- Molecule 7: 50S ribosomal protein L5

Chain AD:  99% .

ALA K2 K178

- Molecule 8: 50S ribosomal protein L6

Chain AE:  95%  5%

SER ARG VAL ALA K5 K171 GLU ALA LYS LYS

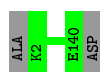
- Molecule 9: 50S ribosomal protein L9

Chain AF:  100%

There are no outlier residues recorded for this chain.

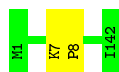
- Molecule 10: 50S ribosomal protein L11

Chain AG:  99% .



- Molecule 11: 50S ribosomal protein L13

Chain AH: 99%



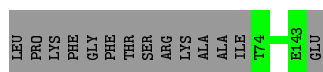
- Molecule 12: 50S ribosomal protein L14

Chain AI: 99%



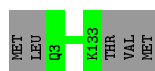
- Molecule 13: 50S ribosomal protein L15

Chain AJ: 49% 51%



- Molecule 14: 50S ribosomal protein L16

Chain AK: 96%



- Molecule 15: 50S ribosomal protein L17

Chain AL: 75% 22%



- Molecule 16: 50S ribosomal protein L18

Chain AM: 97%



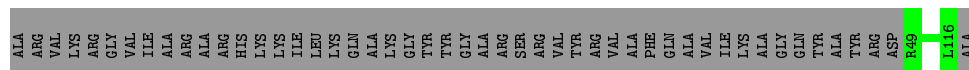
- Molecule 17: 50S ribosomal protein L19

Chain AN: 100%

There are no outlier residues recorded for this chain.

- Molecule 18: 50S ribosomal protein L20

Chain AO:  58% 42%



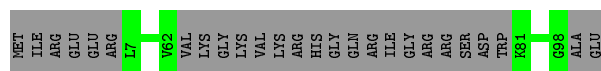
- Molecule 19: 50S ribosomal protein L22

Chain AQ:  95% . .



- Molecule 20: 50S ribosomal protein L23

Chain AR:  74% 26%



- Molecule 21: 50S ribosomal protein L24

Chain AS:  96% .




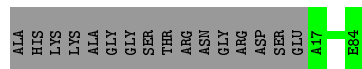
- Molecule 22: 50S ribosomal protein L25

Chain AT:  100%

There are no outlier residues recorded for this chain.

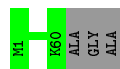
- Molecule 23: 50S ribosomal protein L27

Chain AU:  81% 19%



- Molecule 24: 50S ribosomal protein L29

Chain AW:  95% 5%



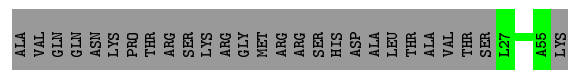
- Molecule 25: 50S ribosomal protein L30

Chain AX:  95% 



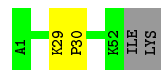
- Molecule 26: 50S ribosomal protein L32

Chain AZ:  52% 



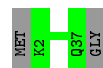
- Molecule 27: 50S ribosomal protein L33

Chain A1:  93% 



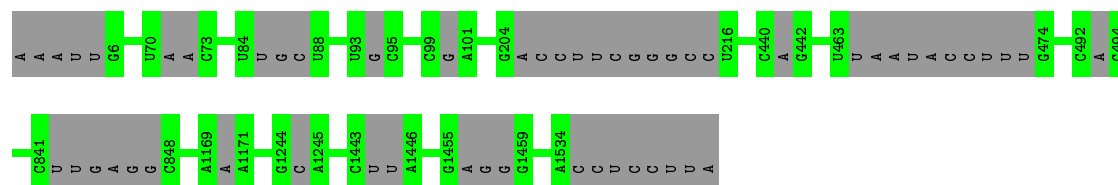
- Molecule 28: 50S ribosomal protein L36

Chain A4:  95% 



- Molecule 29: 16S RIBOSOMAL RNA

Chain BA:  96% 



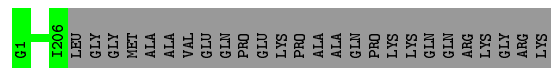
- Molecule 30: 30S RIBOSOMAL PROTEIN S2

Chain BB:  98% 



- Molecule 31: 30S RIBOSOMAL PROTEIN S3

Chain BC:  89% 



- Molecule 32: 30S RIBOSOMAL PROTEIN S4

Chain BD:  100%



- Molecule 33: 30S RIBOSOMAL PROTEIN S5

Chain BE:  89% 11%




- Molecule 34: 30S RIBOSOMAL PROTEIN S6

Chain BF:  70% 30%



- Molecule 35: 30S RIBOSOMAL PROTEIN S7

Chain BG:  77% 23%




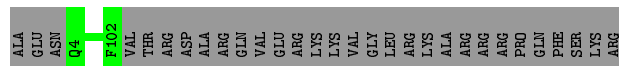
- Molecule 36: 30S RIBOSOMAL PROTEIN S8

Chain BH:  98%



- Molecule 37: 30S RIBOSOMAL PROTEIN S9

Chain BI:  77% 23%




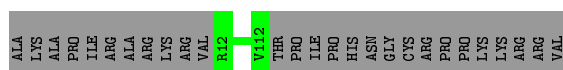
- Molecule 38: 30S RIBOSOMAL PROTEIN S10

Chain BJ:  93% 7%



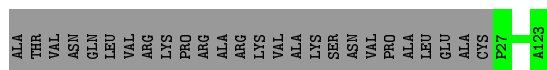
- Molecule 39: 30S RIBOSOMAL PROTEIN S11

Chain BK:  79% 21%



- Molecule 40: 30S RIBOSOMAL PROTEIN S12

Chain BL: 79% 21%



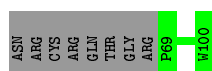
- Molecule 41: 30S RIBOSOMAL PROTEIN S13

Chain BM: 98% .



- Molecule 42: 30S RIBOSOMAL PROTEIN S14

Chain BN: 32% 68%



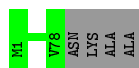
- Molecule 43: 30S RIBOSOMAL PROTEIN S15

Chain BO: 98% .



- Molecule 44: 30S RIBOSOMAL PROTEIN S16

Chain BP: 95% 5%



- Molecule 45: 30S RIBOSOMAL PROTEIN S17

Chain BQ: 95% 5%



- Molecule 46: 30S RIBOSOMAL PROTEIN S18

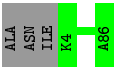
Chain BR: 69% 31%



- Molecule 47: 30S RIBOSOMAL PROTEIN S19



- Molecule 48: 30S RIBOSOMAL PROTEIN S20



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of 3D-maps	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1000	Depositor
Minimum defocus (nm)	730	Depositor
Maximum defocus (nm)	4340	Depositor
Magnification	51200	Depositor
Image detector	KODAK SO163 FILM	Depositor

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	1	0
2	A9	108	0	0	0	0
3	A6	76	0	0	0	0
4	AA	227	0	0	0	0
5	AB	156	0	0	0	0
6	AC	142	0	0	0	0
7	AD	177	0	0	0	0
8	AE	167	0	0	0	0
9	AF	149	0	0	0	0
10	AG	139	0	0	0	0
11	AH	142	0	0	1	0
12	AI	122	0	0	0	0
13	AJ	70	0	0	0	0
14	AK	131	0	0	0	0
15	AL	99	0	0	2	0
16	AM	113	0	0	0	0
17	AN	114	0	0	0	0
18	AO	68	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	AQ	106	0	0	1	0
20	AR	74	0	0	0	0
21	AS	99	0	0	0	0
22	AT	94	0	0	0	0
23	AU	68	0	0	0	0
24	AW	60	0	0	0	0
25	AX	56	0	0	1	0
26	AZ	29	0	0	0	0
27	A1	52	0	0	1	0
28	A4	36	0	0	0	0
29	BA	1487	0	0	0	0
30	BB	236	0	0	0	0
31	BC	206	0	0	0	0
32	BD	204	0	0	0	0
33	BE	148	0	0	0	0
34	BF	95	0	0	0	0
35	BG	137	0	0	0	0
36	BH	127	0	0	0	0
37	BI	99	0	0	0	0
38	BJ	96	0	0	0	0
39	BK	101	0	0	0	0
40	BL	97	0	0	0	0
41	BM	115	0	0	0	0
42	BN	32	0	0	0	0
43	BO	86	0	0	0	0
44	BP	78	0	0	0	0
45	BQ	79	0	0	0	0
46	BR	51	0	0	0	0
47	BS	65	0	0	0	0
48	BT	83	0	0	0	0
All	All	9032	0	0	6	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 6 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:A0:929:U:P	25:AX:25:GLY:CA	2.30	1.20
27:A1:29:LYS:CA	27:A1:30:PRO:CA	2.94	0.46
11:AH:7:LYS:CA	11:AH:8:PRO:CA	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AL:49:GLU:CA	15:AL:50:PRO:CA	2.96	0.44
19:AQ:79:GLY:CA	19:AQ:80:PRO:CA	2.97	0.43

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	-	-
29	BA	0/1543	-	-
3	A6	0/76	-	-
All	All	0/4643	-	-

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 carbohydrates 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 [i](#)

There are no chain breaks in this entry.