



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:48 PM UTC

PDB ID : 8PHB / pdb_00008phb
Title : Crystal structure of apo CamI
Authors : Tamulaitiene, G.; Tamulaitis, G.; Mogila, I.; Keda, K.
Deposited on : 2023-06-19
Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

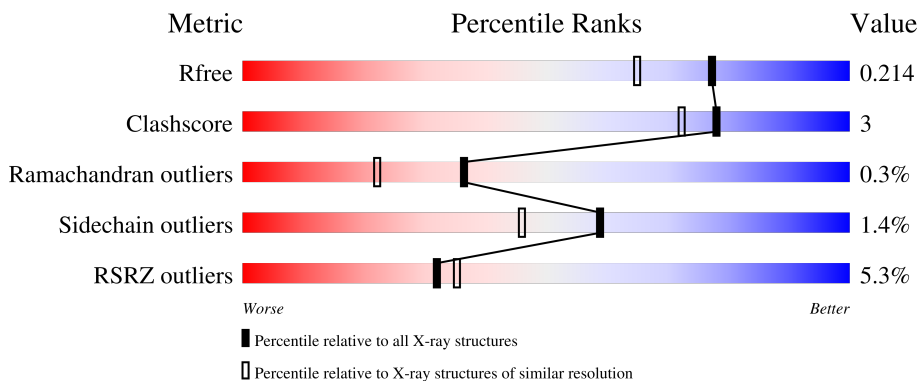
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
R_{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 of the lower 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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	406	 6% 85% 8% 7%
1	B	406	 4% 86% 6% 8%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6356 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 CRISPR-associated protein, APE2256 family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	379	3027	1936	524	555	12	0	15	0
1	B	372	2962	1886	511	553	12	0	14	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP D3RW14
A	2	ALA	-	expression tag	UNP D3RW14
A	382	GLY	-	expression tag	UNP D3RW14
A	383	GLU	-	expression tag	UNP D3RW14
A	384	GLY	-	expression tag	UNP D3RW14
A	385	TRP	-	expression tag	UNP D3RW14
A	386	SER	-	expression tag	UNP D3RW14
A	387	HIS	-	expression tag	UNP D3RW14
A	388	PRO	-	expression tag	UNP D3RW14
A	389	GLN	-	expression tag	UNP D3RW14
A	390	PHE	-	expression tag	UNP D3RW14
A	391	GLU	-	expression tag	UNP D3RW14
A	392	LYS	-	expression tag	UNP D3RW14
A	393	GLY	-	expression tag	UNP D3RW14
A	394	VAL	-	expression tag	UNP D3RW14
A	395	GLU	-	expression tag	UNP D3RW14
A	396	GLY	-	expression tag	UNP D3RW14
A	397	HIS	-	expression tag	UNP D3RW14
A	398	HIS	-	expression tag	UNP D3RW14
A	399	HIS	-	expression tag	UNP D3RW14
A	400	HIS	-	expression tag	UNP D3RW14
A	401	HIS	-	expression tag	UNP D3RW14
A	402	HIS	-	expression tag	UNP D3RW14
A	403	HIS	-	expression tag	UNP D3RW14
A	404	HIS	-	expression tag	UNP D3RW14

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Chain	Residue	Modelled	Actual	Comment	Reference
A	405	HIS	-	expression tag	UNP D3RW14
A	406	HIS	-	expression tag	UNP D3RW14
B	1	MET	-	initiating methionine	UNP D3RW14
B	2	ALA	-	expression tag	UNP D3RW14
B	382	GLY	-	expression tag	UNP D3RW14
B	383	GLU	-	expression tag	UNP D3RW14
B	384	GLY	-	expression tag	UNP D3RW14
B	385	TRP	-	expression tag	UNP D3RW14
B	386	SER	-	expression tag	UNP D3RW14
B	387	HIS	-	expression tag	UNP D3RW14
B	388	PRO	-	expression tag	UNP D3RW14
B	389	GLN	-	expression tag	UNP D3RW14
B	390	PHE	-	expression tag	UNP D3RW14
B	391	GLU	-	expression tag	UNP D3RW14
B	392	LYS	-	expression tag	UNP D3RW14
B	393	GLY	-	expression tag	UNP D3RW14
B	394	VAL	-	expression tag	UNP D3RW14
B	395	GLU	-	expression tag	UNP D3RW14
B	396	GLY	-	expression tag	UNP D3RW14
B	397	HIS	-	expression tag	UNP D3RW14
B	398	HIS	-	expression tag	UNP D3RW14
B	399	HIS	-	expression tag	UNP D3RW14
B	400	HIS	-	expression tag	UNP D3RW14
B	401	HIS	-	expression tag	UNP D3RW14
B	402	HIS	-	expression tag	UNP D3RW14
B	403	HIS	-	expression tag	UNP D3RW14
B	404	HIS	-	expression tag	UNP D3RW14
B	405	HIS	-	expression tag	UNP D3RW14
B	406	HIS	-	expression tag	UNP D3RW14

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	166	Total O 166 166	0	0
2	B	201	Total O 201 201	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.24Å 90.43Å 65.62Å 90.00° 99.56° 90.00°	Depositor
Resolution (Å)	64.71 – 1.70 64.70 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (64.71-1.70) 99.2 (64.70-1.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 1.70Å)	Xtrriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.186 , 0.215 0.185 , 0.214	Depositor DCC
R_{free} test set	8138 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtrriage
Anisotropy	0.493	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.076 for l,-k,h	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6356	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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 >5	RMSZ	# Z >5
1	A	0.29	0/3090	0.44	0/4206
1	B	0.32	0/3022	0.48	0/4109
All	All	0.31	0/6112	0.46	0/8315

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	3027	0	2927	24	0
1	B	2962	0	2865	12	0
2	A	166	0	0	2	0
2	B	201	0	0	1	0
All	All	6356	0	5792	33	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 3.

The worst 5 of 33 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:200:GLU:HG3	1:A:333:TRP:HE1	1.49	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:PHE:HB3	1:A:196[B]:ARG:HG3	1.74	0.69
1:A:168[A]:MET:HE2	1:A:190:MET:H	1.56	0.68
1:A:7[A]:THR:HG21	2:A:535:HOH:O	1.94	0.67
1:A:390:PHE:HB2	1:B:330:VAL:HB	1.77	0.65

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 X-ray entries followed by that with respect to entries of similar resolution.

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	384/406 (95%)	377 (98%)	6 (2%)	1 (0%)	36	22
1	B	376/406 (93%)	371 (99%)	4 (1%)	1 (0%)	36	22
All	All	760/812 (94%)	748 (98%)	10 (1%)	2 (0%)	36	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	156	PHE
1	A	156	PHE

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	305/341 (89%)	300 (98%)	5 (2%)	55	41
1	B	304/341 (89%)	298 (98%)	6 (2%)	48	32
All	All	609/682 (89%)	598 (98%)	11 (2%)	59	36

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	180[A]	GLN
1	B	180[B]	GLN
1	B	182[B]	SER
1	B	182[A]	SER
1	A	324	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	379/406 (93%)	0.48	23 (6%) 27 29	12, 34, 59, 81	22 (5%)
1	B	372/406 (91%)	0.29	17 (4%) 37 41	12, 31, 52, 78	19 (5%)
All	All	751/812 (92%)	0.39	40 (5%) 32 35	12, 33, 57, 81	41 (5%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	386	SER	5.6
1	A	385	TRP	4.8
1	B	232	ILE	4.2
1	B	390	PHE	4.0
1	B	388	PRO	3.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.