



wwPDB X-ray Structure Validation Summary Report

Mar 31, 2014 – 05:44 PM BST

PDB ID : 3V2C
Title : Crystal structure of YfiA bound to the 70S ribosome. This PDB entry contains coordinates for the 30S subunit with bound YfiA of the 1st ribosome in the ASU
Authors : Polikanov, Y.S.; Blaha, G.M.; Steitz, T.A.
Deposited on : 2011-12-12
Resolution : 2.70 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>

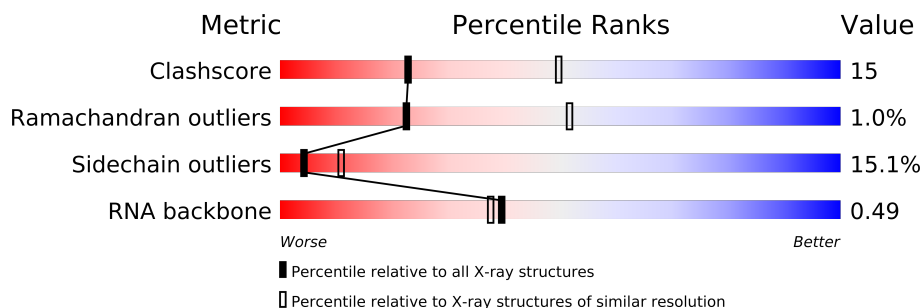
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.70 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	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RNA backbone	1838	1042 (3.20-2.20)

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	1522	
2	B	256	
3	C	239	
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	
15	O	89	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	
22	Y	119	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 51116 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 Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1493	Total	C	N	O	P	0	0	0
			32102	14287	5955	10367	1493			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	229	Total	C	N	O	S	0	0	0
			1777	1134	318	320	5			

- 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
			1450	906	279	264	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1520	960	283	272	5			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	148	Total	C	N	O	S	0	0	0
			1105	699	204	198	4			

- 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
			781	495	137	146	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1167	727	224	210	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1045	665	188	190	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	125	Total	C	N	O	0	0	0
			852	533	163	156			

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	96	Total	C	N	O	0	0	0
			659	408	131	120			

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	114	Total	C	N	O	S	0	0	0
			828	516	155	154	3			

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	122	Total	C	N	O	S	0	0	0
			909	570	179	159	1			

- 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
			801	494	164	142	1			

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			478	303	99	72	4			

- 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
			724	453	143	126	2			

- 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
			651	416	123	111	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	68	Total	C	N	O	0	0	0
			514	329	98	87			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	0
			560	351	108	99	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	96	Total	C	N	O	S	0	0	0
			699	430	150	117	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a protein called Ribosome-associated inhibitor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Y	95	Total	C	N	O	S	0	0	0
			754	472	142	137	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	114	HIS	-	EXPRESSION TAG	UNP P0AD49
Y	115	HIS	-	EXPRESSION TAG	UNP P0AD49
Y	116	HIS	-	EXPRESSION TAG	UNP P0AD49
Y	117	HIS	-	EXPRESSION TAG	UNP P0AD49
Y	118	HIS	-	EXPRESSION TAG	UNP P0AD49
Y	119	HIS	-	EXPRESSION TAG	UNP P0AD49

- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	P	1	Total	Mg	0	0
			1	1		
23	D	2	Total	Mg	0	0
			2	2		
23	E	1	Total	Mg	0	0
			1	1		
23	I	1	Total	Mg	0	0
			1	1		
23	A	223	Total	Mg	0	0
			223	223		
23	O	1	Total	Mg	0	0
			1	1		
23	L	1	Total	Mg	0	0
			1	1		
23	F	1	Total	Mg	0	0
			1	1		
23	M	2	Total	Mg	0	0
			2	2		

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total 1	Zn 1	0	0
24	N	1	Total 1	Zn 1	0	0

- Molecule 25 is water.

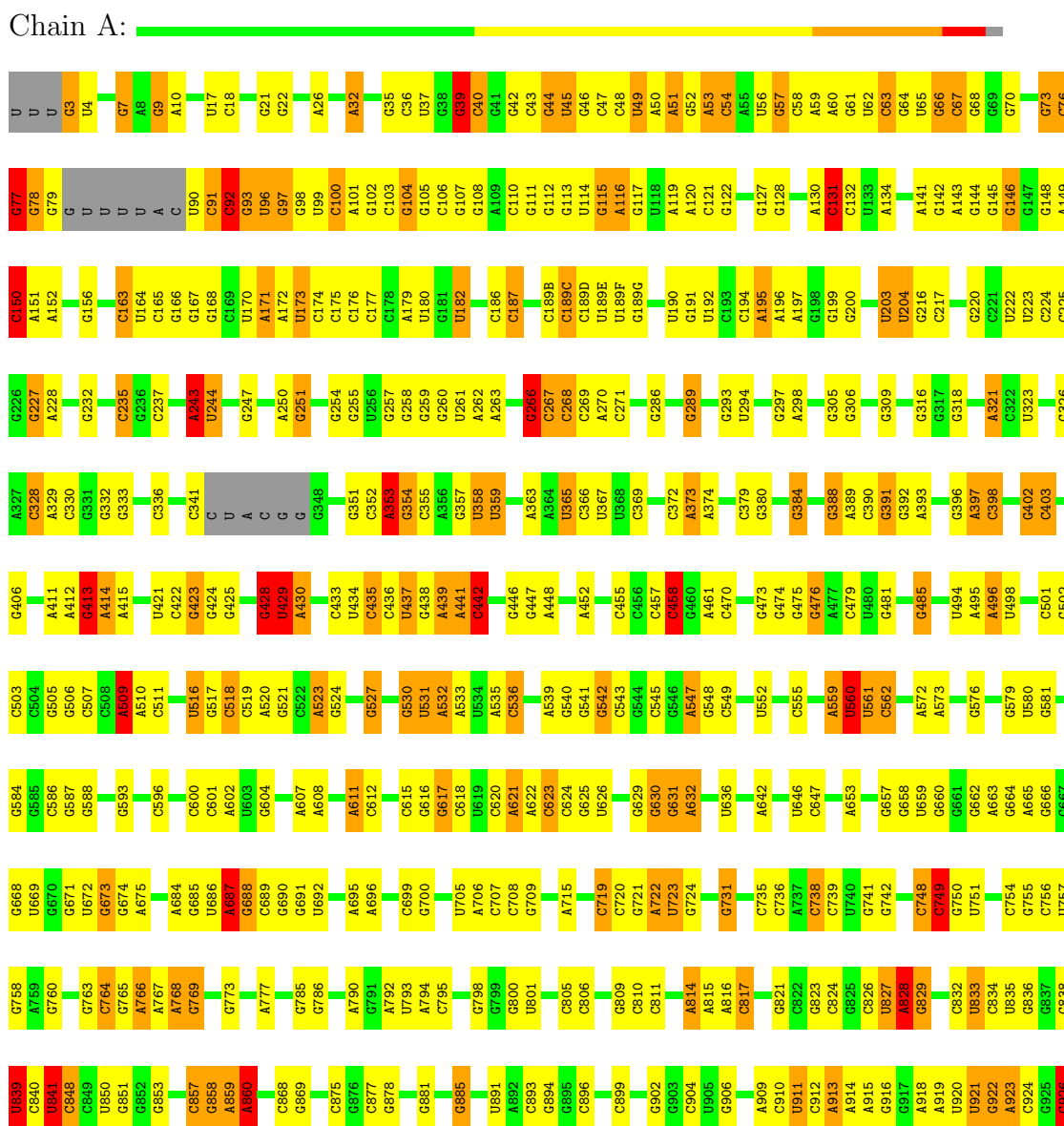
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	460	Total 460	O 460	0	0
25	D	3	Total 3	O 3	0	0
25	E	2	Total 2	O 2	0	0
25	F	2	Total 2	O 2	0	0
25	G	2	Total 2	O 2	0	0
25	J	1	Total 1	O 1	0	0
25	K	1	Total 1	O 1	0	0
25	L	3	Total 3	O 3	0	0
25	M	1	Total 1	O 1	0	0
25	O	4	Total 4	O 4	0	0
25	Q	3	Total 3	O 3	0	0
25	Y	1	Total 1	O 1	0	0

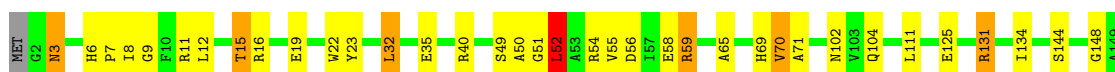
3 Residue-property plots

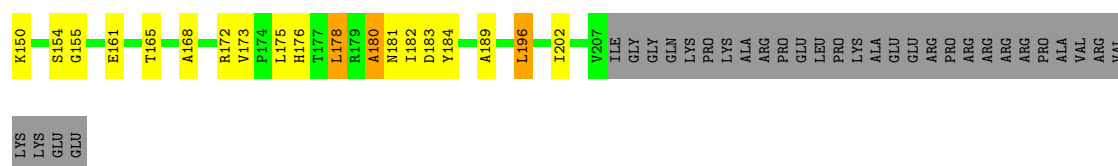
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 Ribosomal RNA

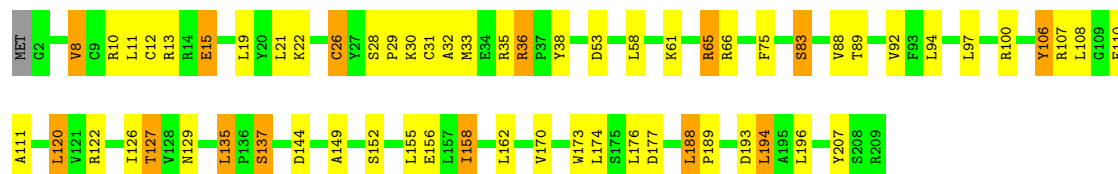






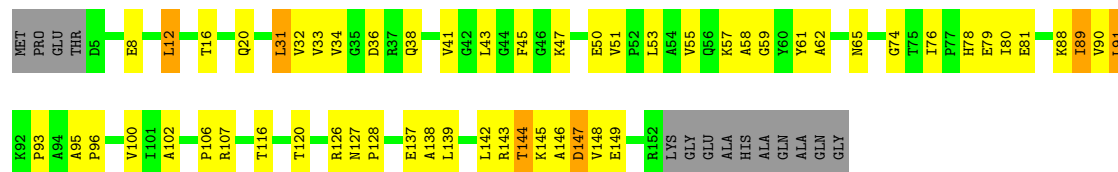
- Molecule 4: 30S Ribosomal Protein S4

Chain D:



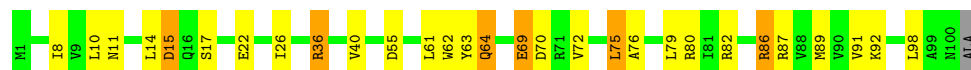
- Molecule 5: 30S Ribosomal Protein S5

Chain E:



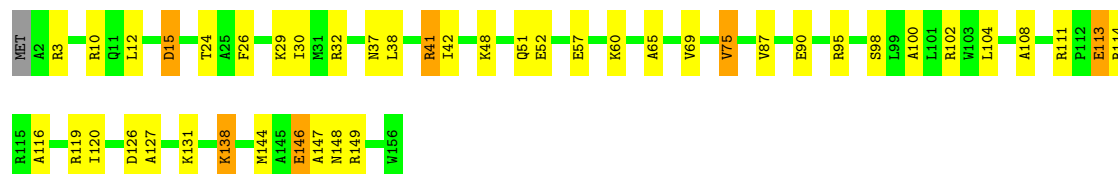
- Molecule 6: 30S Ribosomal Protein S6

Chain F:



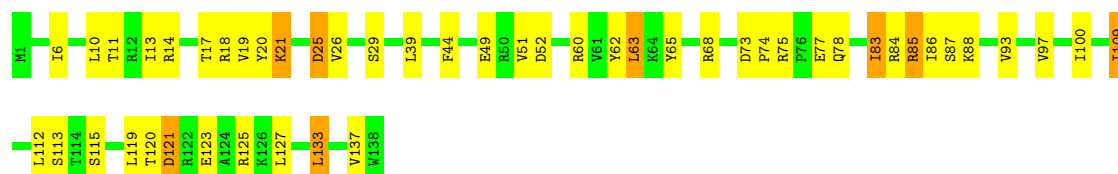
- Molecule 7: 30S Ribosomal Protein S7

Chain G:



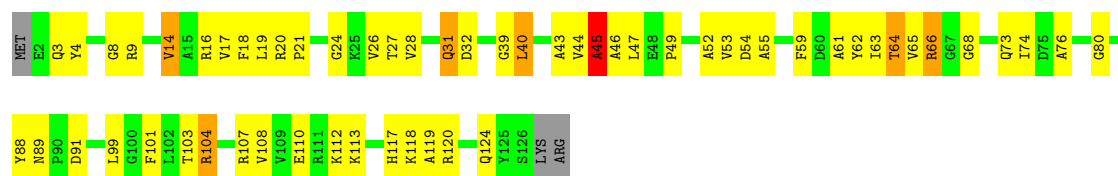
- Molecule 8: 30S Ribosomal Protein S8

Chain H:



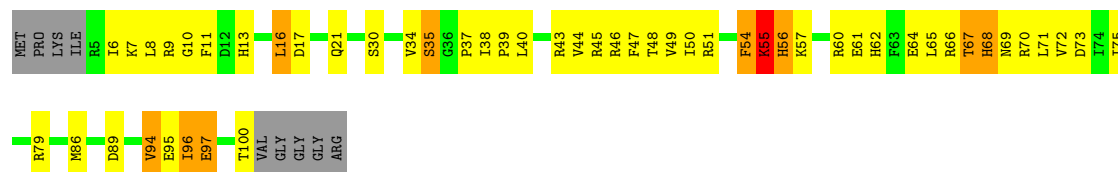
- Molecule 9: 30S Ribosomal Protein S9

Chain I: 



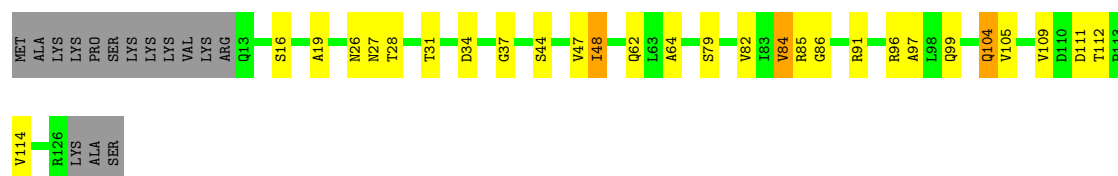
• Molecule 10: 30S Ribosomal Protein S10

Chain J: 



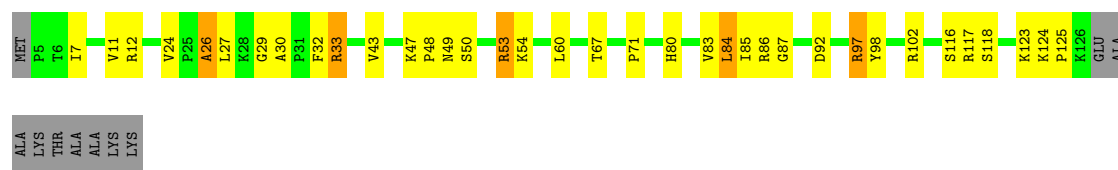
• Molecule 11: 30S Ribosomal Protein S11

Chain K: 



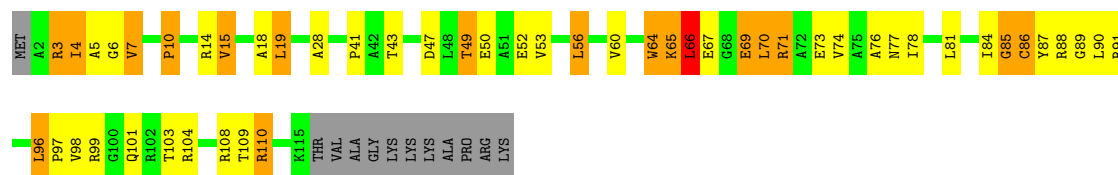
• Molecule 12: 30S Ribosomal Protein S12

Chain L: 



• Molecule 13: 30S Ribosomal Protein S13

Chain M: 



• Molecule 14: 30S Ribosomal Protein S14

Chain N: 



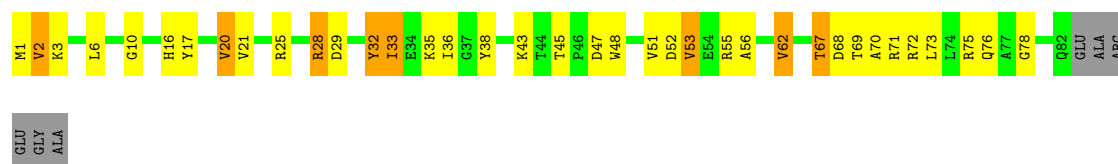
• Molecule 15: 30S Ribosomal Protein S15

Chain O:



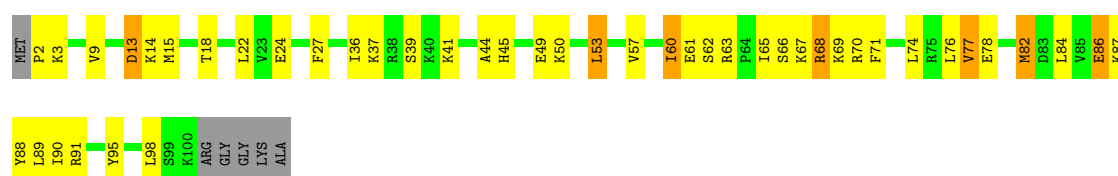
- Molecule 16: 30S Ribosomal Protein S16

Chain P:



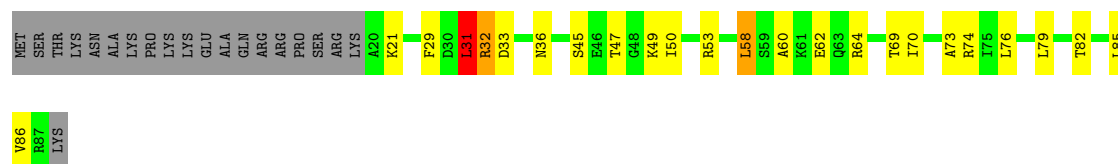
- Molecule 17: 30S Ribosomal Protein S17

Chain Q:



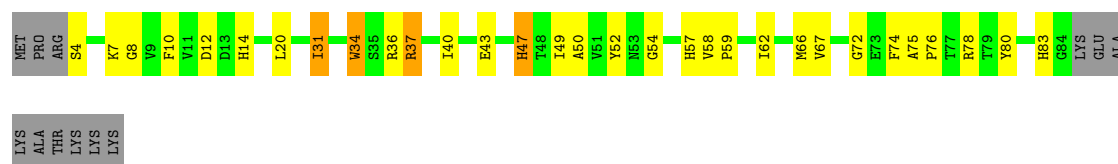
- Molecule 18: 30S Ribosomal Protein S18

Chain R:



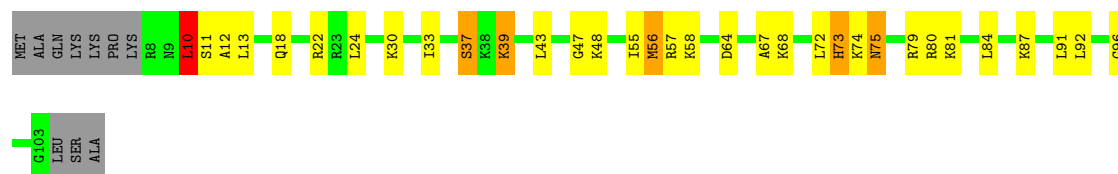
- Molecule 19: 30S Ribosomal Protein S19

Chain S:



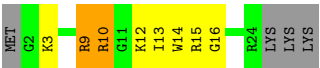
- Molecule 20: 30S Ribosomal Protein S20

Chain T:



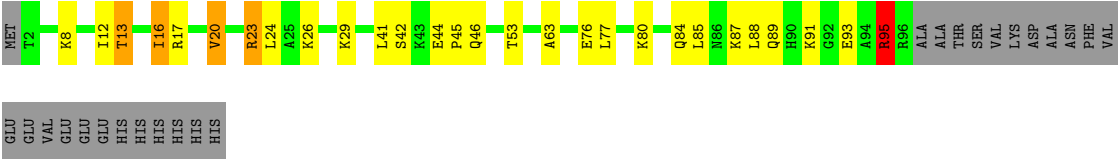
- Molecule 21: 30S Ribosomal Protein THX

Chain U: 



- Molecule 22: Ribosome-associated inhibitor A

Chain Y: 



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	209.63Å 449.30Å 620.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.71 – 2.70	Depositor
% Data completeness (in resolution range)	98.4 (49.71-2.70)	Depositor
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.217 , 0.254	Depositor
Wilson B-factor (Å ²)	55.6	Xtriage
Anisotropy	0.155	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 1557851 reflections	Xtriage
Total number of atoms	51116	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.42% 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: ZN, 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	1.00	41/35935 (0.1%)	1.48	589/56084 (1.1%)
2	B	0.57	0/1811	0.74	0/2452
3	C	0.63	1/1474 (0.1%)	0.84	1/2003 (0.0%)
4	D	0.73	2/1550 (0.1%)	0.87	1/2106 (0.0%)
5	E	0.60	0/1121	0.78	0/1517
6	F	0.61	0/794	0.79	0/1082
7	G	0.59	0/1186	0.74	0/1603
8	H	0.52	0/1065	0.71	0/1445
9	I	0.60	0/867	0.85	0/1180
10	J	0.65	0/672	0.83	0/919
11	K	0.59	0/843	0.74	0/1144
12	L	0.67	0/925	0.83	0/1251
13	M	0.66	0/811	0.91	0/1103
14	N	0.62	0/487	0.83	0/649
15	O	0.59	0/735	0.84	2/981 (0.2%)
16	P	0.60	0/667	0.83	0/905
17	Q	0.59	0/836	0.76	0/1117
18	R	0.51	0/519	0.82	1/699 (0.1%)
19	S	0.58	0/574	0.85	1/781 (0.1%)
20	T	0.59	0/701	0.86	2/930 (0.2%)
21	U	0.57	0/203	0.73	0/266
22	Y	0.67	0/766	0.87	0/1034
All	All	0.89	44/54542 (0.1%)	1.31	597/81251 (0.7%)

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
2	B	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	2
4	D	0	1
9	I	0	3
10	J	0	3
13	M	0	2
18	R	0	1
All	All	0	13

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1459	C	N1-C2	18.78	1.58	1.40
1	A	1442(A)	G	N9-C4	13.88	1.49	1.38
1	A	1459	C	C1'-N1	11.90	1.66	1.48
1	A	1442(A)	G	C2-N3	11.18	1.41	1.32
1	A	1459	C	C2-N3	11.00	1.44	1.35

The worst 5 of 597 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1459	C	C6-N1-C2	-31.41	107.74	120.30
1	A	1459	C	N3-C2-O2	-28.10	102.23	121.90
1	A	1442(A)	G	N3-C4-C5	-24.94	116.13	128.60
1	A	1459	C	N1-C2-O2	19.91	130.84	118.90
1	A	1442(A)	G	C6-N1-C2	-19.29	113.52	125.10

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	14	GLY	Peptide
3	C	180	ALA	Peptide
3	C	50	ALA	Peptide
4	D	29	PRO	Peptide
9	I	39	GLY	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	32102	0	16201	698	0
2	B	1777	0	1747	75	0
3	C	1450	0	1314	42	0
4	D	1520	0	1406	44	0
5	E	1105	0	1130	37	0
6	F	781	0	741	17	0
7	G	1167	0	1108	34	0
8	H	1045	0	1033	31	0
9	I	852	0	742	47	0
10	J	659	0	552	40	0
11	K	828	0	822	15	0
12	L	909	0	927	29	0
13	M	801	0	743	42	0
14	N	478	0	496	25	0
15	O	724	0	749	23	0
16	P	651	0	638	34	0
17	Q	823	0	891	29	0
18	R	514	0	530	13	0
19	S	560	0	466	31	0
20	T	699	0	746	24	0
21	U	199	0	208	6	0
22	Y	754	0	776	24	0
23	A	223	0	0	0	0
23	D	2	0	0	0	0
23	E	1	0	0	0	0
23	F	1	0	0	0	0
23	I	1	0	0	0	0
23	L	1	0	0	0	0
23	M	2	0	0	0	0
23	O	1	0	0	0	0
23	P	1	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	460	0	0	25	0
25	D	3	0	0	2	0
25	E	2	0	0	0	0
25	F	2	0	0	0	0
25	G	2	0	0	0	0
25	J	1	0	0	0	0
25	K	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	L	3	0	0	0	0
25	M	1	0	0	0	0
25	O	4	0	0	0	0
25	Q	3	0	0	0	0
25	Y	1	0	0	0	0
All	All	51116	0	33966	1219	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 15.

The worst 5 of 1219 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:40:C:N4	1:A:402:G:H1	1.47	1.12
1:A:1003:G:H1	1:A:1037:C:H42	1.00	0.97
1:A:1502:A:H2	1:A:1505:G:H1	1.10	0.93
1:A:1025:U:O2	1:A:1036:G:O6	1.86	0.93
1:A:40:C:N3	1:A:402:G:N2	2.16	0.93

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	227/256 (89%)	185 (82%)	40 (18%)	2 (1%)	25	55
3	C	204/239 (85%)	176 (86%)	28 (14%)	0	100	100
4	D	206/209 (99%)	186 (90%)	20 (10%)	0	100	100
5	E	146/162 (90%)	128 (88%)	17 (12%)	1 (1%)	30	62
6	F	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
7	G	153/156 (98%)	132 (86%)	20 (13%)	1 (1%)	30	62
8	H	136/138 (99%)	129 (95%)	7 (5%)	0	100	100
9	I	123/128 (96%)	108 (88%)	13 (11%)	2 (2%)	14	35

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	94/105 (90%)	72 (77%)	15 (16%)	7 (7%)	2	1
11	K	112/129 (87%)	103 (92%)	9 (8%)	0	100	100
12	L	120/132 (91%)	109 (91%)	10 (8%)	1 (1%)	27	58
13	M	112/126 (89%)	86 (77%)	22 (20%)	4 (4%)	5	11
14	N	58/61 (95%)	50 (86%)	7 (12%)	1 (2%)	14	33
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	80/88 (91%)	74 (92%)	5 (6%)	1 (1%)	18	43
17	Q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	22	51
18	R	66/88 (75%)	55 (83%)	11 (17%)	0	100	100
19	S	79/93 (85%)	67 (85%)	11 (14%)	1 (1%)	18	43
20	T	94/106 (89%)	77 (82%)	17 (18%)	0	100	100
21	U	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
22	Y	93/119 (78%)	85 (91%)	7 (8%)	1 (1%)	21	49
All	All	2405/2657 (90%)	2107 (88%)	275 (11%)	23 (1%)	22	51

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	56	HIS
13	M	84	ILE
7	G	147	ALA
10	J	55	LYS
10	J	57	LYS

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	177/220 (80%)	148 (84%)	29 (16%)	3	9
3	C	114/188 (61%)	97 (85%)	17 (15%)	4	11
4	D	139/181 (77%)	119 (86%)	20 (14%)	5	12
5	E	108/123 (88%)	95 (88%)	13 (12%)	7	17

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	77/90 (86%)	66 (86%)	11 (14%)	5	12
7	G	104/127 (82%)	91 (88%)	13 (12%)	7	16
8	H	103/119 (87%)	87 (84%)	16 (16%)	4	10
9	I	62/99 (63%)	53 (86%)	9 (14%)	5	12
10	J	52/92 (56%)	41 (79%)	11 (21%)	1	4
11	K	81/99 (82%)	73 (90%)	8 (10%)	11	26
12	L	92/109 (84%)	83 (90%)	9 (10%)	12	26
13	M	63/101 (62%)	46 (73%)	17 (27%)	1	2
14	N	46/50 (92%)	38 (83%)	8 (17%)	3	7
15	O	77/80 (96%)	64 (83%)	13 (17%)	3	8
16	P	63/74 (85%)	50 (79%)	13 (21%)	2	5
17	Q	94/97 (97%)	82 (87%)	12 (13%)	6	15
18	R	49/77 (64%)	40 (82%)	9 (18%)	2	6
19	S	43/80 (54%)	37 (86%)	6 (14%)	5	12
20	T	62/82 (76%)	53 (86%)	9 (14%)	5	12
21	U	18/22 (82%)	15 (83%)	3 (17%)	3	8
22	Y	82/104 (79%)	70 (85%)	12 (15%)	5	11
All	All	1706/2214 (77%)	1448 (85%)	258 (15%)	4	11

5 of 258 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	121	ASP
11	K	104	GLN
20	T	39	LYS
9	I	31	GLN
10	J	54	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	73	GLN
9	I	124	GLN
16	P	16	HIS
7	G	28	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	P	14	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1490/1522 (97%)	306 (20%)	32 (2%)

5 of 306 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	7	G
1	A	9	G
1	A	32	A
1	A	39	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	687	A
1	A	991	U
1	A	1456	G
1	A	913	A
1	A	1064	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 235 ligands modelled in this entry, 235 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.