



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 22, 2017 – 08:30 AM EDT

PDB ID : 5FL2
EMDB ID: : EMD-3206
Title : Revisited cryo-EM structure of Inducible lysine decarboxylase complexed with LARA domain of RavA ATPase
Authors : Kandiah, E.; Carriel, D.; Perard, J.; Malet, H.; Bacia, M.; Liu, K.; Chan, S.W.S.; Houry, W.A.; Ollagnier de Choudens, S.; Elsen, S.; Gutsche, I.
Deposited on : unknown
Resolution : 6.20 Å(reported)
Based on PDB ID : 3N75

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

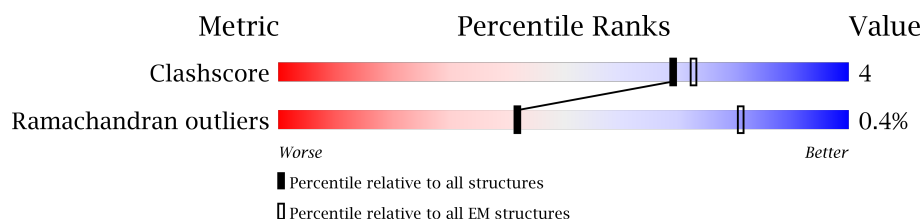
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.20 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

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	711	 95% .
2	K	106	 96% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4027 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 protein called LYSINE DECARBOXYLASE, INDUCIBLE.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	710	Total	C	N	O	0	0
			3506	2086	710	710		

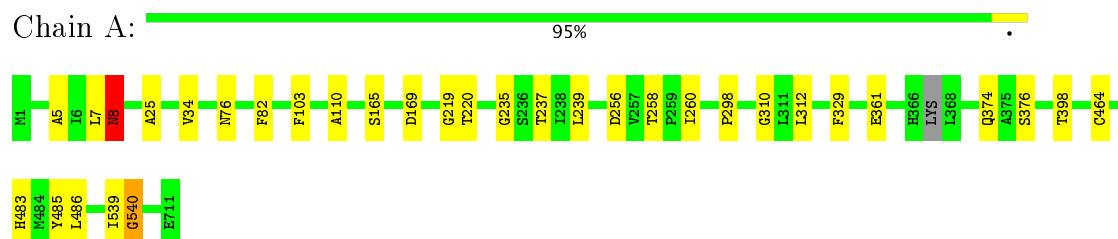
- Molecule 2 is a protein called ATPASE RAVA.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	K	106	Total	C	N	O	0	0
			521	309	106	106		

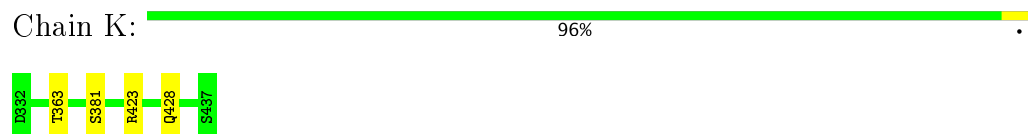
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: LYSINE DECARBOXYLASE, INDUCIBLE



- Molecule 2: ATPASE RAVA



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	INDIVIDUAL PARTICLE WITH FULL CTF CORRECTION AFTER FIRST PEAK	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	51660	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	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	0.57	3/3504 (0.1%)	0.71	5/4876 (0.1%)
2	K	0.31	0/520	0.51	0/721
All	All	0.54	3/4024 (0.1%)	0.69	5/5597 (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	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	8	ASN	N-CA	6.52	1.59	1.46
1	A	8	ASN	CA-C	6.39	1.69	1.52
1	A	540	GLY	N-CA	5.38	1.54	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	ASN	N-CA-C	14.55	150.29	111.00
1	A	540	GLY	N-CA-C	8.17	133.52	113.10
1	A	8	ASN	N-CA-CB	-5.97	99.86	110.60
1	A	76	ASN	N-CA-C	5.14	124.89	111.00
1	A	8	ASN	CB-CA-C	-5.03	100.34	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	539	ILE	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	3506	0	1567	23	0
2	K	521	0	235	2	0
All	All	4027	0	1802	25	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 4.

The worst 5 of 25 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:25:ALA:CB	1:A:110:ALA:CB	2.51	0.88
1:A:25:ALA:CB	1:A:110:ALA:HB3	2.07	0.84
1:A:25:ALA:HB3	1:A:110:ALA:CB	2.09	0.83
1:A:312:LEU:O	1:A:483:HIS:O	2.03	0.77
1:A:219:GLY:N	1:A:374:GLN:O	2.21	0.73

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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
1	A	706/711 (99%)	677 (96%)	26 (4%)	3 (0%)	38 77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	104/106 (98%)	96 (92%)	8 (8%)	0	100	100
All	All	810/817 (99%)	773 (95%)	34 (4%)	3 (0%)	42	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	540	GLY
1	A	398	THR

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](#)

There are no RNA molecules in this entry.

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.