



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:01 AM UTC

PDB ID : 3IZ2 / pdb_00003iz2
EMDB ID : EMD-1749
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)
Based on initial model : 2ZW3

This is a wwPDB EM Validation Summary Report for a publicly released PDB 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

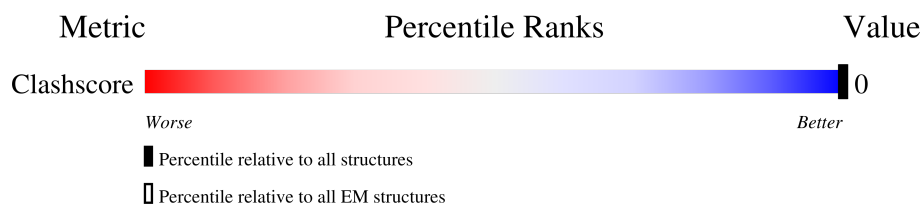
1 Overall quality at a glance

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)	EM structures (#Entries)
Clashscore	229148	23984

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 of 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	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 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	AltConf	Trace
1	A	185	Total C 185 185	0	185
1	B	185	Total C 185 185	0	185
1	C	185	Total C 185 185	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
B	236	HIS	-	expression tag	UNP P29033

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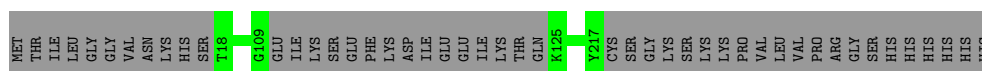
Chain	Residue	Modelled	Actual	Comment	Reference
B	237	HIS	-	expression tag	UNP P29033
B	238	HIS	-	expression tag	UNP P29033
C	7	MET	-	expression tag	UNP P29033
C	227	LEU	-	expression tag	UNP P29033
C	228	VAL	-	expression tag	UNP P29033
C	229	PRO	-	expression tag	UNP P29033
C	230	ARG	-	expression tag	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, DNA and oligosaccharide 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.

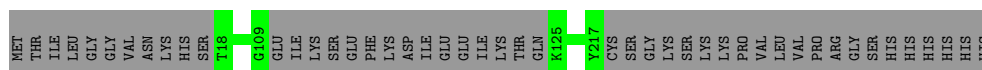
- Molecule 1: Gap junction beta-2 protein

Chain A: 



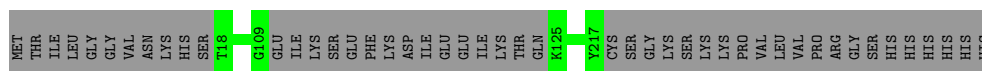
- Molecule 1: Gap junction beta-2 protein

Chain B: 



- Molecule 1: Gap junction beta-2 protein

Chain C: 



4 Experimental information

Property	Value	Source
EM reconstruction method	CRYSTALLOGRAPHY	Depositor
Imposed symmetry	2D CRYSTAL, a =Not provided Å, b =Not provided Å, c =Not provided Å, γ =Not provided°, space group=Not provided	Depositor
Number of images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Each image	Depositor
Microscope	JEOL KYOTO-3000SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	544	Depositor
Maximum defocus (nm)	2214	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	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	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 [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 oligosaccharides 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 Map visualisation

This section contains visualisations of the EMDB entry EMD-1749. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.