



wwPDB EM Map/Model Validation Report i

Apr 10, 2016 – 01:39 PM BST

PDB ID : 3IZD
EMDB ID: : EMD-1667
Title : Model of the large subunit RNA expansion segment ES27L-out based on a 6.1 Å cryo-EM map of *Saccharomyces cerevisiae* translating 80S ribosome. 3IZD is a small part (an expansion segment) which is in an alternative conformation to what is in already 3IZF.
Authors : Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on : 2010-10-13
Resolution : 8.60 Å(reported)

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

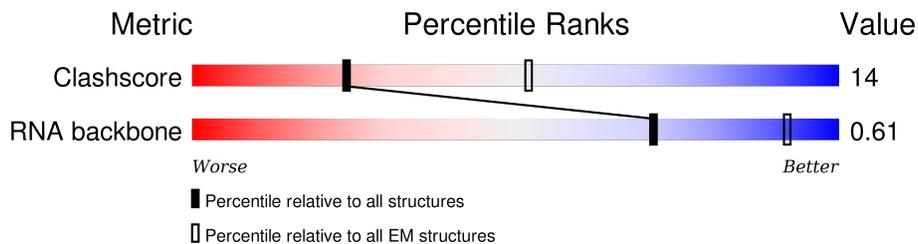
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.60 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	A	151	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3044 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 rRNA expansion segment ES27L in an "out" conformation.

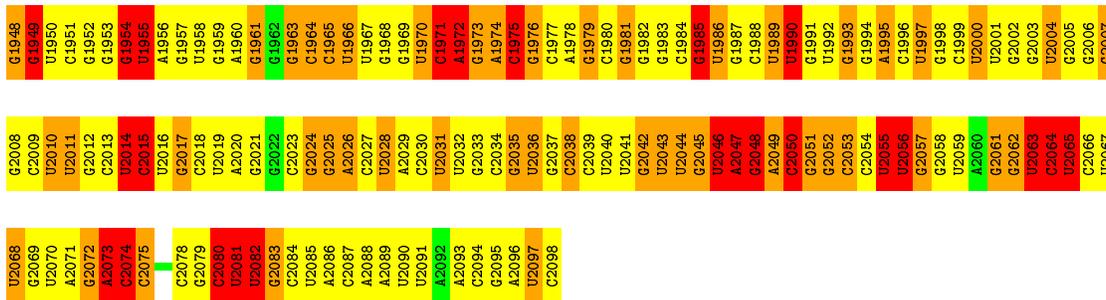
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	151	3044	1346	504	1043	151	0	0

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: rRNA expansion segment ES27L in an "out" conformation

Chain A:  49% 31% 16%



4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	2.89	189/3384 (5.6%)	2.84	321/5256 (6.1%)

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	1	0

The worst 5 of 189 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2038	C	O3'-P	-33.65	1.20	1.61
1	A	1985	G	O3'-P	31.35	1.98	1.61
1	A	2035	G	O3'-P	-28.25	1.27	1.61
1	A	2047	A	O3'-P	28.07	1.94	1.61
1	A	1961	G	C2'-C1'	26.77	1.82	1.53

The worst 5 of 321 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2047	A	P-O5'-C5'	36.05	178.58	120.90
1	A	2082	U	P-O3'-C3'	30.68	156.51	119.70
1	A	2073	A	P-O3'-C3'	29.66	155.29	119.70
1	A	2079	G	O5'-P-OP2	-29.48	75.32	110.70
1	A	2055	U	P-O3'-C3'	28.80	154.26	119.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1954	G	C4'

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	A	3044	0	1506	58	0
All	All	3044	0	1506	58	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 14.

The worst 5 of 58 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:1972:A:C4'	1:A:1972:A:C3'	1.80	1.57
1:A:1961:G:C2'	1:A:1961:G:C1'	1.82	1.48
1:A:1971:C:C1'	1:A:1971:C:O4'	1.63	1.36
1:A:2080:C:O4'	1:A:2080:C:C1'	1.64	1.22
1:A:1985:G:O3'	1:A:1986:U:P	1.98	1.20

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	138/151 (91%)	28 (20%)	18 (13%)

5 of 28 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1949	G
1	A	1954	G
1	A	1955	U
1	A	1966	U
1	A	1972	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2014	U
1	A	2038	C
1	A	2075	C
1	A	1985	G
1	A	1989	U

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.