



Full wwPDB EM Model Validation Report ⓘ

Apr 13, 2020 – 10:20 AM EDT

PDB ID : 6JR3
EMDB ID : EMD-9878
Title : Crystal structure of insulin hexamer fitted into cryo EM density map where each dimer was kept as rigid body
Authors : Sengupta, J.; Pathak, B.K.; Bhakta, S.
Deposited on : 2019-04-02
Resolution : 14.50 Å(reported)
Based on initial model : 1EV6

This is a Full wwPDB EM Model Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.10.1

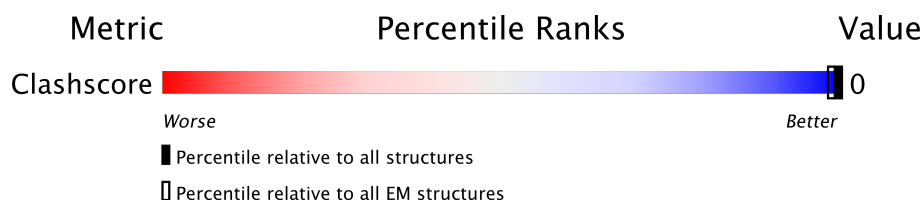
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 14.50 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.



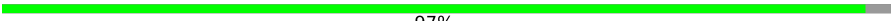
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. 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 respectively. 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	21	 100%
1	C	21	 100%
1	E	21	 100%
1	G	21	 100%
1	I	21	 100%
1	K	21	 100%
2	B	30	 97% .
2	D	30	 97% .
2	F	30	 97% .
2	H	30	 97% .
2	J	30	 97% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	L	30	 97%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 300 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 Insulin A chain.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	21	Total C 21 21	0	21
1	C	21	Total C 21 21	0	21
1	G	21	Total C 21 21	0	21
1	E	21	Total C 21 21	0	21
1	I	21	Total C 21 21	0	21
1	K	21	Total C 21 21	0	21

- Molecule 2 is a protein called Insulin B chain.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	29	Total C 29 29	0	29
2	D	29	Total C 29 29	0	29
2	H	29	Total C 29 29	0	29
2	F	29	Total C 29 29	0	29
2	J	29	Total C 29 29	0	29
2	L	29	Total C 29 29	0	29

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 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: Insulin A chain

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Insulin A chain

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Insulin A chain

Chain G:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Insulin A chain

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Insulin A chain

Chain I:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Insulin A chain

Chain K:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: Insulin B chain

Chain B:  97%



- Molecule 2: Insulin B chain

Chain D:  97% .



- Molecule 2: Insulin B chain

Chain H:  97% .



- Molecule 2: Insulin B chain

Chain F:  97% .



- Molecule 2: Insulin B chain

Chain J:  97% .



- Molecule 2: Insulin B chain

Chain L:  97% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	11000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI EAGLE (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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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	21	0	0	0	0
1	C	21	0	0	0	0
1	E	21	0	0	0	0
1	G	21	0	0	0	0
1	I	21	0	0	0	0
1	K	21	0	0	0	0
2	B	29	0	0	0	0
2	D	29	0	0	0	0
2	F	29	0	0	0	0
2	H	29	0	0	0	0
2	J	29	0	0	0	0
2	L	29	0	0	0	0
All	All	300	0	0	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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.