



## Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2017 – 04:22 pm GMT

PDB ID : 3IZ2  
Title : C-alpha model fitted into the EM structure of Cx26M34Adel2-7  
Authors : Oshima, A.; Tani, K.; Toloue, M.M.; Hiroaki, Y.; Smock, A.; Inukai, S.; Cone, A.; Nicholson, B.J.; Sosinsky, G.E.; Fujiyoshi, Y.  
Deposited on : 2010-08-19  
Resolution : 10.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	recalc29102

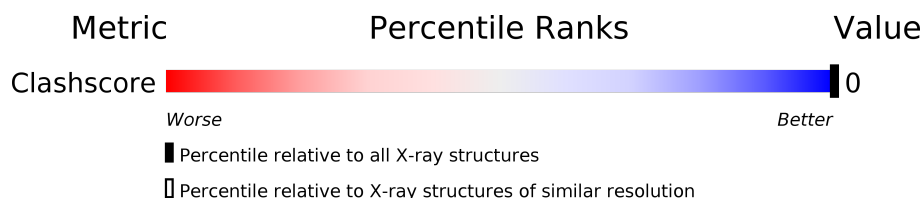
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON CRYSTALLOGRAPHY*

The reported resolution of this entry is 10.00 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	112137	1037 (15.00-3.80)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	232	 80% 20%
1	B	232	 80% 20%
1	C	232	 80% 20%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 555 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 protein called Gap junction beta-2 protein.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	185	Total C 185 185	0	0	185
1	B	185	Total C 185 185	0	0	185
1	C	185	Total C 185 185	0	0	185

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	EXPRESSION TAG	UNP P29033
A	227	LEU	-	EXPRESSION TAG	UNP P29033
A	228	VAL	-	EXPRESSION TAG	UNP P29033
A	229	PRO	-	EXPRESSION TAG	UNP P29033
A	230	ARG	-	EXPRESSION TAG	UNP P29033
A	231	GLY	-	EXPRESSION TAG	UNP P29033
A	232	SER	-	EXPRESSION TAG	UNP P29033
A	233	HIS	-	EXPRESSION TAG	UNP P29033
A	234	HIS	-	EXPRESSION TAG	UNP P29033
A	235	HIS	-	EXPRESSION TAG	UNP P29033
A	236	HIS	-	EXPRESSION TAG	UNP P29033
A	237	HIS	-	EXPRESSION TAG	UNP P29033
A	238	HIS	-	EXPRESSION TAG	UNP P29033
B	7	MET	-	EXPRESSION TAG	UNP P29033
B	227	LEU	-	EXPRESSION TAG	UNP P29033
B	228	VAL	-	EXPRESSION TAG	UNP P29033
B	229	PRO	-	EXPRESSION TAG	UNP P29033
B	230	ARG	-	EXPRESSION TAG	UNP P29033
B	231	GLY	-	EXPRESSION TAG	UNP P29033
B	232	SER	-	EXPRESSION TAG	UNP P29033
B	233	HIS	-	EXPRESSION TAG	UNP P29033
B	234	HIS	-	EXPRESSION TAG	UNP P29033
B	235	HIS	-	EXPRESSION TAG	UNP P29033

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Chain	Residue	Modelled	Actual	Comment	Reference
B	236	HIS	-	EXPRESSION TAG	UNP P29033
B	237	HIS	-	EXPRESSION TAG	UNP P29033
B	238	HIS	-	EXPRESSION TAG	UNP P29033
C	7	MET	-	EXPRESSION TAG	UNP P29033
C	227	LEU	-	EXPRESSION TAG	UNP P29033
C	228	VAL	-	EXPRESSION TAG	UNP P29033
C	229	PRO	-	EXPRESSION TAG	UNP P29033
C	230	ARG	-	EXPRESSION TAG	UNP P29033
C	231	GLY	-	EXPRESSION TAG	UNP P29033
C	232	SER	-	EXPRESSION TAG	UNP P29033
C	233	HIS	-	EXPRESSION TAG	UNP P29033
C	234	HIS	-	EXPRESSION TAG	UNP P29033
C	235	HIS	-	EXPRESSION TAG	UNP P29033
C	236	HIS	-	EXPRESSION TAG	UNP P29033
C	237	HIS	-	EXPRESSION TAG	UNP P29033
C	238	HIS	-	EXPRESSION TAG	UNP P29033

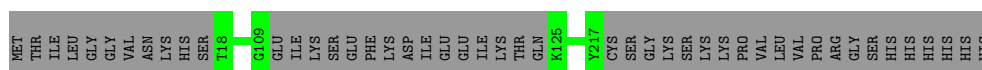
### 3 Residue-property plots [i](#)

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 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.

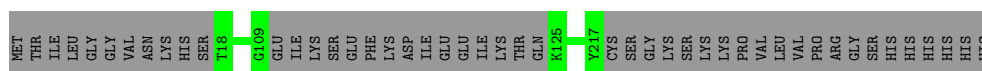
- Molecule 1: Gap junction beta-2 protein

Chain A: 




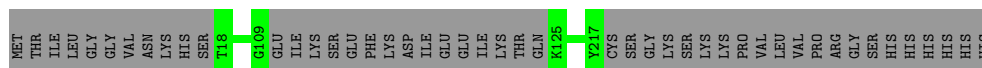
- Molecule 1: Gap junction beta-2 protein

Chain B: 



- Molecule 1: Gap junction beta-2 protein

Chain C: 



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.40Å 112.20Å 300.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 10.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-10.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	unknown	Depositor
R, $R_{free}$	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	555	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	128.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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	185	0	0	0	0
1	B	185	0	0	0	0
1	C	185	0	0	0	0
All	All	555	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

#### 5.3.1 Protein backbone

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.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.