



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 07:10 AM EDT

PDB ID : 5LMP
EMDB ID: : EMD-4075
Title : Structure of bacterial 30S-IF1-IF3-mRNA translation pre-initiation complex (state-1C)
Authors : Hussain, T.; Llacer, J.L.; Wimberly, B.T.; Ramakrishnan, V.
Deposited on : unknown
Resolution : 5.35 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model 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

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

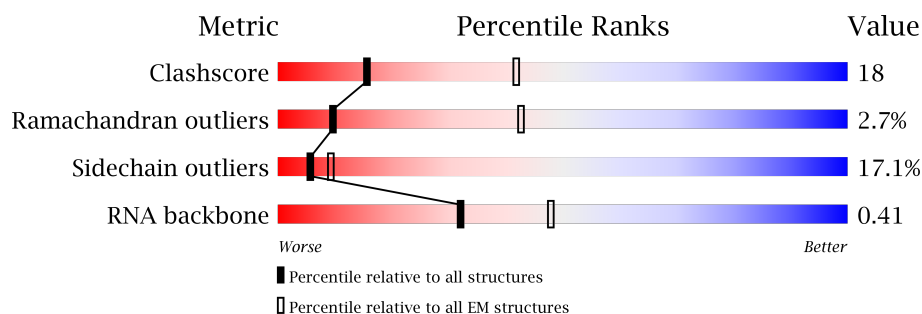
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.35 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	A	1522	27% 55% 17% ..
2	B	256	51% 30% 10% 9%
3	C	239	54% 29% • 14%
4	D	209	58% 33% 8% •
5	E	162	56% 24% 12% • 7%
6	F	101	65% 28% 7%
7	G	156	78% 19% ..
8	H	138	54% 41% •

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Mol	Chain	Length	Quality of chain
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	V	27	
22	W	72	
23	X	171	
24	Y	39	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
26	ZN	D	300	-	-	X	-
26	ZN	N	101	-	-	X	-

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 54132 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1514	Total	C	N	O	P	0	0
			32525	14481	6019	10514	1511		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	127	Total	C	N	O	0	0
			1010	639	197	174		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			792	498	156	137	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	117	Total	C	N	O	S	0	0
			933	577	192	162	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	73	Total	C	N	O	0	0
			598	381	118	99		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	80	Total	C	N	O	S	0	0
			647	414	119	112	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a protein called Translation initiation factor IF-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	71	Total	C	N	O	S	0	0
			570	362	103	103	2		

- Molecule 23 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	168	Total	C	N	O	S	0	0
			1356	853	249	245	9		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	20	Total	C	N	O	P	0	0
			439	196	89	134	20		

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

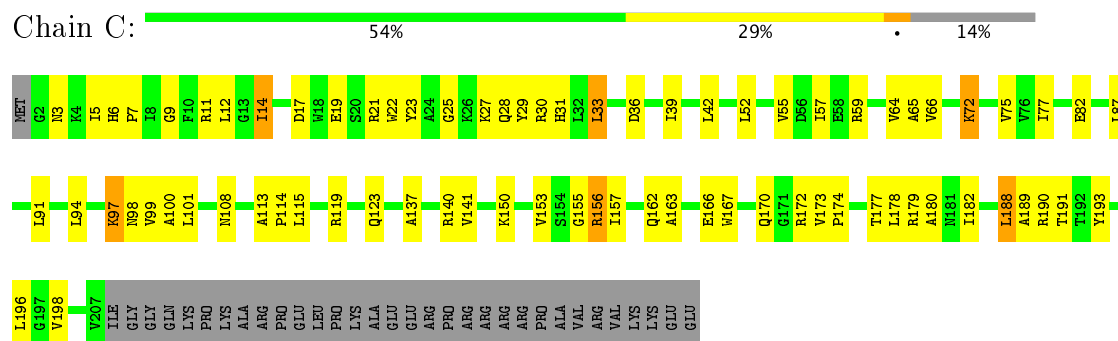
Mol	Chain	Residues	Atoms		AltConf
25	A	108	Total	Mg	0
			108	108	

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

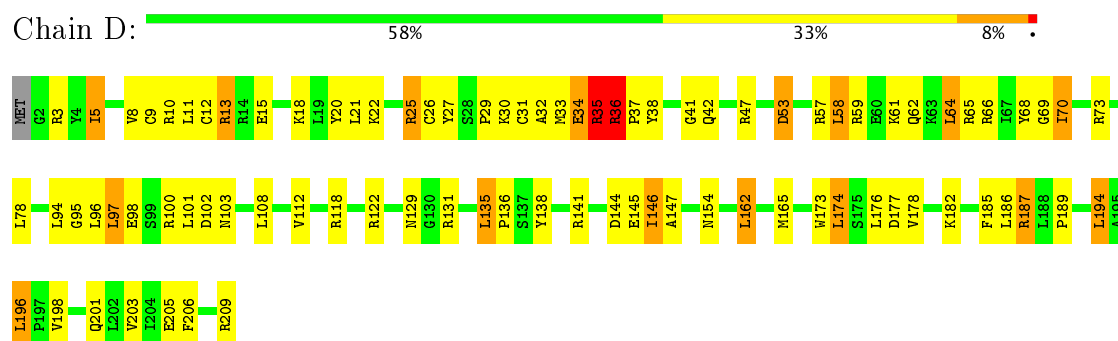
Mol	Chain	Residues	Atoms		AltConf
26	D	1	Total	Zn	0
			1	1	
26	N	1	Total	Zn	0
			1	1	

- Molecule 1: 16S rRNA

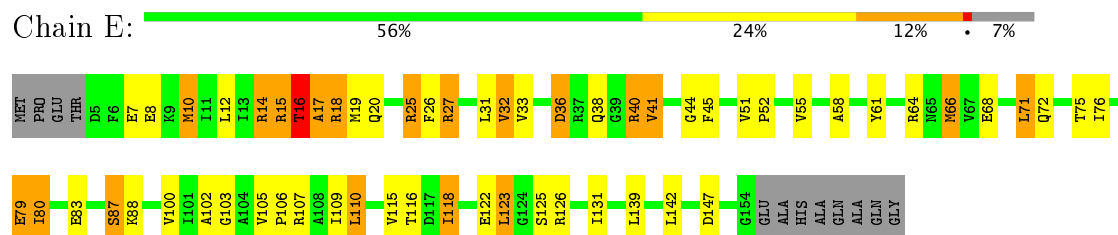




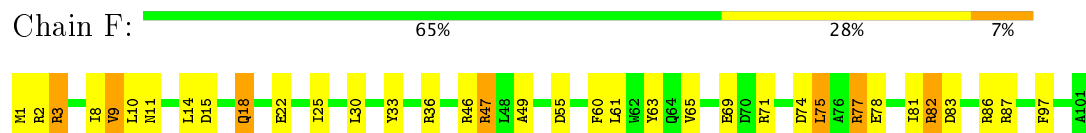
- Molecule 4: 30S ribosomal protein S4



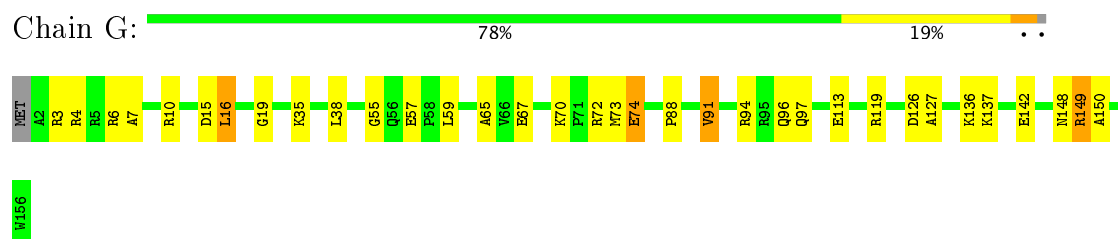
- Molecule 5: 30S ribosomal protein S5



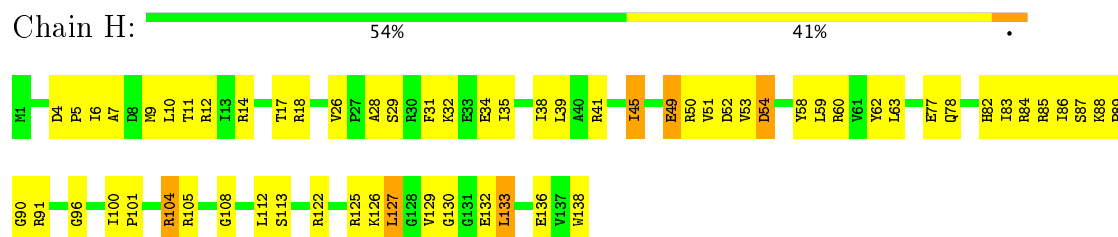
- Molecule 6: 30S ribosomal protein S6



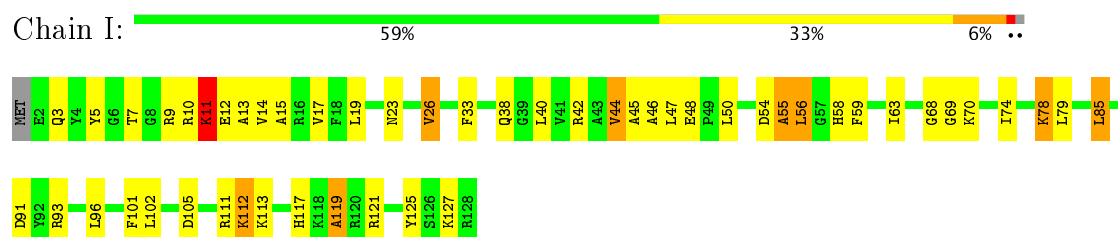
- Molecule 7: 30S ribosomal protein S7



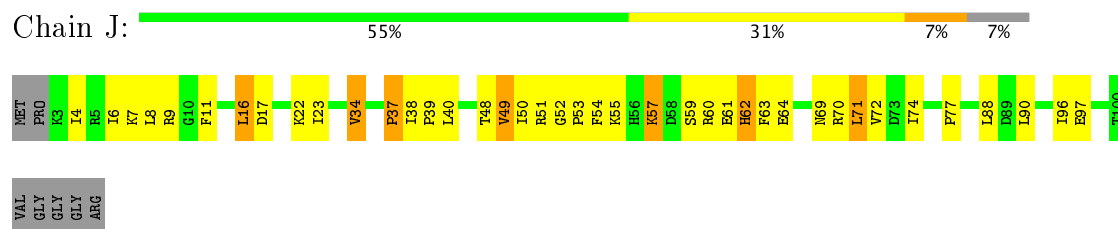
- Molecule 8: 30S ribosomal protein S8



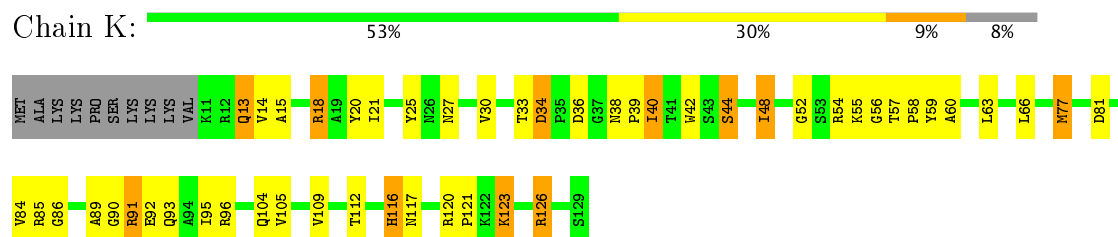
- Molecule 9: 30S ribosomal protein S9



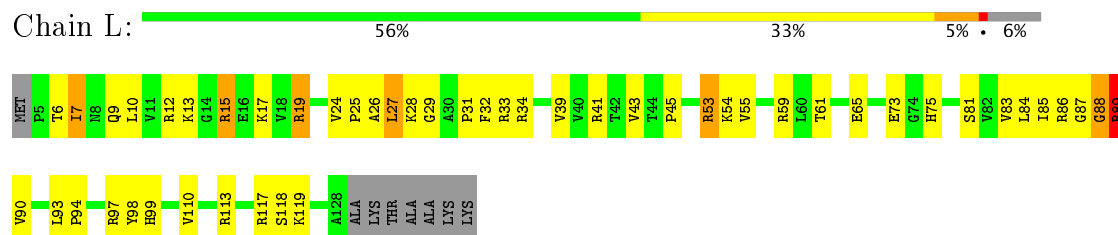
- Molecule 10: 30S ribosomal protein S10



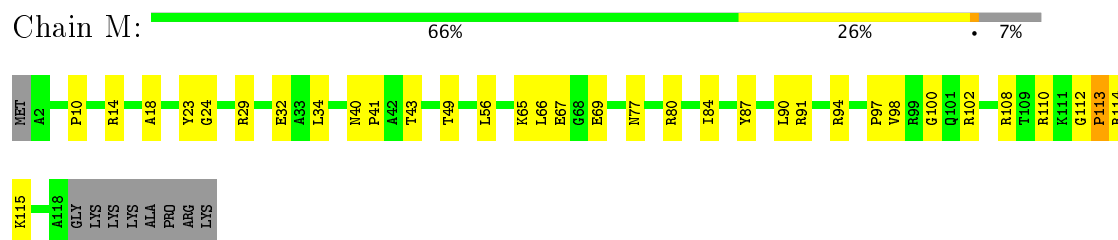
- Molecule 11: 30S ribosomal protein S11



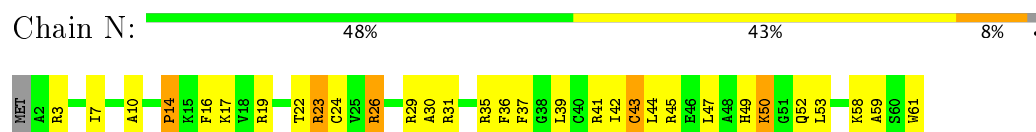
- Molecule 12: 30S ribosomal protein S12



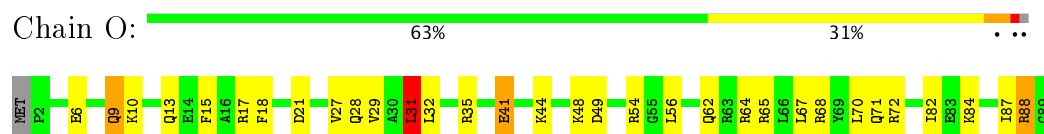
- Molecule 13: 30S ribosomal protein S13



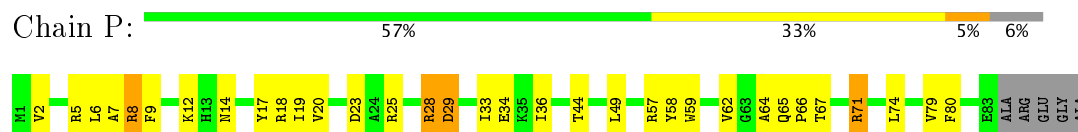
- Molecule 14: 30S ribosomal protein S14 type Z



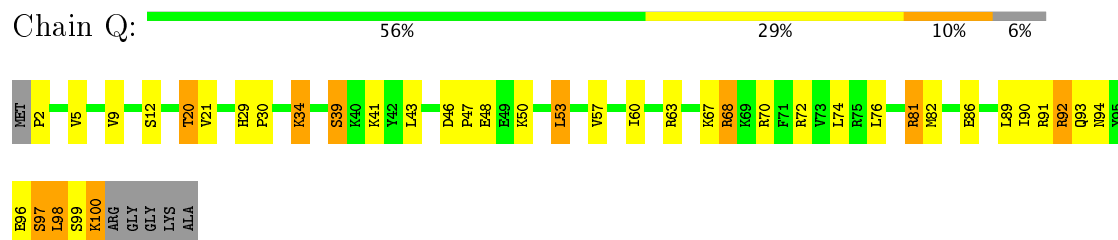
- Molecule 15: 30S ribosomal protein S15



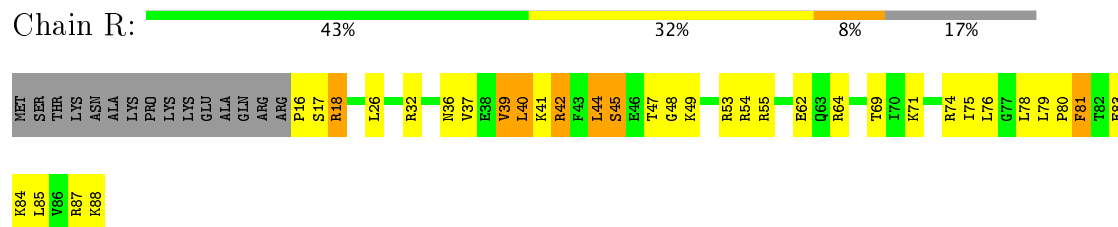
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

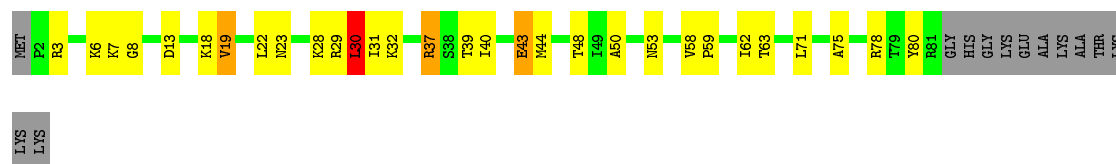


- Molecule 18: 30S ribosomal protein S18



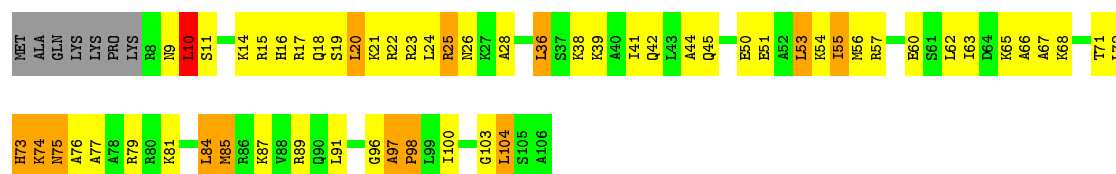
- Molecule 19: 30S ribosomal protein S19

Chain S: 



- Molecule 20: 30S ribosomal protein S20

Chain T: 



- Molecule 21: 30S ribosomal protein Thx

Chain V: 



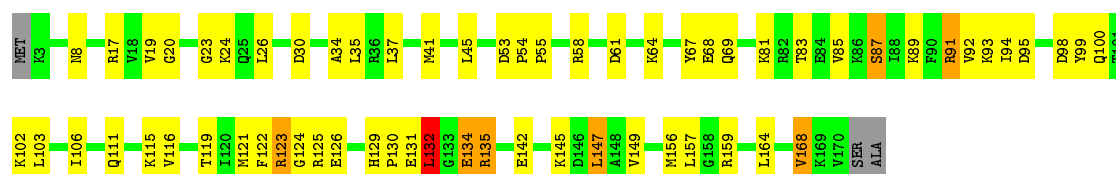
- Molecule 22: Translation initiation factor IF-1

Chain W: 



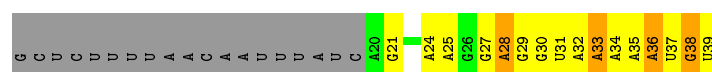
- Molecule 23: Translation initiation factor IF-3

Chain X: 



- Molecule 24: mRNA

Chain Y: 



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	18830	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	OTHER	Depositor

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 > 2$	RMSZ	# $ Z > 2$
1	A	0.38	0/36397	0.75	21/56783 (0.0%)
10	J	0.61	0/805	0.75	0/1082
11	K	0.59	0/900	0.79	0/1213
12	L	0.51	1/986 (0.1%)	0.81	1/1320 (0.1%)
13	M	0.63	0/943	0.83	0/1265
14	N	0.53	0/501	0.80	0/664
15	O	0.54	0/745	0.92	1/992 (0.1%)
16	P	0.50	0/716	0.81	0/963
17	Q	0.52	0/836	0.79	0/1117
18	R	0.59	0/604	0.85	0/801
19	S	0.69	0/661	0.80	0/890
2	B	0.69	0/1935	0.88	0/2609
20	T	0.55	0/765	0.98	1/1007 (0.1%)
21	V	1.04	1/212 (0.5%)	0.76	0/277
22	W	0.67	0/580	0.92	3/782 (0.4%)
23	X	0.68	0/1375	0.90	2/1844 (0.1%)
24	Y	0.59	0/494	0.84	0/770
3	C	0.54	0/1636	0.84	4/2205 (0.2%)
4	D	0.56	0/1733	0.90	3/2318 (0.1%)
5	E	0.53	0/1162	0.97	3/1564 (0.2%)
6	F	0.50	0/856	0.81	1/1154 (0.1%)
7	G	0.58	0/1276	0.81	1/1709 (0.1%)
8	H	0.53	0/1136	0.86	1/1527 (0.1%)
9	I	0.57	0/1029	0.98	2/1379 (0.1%)
All	All	0.47	2/58283 (0.0%)	0.79	44/86235 (0.1%)

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
1	A	0	2
23	X	0	1
9	I	1	0
All	All	1	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	V	2	GLY	N-CA	12.09	1.64	1.46
12	L	19	ARG	CZ-NH1	5.07	1.39	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	11	LYS	CB-CA-C	20.48	151.36	110.40
5	E	16	THR	N-CA-CB	-12.74	86.10	110.30
5	E	15	ARG	N-CA-C	-11.21	80.73	111.00
23	X	91	ARG	NE-CZ-NH2	10.39	125.49	120.30
22	W	23	ARG	CB-CA-C	-9.87	90.66	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	I	11	LYS	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1445	C	Sidechain
1	A	218	C	Sidechain
23	X	53	ASP	Peptide

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	A	32525	0	16434	1096	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1900	0	1951	49	0
3	C	1612	0	1677	84	0
4	D	1703	0	1766	91	0
5	E	1146	0	1207	59	0
6	F	843	0	857	19	0
7	G	1257	0	1296	17	0
8	H	1116	0	1177	38	0
9	I	1010	0	1035	26	0
10	J	792	0	835	38	0
11	K	885	0	904	30	0
12	L	970	0	1057	34	0
13	M	933	0	992	17	0
14	N	492	0	533	42	0
15	O	734	0	771	13	0
16	P	700	0	720	23	0
17	Q	823	0	888	40	0
18	R	598	0	670	23	0
19	S	647	0	673	20	0
20	T	763	0	861	82	0
21	V	208	0	221	3	0
22	W	570	0	598	21	0
23	X	1356	0	1401	30	0
24	Y	439	0	218	10	0
25	A	108	0	0	0	0
26	D	1	0	0	3	0
26	N	1	0	0	2	0
All	All	54132	0	38742	1696	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 18.

The worst 5 of 1696 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:A:1256:A:H3'	3:C:27:LYS:NZ	1.22	1.48
4:D:36:ARG:HD2	4:D:38:TYR:CZ	1.47	1.46
17:Q:41:LYS:NZ	17:Q:92:ARG:NH2	1.65	1.44
1:A:1256:A:C3'	3:C:27:LYS:HZ1	1.28	1.42
3:C:57:ILE:HG12	3:C:66:VAL:CG2	1.51	1.39

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 PDB entries followed by that with respect to all EM entries.

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	232/256 (91%)	182 (78%)	36 (16%)	14 (6%)	2	22
3	C	204/239 (85%)	181 (89%)	21 (10%)	2 (1%)	18	61
4	D	206/209 (99%)	182 (88%)	21 (10%)	3 (2%)	12	53
5	E	148/162 (91%)	127 (86%)	20 (14%)	1 (1%)	25	68
6	F	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	18	61
7	G	153/156 (98%)	134 (88%)	17 (11%)	2 (1%)	14	56
8	H	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	25	68
9	I	125/128 (98%)	98 (78%)	19 (15%)	8 (6%)	1	22
10	J	96/105 (91%)	79 (82%)	13 (14%)	4 (4%)	3	30
11	K	117/129 (91%)	100 (86%)	15 (13%)	2 (2%)	11	51
12	L	122/132 (92%)	97 (80%)	21 (17%)	4 (3%)	4	36
13	M	115/126 (91%)	100 (87%)	13 (11%)	2 (2%)	11	51
14	N	58/61 (95%)	47 (81%)	7 (12%)	4 (7%)	1	20
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	81/88 (92%)	72 (89%)	9 (11%)	0	100	100
17	Q	97/105 (92%)	86 (89%)	9 (9%)	2 (2%)	8	46
18	R	71/88 (81%)	63 (89%)	4 (6%)	4 (6%)	2	24
19	S	78/93 (84%)	64 (82%)	10 (13%)	4 (5%)	2	26
20	T	97/106 (92%)	85 (88%)	8 (8%)	4 (4%)	3	31
21	V	22/27 (82%)	17 (77%)	4 (18%)	1 (4%)	3	29
22	W	69/72 (96%)	63 (91%)	5 (7%)	1 (1%)	13	54
23	X	166/171 (97%)	143 (86%)	18 (11%)	5 (3%)	5	38
All	All	2578/2781 (93%)	2218 (86%)	291 (11%)	69 (3%)	10	40

5 of 69 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	9	GLU
2	B	16	HIS
2	B	24	TRP
2	B	229	VAL
7	G	55	GLY

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 PDB entries followed by that with respect to all EM entries.

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	202/220 (92%)	152 (75%)	50 (25%)	1	5
3	C	160/188 (85%)	138 (86%)	22 (14%)	4	24
4	D	180/181 (99%)	137 (76%)	43 (24%)	1	6
5	E	115/123 (94%)	86 (75%)	29 (25%)	0	5
6	F	90/90 (100%)	78 (87%)	12 (13%)	4	24
7	G	126/127 (99%)	112 (89%)	14 (11%)	7	30
8	H	119/119 (100%)	100 (84%)	19 (16%)	3	18
9	I	98/99 (99%)	84 (86%)	14 (14%)	4	22
10	J	87/92 (95%)	77 (88%)	10 (12%)	6	28
11	K	90/99 (91%)	72 (80%)	18 (20%)	1	9
12	L	104/109 (95%)	89 (86%)	15 (14%)	4	22
13	M	94/101 (93%)	85 (90%)	9 (10%)	10	36
14	N	49/50 (98%)	44 (90%)	5 (10%)	8	33
15	O	79/80 (99%)	61 (77%)	18 (23%)	1	7
16	P	72/74 (97%)	63 (88%)	9 (12%)	5	26
17	Q	94/97 (97%)	78 (83%)	16 (17%)	2	16
18	R	64/77 (83%)	53 (83%)	11 (17%)	2	15
19	S	71/80 (89%)	61 (86%)	10 (14%)	4	23
20	T	76/82 (93%)	57 (75%)	19 (25%)	1	5
21	V	19/22 (86%)	18 (95%)	1 (5%)	26	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	W	62/63 (98%)	52 (84%)	10 (16%)	3	18
23	X	145/150 (97%)	123 (85%)	22 (15%)	3	20
All	All	2196/2323 (94%)	1820 (83%)	376 (17%)	6	15

5 of 376 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	H	9	MET
10	J	71	LEU
22	W	32	ILE
8	H	41	ARG
9	I	38	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
8	H	15	ASN
12	L	8	ASN
20	T	18	GLN
11	K	27	ASN
12	L	9	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1505/1522 (98%)	439 (29%)	103 (6%)
24	Y	19/39 (48%)	11 (57%)	3 (15%)
All	All	1524/1561 (97%)	450 (29%)	106 (6%)

5 of 450 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	18	C

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	595	G
1	A	884	U
1	A	1447	A
1	A	687	A
1	A	777	A

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](#)

Of 110 ligands modelled in this entry, 110 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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	7

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	84:U	O3'	88:A	P	5.54
1	A	93:G	O3'	96:U	P	5.11
1	A	204:U	O3'	216:G	P	4.54
1	A	1442(A):G	O3'	1442(B):A	P	3.89
1	A	841:U	O3'	848:C	P	3.88