



wwPDB X-ray Structure Validation Summary Report

Mar 31, 2014 – 06:15 PM BST

PDB ID : 3OFO
Title : Crystal structure of the E. coli ribosome bound to erythromycin. This file contains the 30S subunit of the first 70S ribosome.
Authors : Dunkle, J.A.; Xiong, L.; Mankin, A.S.; Cate, J.H.D.
Deposited on : 2010-08-15
Resolution : 3.10 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

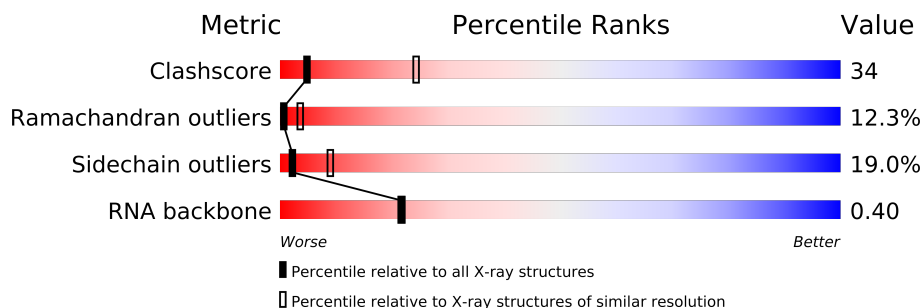
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23004

1 Overall quality at a glance

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RNA backbone	1838	1047 (3.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1533	
2	B	218	
3	C	206	
4	D	205	
5	E	150	
6	F	100	
7	G	151	
8	H	129	
9	I	127	
10	J	98	
11	K	117	
12	L	123	
13	M	114	
14	N	100	
15	O	88	

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Mol	Chain	Length	Quality of chain
16	P	82	
17	Q	80	
18	R	55	
19	S	79	
20	T	85	
21	U	51	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51700 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1533	Total	C	N	O	P	0	0	0
			32895	14671	6036	10655	1533			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	55	Total	C	N	O	0	0	0
			456	288	86	82			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	41	Total	Mg	0	0
			41	41		
22	N	2	Total	Mg	0	0
			2	2		

- Molecule 23 is water.

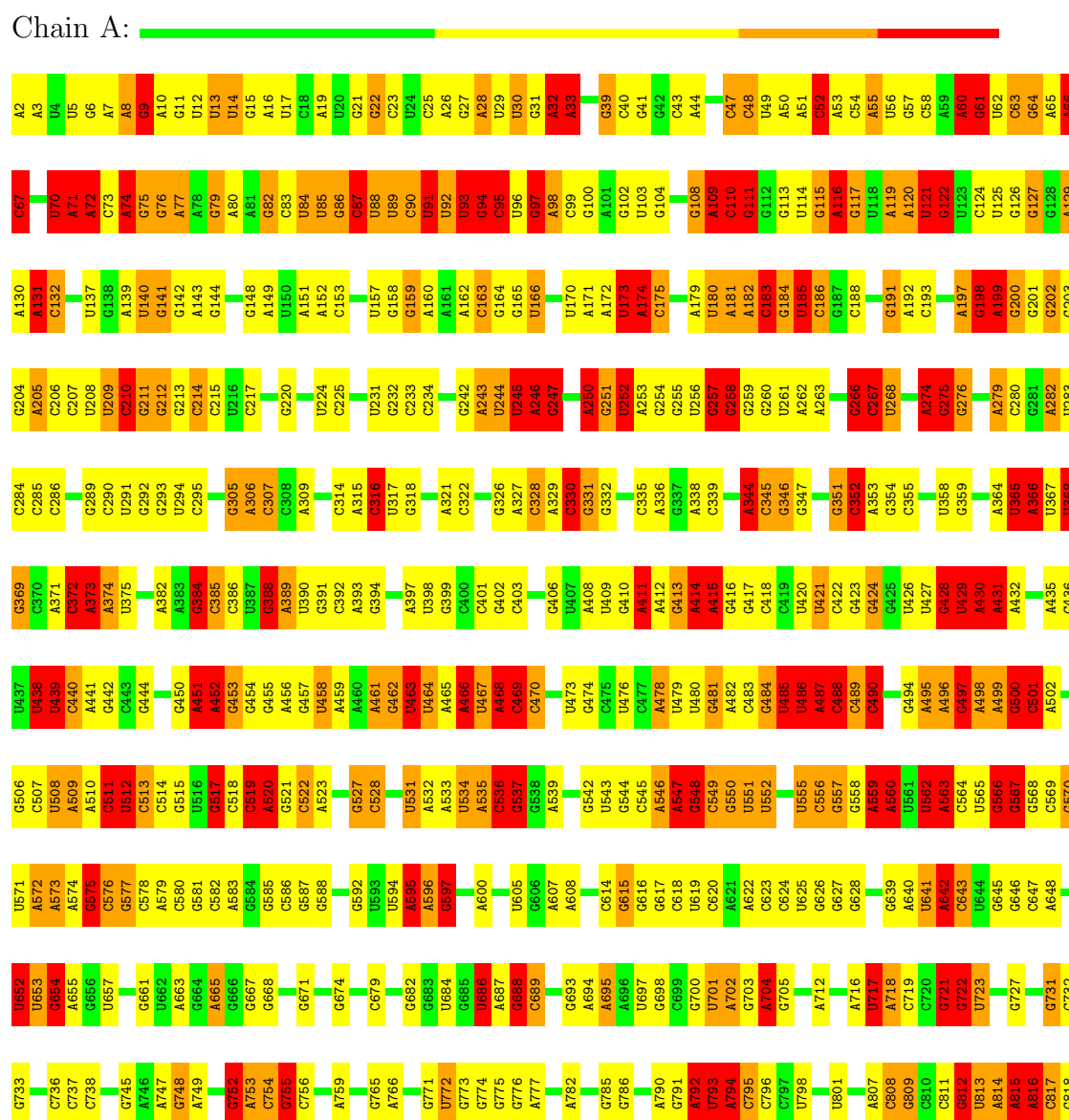
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	198	Total	O	0	0
			198	198		
23	L	1	Total	O	0	0
			1	1		
23	N	7	Total	O	0	0
			7	7		
23	U	2	Total	O	0	0
			2	2		

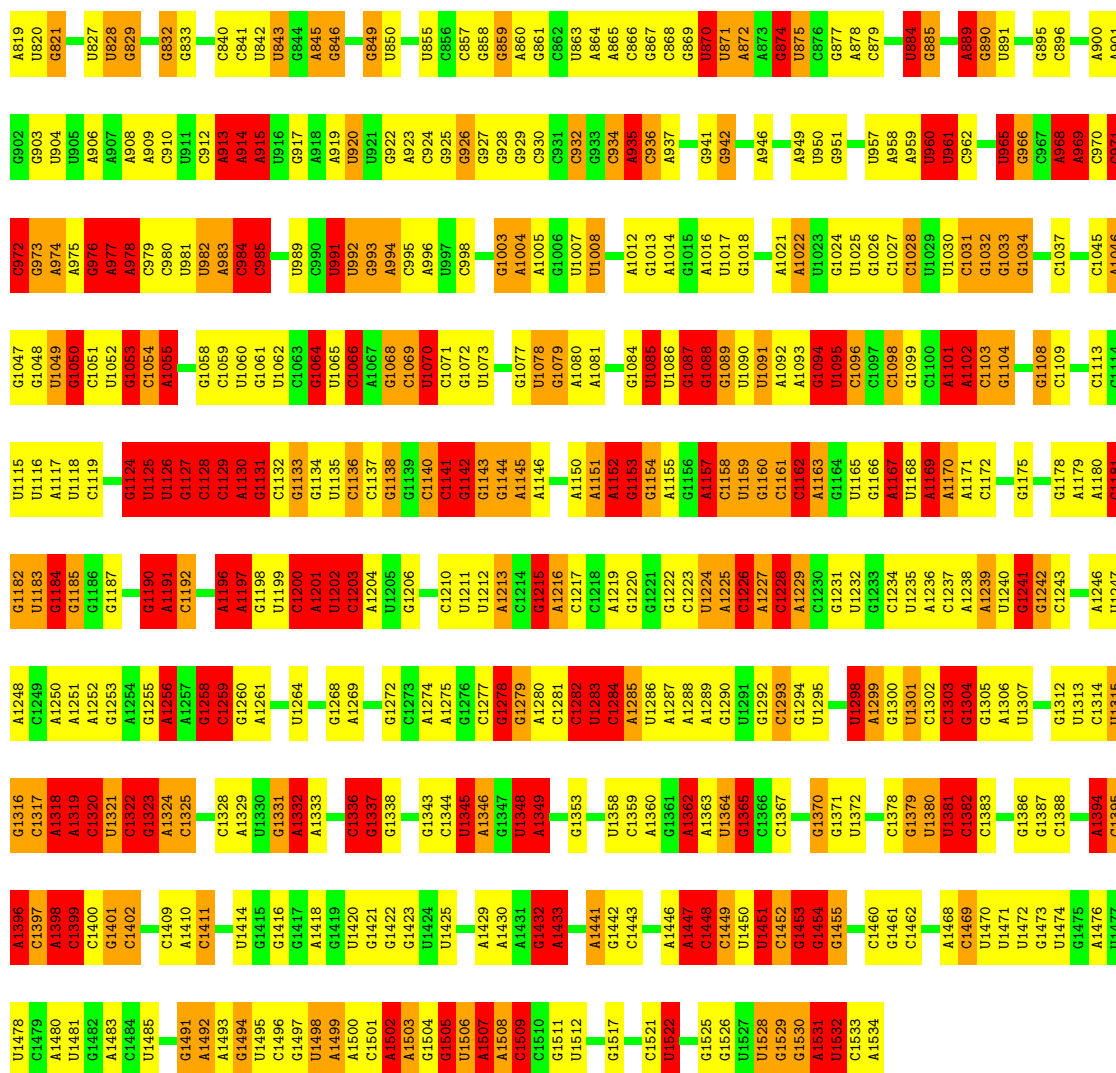
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

Note EDS was not executed.

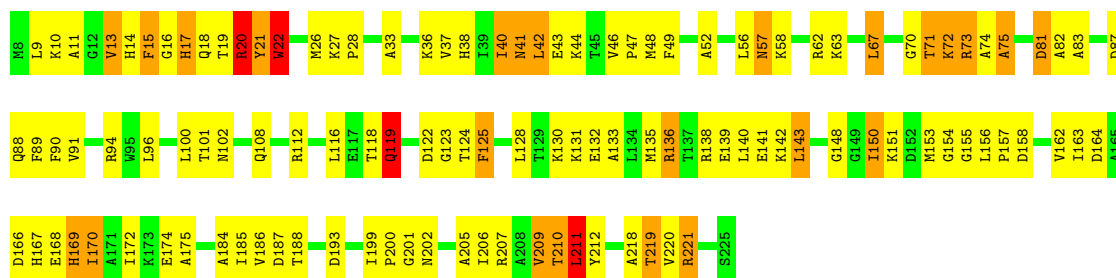
• Molecule 1: 16S rRNA





• Molecule 2: 30S ribosomal protein S2

Chain B:



• Molecule 3: 30S ribosomal protein S3

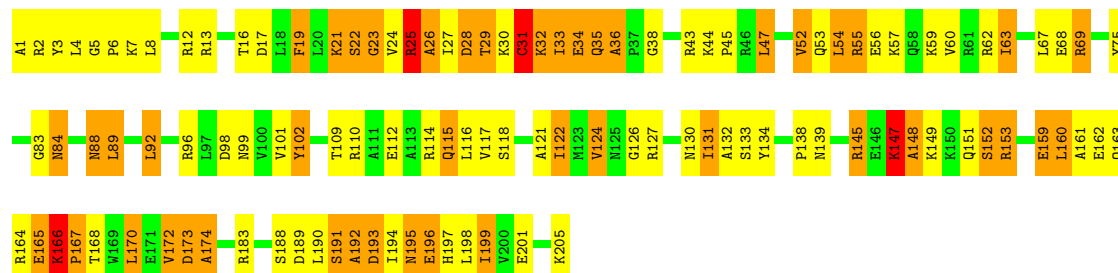
Chain C:





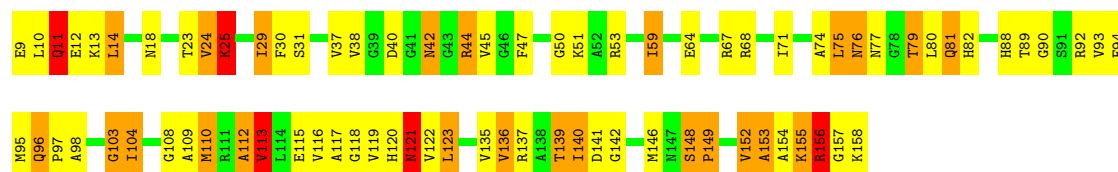
• Molecule 4: 30S ribosomal protein S4

Chain D:



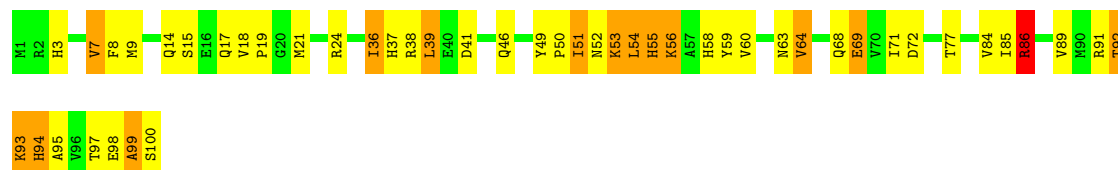
• Molecule 5: 30S ribosomal protein S5

Chain E:



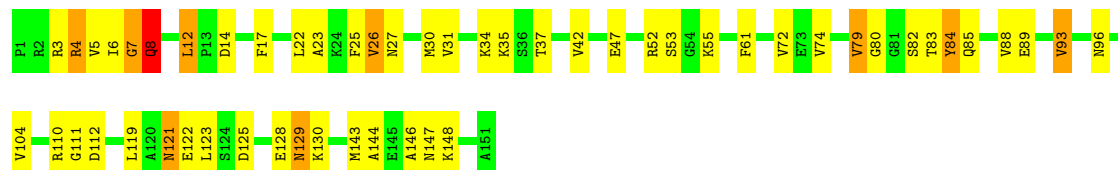
• Molecule 6: 30S ribosomal protein S6

Chain F:



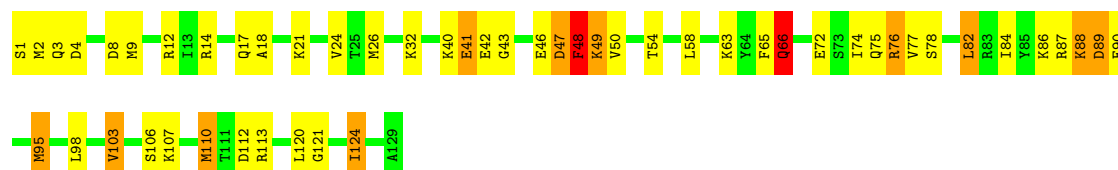
• Molecule 7: 30S ribosomal protein S7

Chain G:

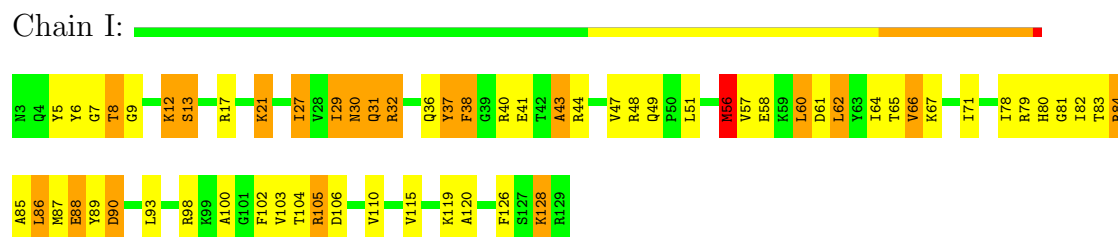


• Molecule 8: 30S ribosomal protein S8

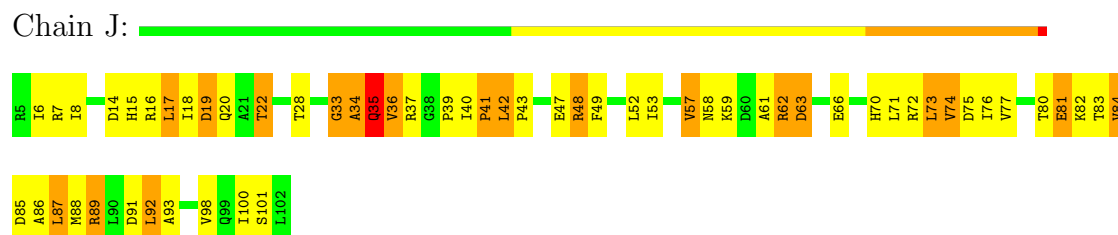
Chain H:



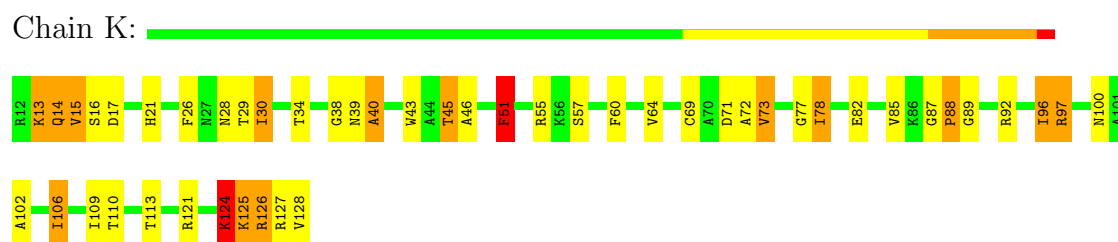
- Molecule 9: 30S ribosomal protein S9



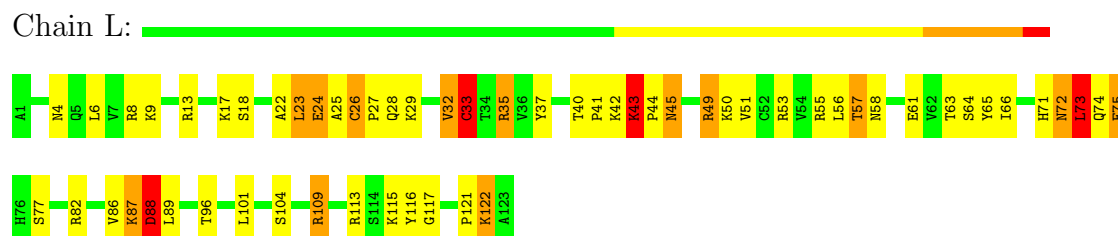
- Molecule 10: 30S ribosomal protein S10



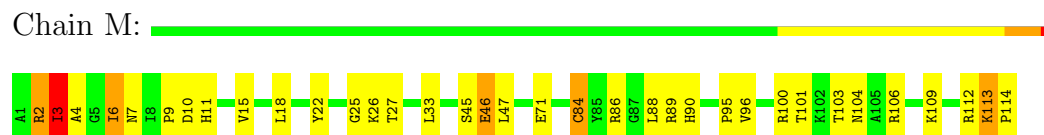
- Molecule 11: 30S ribosomal protein S11



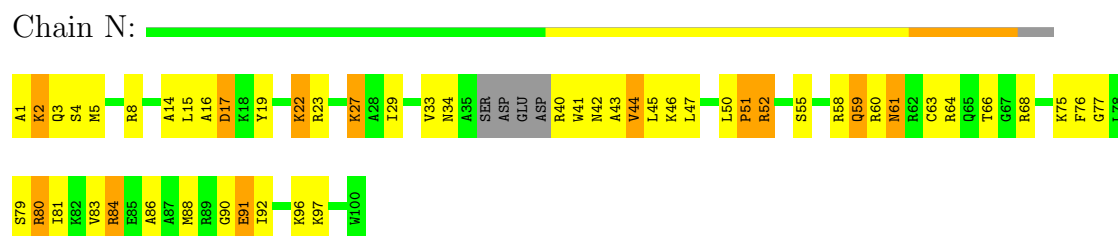
- Molecule 12: 30S ribosomal protein S12



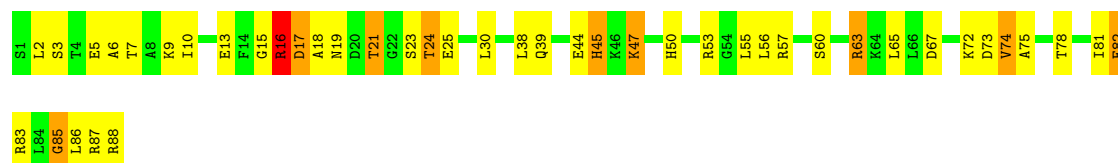
- Molecule 13: 30S ribosomal protein S13



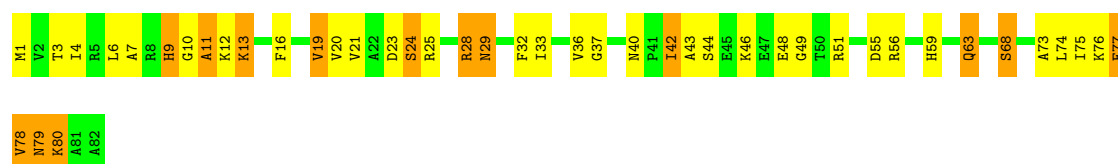
- Molecule 14: 30S ribosomal protein S14



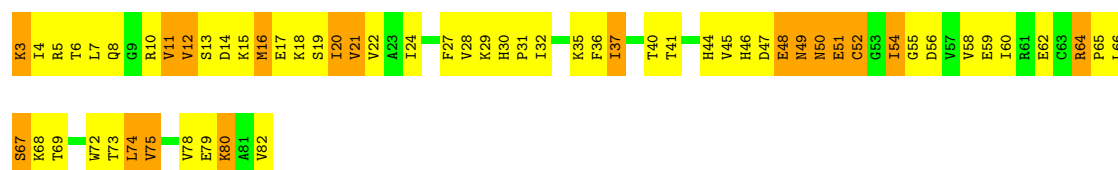
- Molecule 15: 30S ribosomal protein S15

Chain O: 

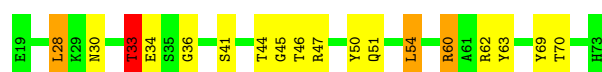
- Molecule 16: 30S ribosomal protein S16

Chain P: 

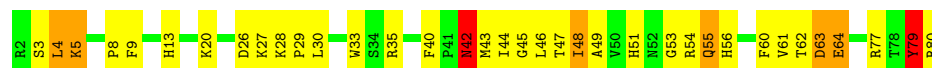
- Molecule 17: 30S ribosomal protein S17

Chain Q: 

- Molecule 18: 30S ribosomal protein S18

Chain R: 

- Molecule 19: 30S ribosomal protein S19

Chain S: 

- Molecule 20: 30S ribosomal protein S20

Chain T: 

- Molecule 21: 30S ribosomal protein S21

Chain U: 

4 Data and refinement statistics

EDS was not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.96Å 434.53Å 623.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.40 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (82.40-3.10)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.13Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.254	Depositor
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.354	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 925668 reflections	Xtriage
Total number of atoms	51700	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	A	0.53	0/36834	1.32	524/57462 (0.9%)
2	B	0.24	0/1736	0.47	0/2338
3	C	0.27	0/1652	0.50	0/2225
4	D	0.30	0/1665	0.52	0/2227
5	E	0.34	0/1119	0.61	0/1504
6	F	0.29	0/836	0.47	0/1128
7	G	0.22	0/1196	0.44	0/1602
8	H	0.32	0/989	0.56	0/1326
9	I	0.23	0/1034	0.45	0/1375
10	J	0.24	0/797	0.47	0/1077
11	K	0.27	0/893	0.53	0/1205
12	L	0.38	0/969	0.69	0/1300
13	M	0.23	0/893	0.49	0/1193
14	N	0.25	0/785	0.48	0/1043
15	O	0.30	0/722	0.49	0/964
16	P	0.31	0/659	0.51	0/884
17	Q	0.37	0/658	0.59	0/881
18	R	0.29	0/463	0.49	0/621
19	S	0.23	0/653	0.46	0/877
20	T	0.34	0/671	0.57	0/888
21	U	0.25	0/431	0.46	0/570
All	All	0.46	0/55655	1.14	524/82690 (0.6%)

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
12	L	0	1
20	T	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	2

There are no bond length outliers.

The worst 5 of 524 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	G	P-O3'-C3'	-15.18	101.49	119.70
1	A	1202	U	N1-C1'-C2'	-14.12	95.64	114.00
1	A	352	C	N1-C1'-C2'	-13.67	96.23	114.00
1	A	52	C	N1-C1'-C2'	-13.24	96.79	114.00
1	A	267	C	N1-C1'-C2'	-12.43	97.84	114.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	22	ALA	Peptide
20	T	6	ALA	Peptide

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32895	0	44	955	0
2	B	1705	0	0	63	0
3	C	1625	0	0	32	0
4	D	1643	0	0	92	0
5	E	1106	0	75	80	0
6	F	818	0	0	29	0
7	G	1182	0	0	27	0
8	H	979	0	0	31	0
9	I	1022	0	0	33	0
10	J	787	0	0	40	0
11	K	877	0	0	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	955	0	0	31	0
13	M	884	0	0	17	0
14	N	774	0	0	31	0
15	O	714	0	0	25	0
16	P	649	0	0	32	0
17	Q	649	0	691	137	0
18	R	456	0	0	13	0
19	S	638	0	0	26	0
20	T	665	0	0	28	0
21	U	426	0	0	28	0
22	A	41	0	0	0	0
22	N	2	0	0	0	0
23	A	198	0	0	5	0
23	L	1	0	0	0	0
23	N	7	0	0	0	0
23	U	2	0	0	0	0
All	All	51700	0	810	1704	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 34.

The worst 5 of 1704 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:152:VAL:HB	5:E:155:LYS:NZ	1.44	1.30
1:A:1531:A:C8	1:A:1531:A:H5'	1.79	1.17
5:E:153:ALA:HA	5:E:156:ARG:CB	1.76	1.15
5:E:155:LYS:HA	5:E:158:LYS:NZ	1.62	1.12
17:Q:12:VAL:HG13	17:Q:13:SER:H	1.00	1.10

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	
2	B	216/218 (99%)	133 (62%)	51 (24%)	32 (15%)	0	2
3	C	204/206 (99%)	144 (71%)	36 (18%)	24 (12%)	1	4
4	D	203/205 (99%)	127 (63%)	43 (21%)	33 (16%)	0	0
5	E	148/150 (99%)	97 (66%)	28 (19%)	23 (16%)	0	1
6	F	98/100 (98%)	71 (72%)	15 (15%)	12 (12%)	1	4
7	G	149/151 (99%)	100 (67%)	37 (25%)	12 (8%)	1	10
8	H	127/129 (98%)	101 (80%)	15 (12%)	11 (9%)	1	9
9	I	125/127 (98%)	81 (65%)	28 (22%)	16 (13%)	0	3
10	J	96/98 (98%)	69 (72%)	10 (10%)	17 (18%)	0	0
11	K	115/117 (98%)	80 (70%)	20 (17%)	15 (13%)	0	3
12	L	121/123 (98%)	88 (73%)	21 (17%)	12 (10%)	1	6
13	M	112/114 (98%)	83 (74%)	19 (17%)	10 (9%)	1	8
14	N	92/100 (92%)	60 (65%)	18 (20%)	14 (15%)	0	1
15	O	86/88 (98%)	59 (69%)	19 (22%)	8 (9%)	1	7
16	P	80/82 (98%)	59 (74%)	12 (15%)	9 (11%)	1	4
17	Q	78/80 (98%)	48 (62%)	24 (31%)	6 (8%)	1	11
18	R	53/55 (96%)	40 (76%)	10 (19%)	3 (6%)	3	18
19	S	77/79 (98%)	51 (66%)	15 (20%)	11 (14%)	0	2
20	T	83/85 (98%)	57 (69%)	21 (25%)	5 (6%)	2	17
21	U	49/51 (96%)	25 (51%)	12 (24%)	12 (24%)	0	0
All	All	2312/2358 (98%)	1573 (68%)	454 (20%)	285 (12%)	1	3

5 of 285 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	TYR
2	B	33	ALA
2	B	37	VAL
2	B	72	LYS
2	B	75	ALA

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 X-ray entries followed by that with respect to entries of similar resolution. 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	
2	B	180/180 (100%)	142 (79%)	38 (21%)	1	7
3	C	170/170 (100%)	136 (80%)	34 (20%)	2	8
4	D	172/172 (100%)	138 (80%)	34 (20%)	2	8
5	E	113/113 (100%)	77 (68%)	36 (32%)	0	1
6	F	87/87 (100%)	71 (82%)	16 (18%)	2	9
7	G	124/124 (100%)	111 (90%)	13 (10%)	10	35
8	H	104/104 (100%)	83 (80%)	21 (20%)	2	8
9	I	105/105 (100%)	82 (78%)	23 (22%)	1	6
10	J	86/86 (100%)	70 (81%)	16 (19%)	2	9
11	K	90/90 (100%)	73 (81%)	17 (19%)	2	9
12	L	103/103 (100%)	76 (74%)	27 (26%)	1	2
13	M	92/92 (100%)	84 (91%)	8 (9%)	15	49
14	N	79/83 (95%)	71 (90%)	8 (10%)	11	38
15	O	76/76 (100%)	59 (78%)	17 (22%)	1	6
16	P	65/65 (100%)	54 (83%)	11 (17%)	3	11
17	Q	74/74 (100%)	60 (81%)	14 (19%)	2	9
18	R	48/48 (100%)	44 (92%)	4 (8%)	16	53
19	S	70/70 (100%)	63 (90%)	7 (10%)	11	38
20	T	65/65 (100%)	48 (74%)	17 (26%)	1	2
21	U	44/44 (100%)	36 (82%)	8 (18%)	2	10
All	All	1947/1951 (100%)	1578 (81%)	369 (19%)	2	9

5 of 369 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	72	VAL
9	I	86	LEU
19	S	60	PHE
8	H	12	ARG
8	H	103	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
17	Q	8	GLN
17	Q	44	HIS
17	Q	46	HIS
17	Q	49	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1532/1533 (99%)	518 (33%)	236 (15%)

5 of 518 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	6	G
1	A	7	A
1	A	8	A
1	A	9	G

5 of 236 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	575	G
1	A	874	G
1	A	1394	A
1	A	596	A
1	A	721	G

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 43 ligands modelled in this entry, 43 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.