



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 29, 2025 – 04:09 PM JST

PDB ID : 8Y68 / pdb\_00008y68  
Title : the crystal structure of apo CASK-CaMK  
Authors : Li, W.; Feng, W.  
Deposited on : 2024-02-02  
Resolution : 2.20 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

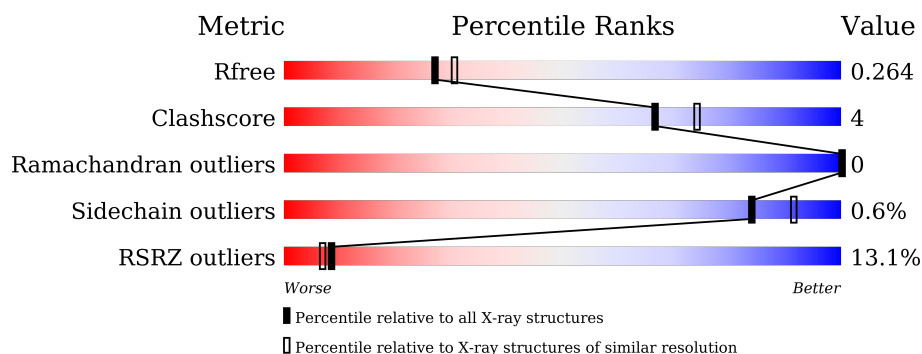
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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  $\geq 3$ , 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	338	<div> <div>11%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>7%</div> </div> </div>
1	B	338	<div> <div>14%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5154 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 Peripheral plasma membrane protein CASK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	1	0
			2519	1616	438	448	17			
1	B	314	Total	C	N	O	S	0	1	0
			2519	1616	438	448	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP O14936
A	-4	PRO	-	expression tag	UNP O14936
A	-3	GLY	-	expression tag	UNP O14936
A	-2	SER	-	expression tag	UNP O14936
A	-1	GLU	-	expression tag	UNP O14936
A	0	PHE	-	expression tag	UNP O14936
B	-5	GLY	-	expression tag	UNP O14936
B	-4	PRO	-	expression tag	UNP O14936
B	-3	GLY	-	expression tag	UNP O14936
B	-2	SER	-	expression tag	UNP O14936
B	-1	GLU	-	expression tag	UNP O14936
B	0	PHE	-	expression tag	UNP O14936

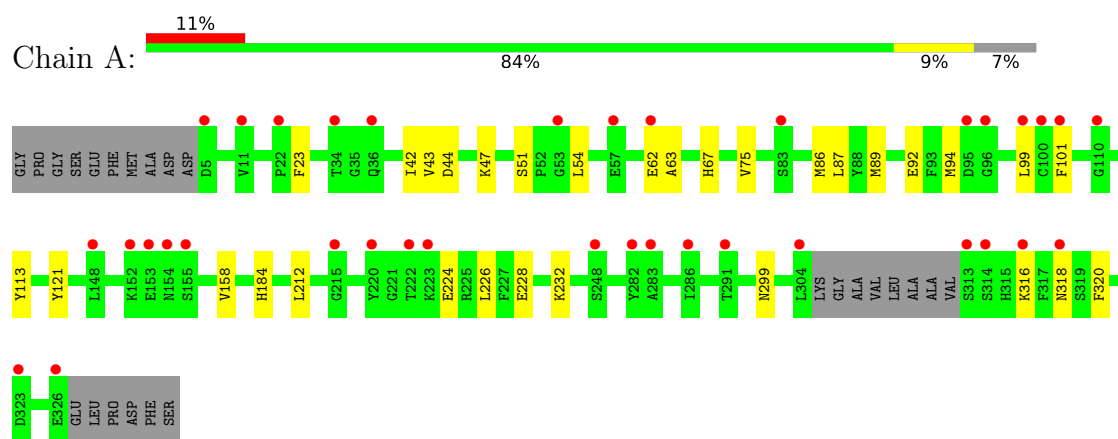
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	53	Total	O	0	0
			53	53		
2	B	63	Total	O	0	0
			63	63		

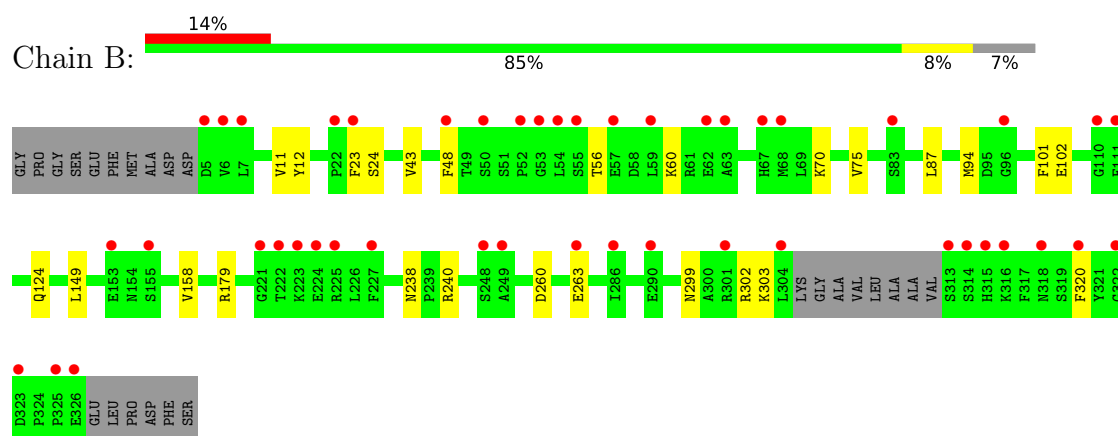
### 3 Residue-property plots [i](#)

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 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.

- Molecule 1: Peripheral plasma membrane protein CASK



- Molecule 1: Peripheral plasma membrane protein CASK



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.49Å 93.68Å 139.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.84 – 2.20 46.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.84-2.20) 89.4 (46.84-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.11 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, $R_{free}$	0.238 , 0.264 0.240 , 0.264	Depositor DCC
$R_{free}$ test set	1998 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.1	Xtriage
Anisotropy	0.523	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 55.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5154	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 56.85 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5766e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.37	0/2584	0.57	0/3486
1	B	0.14	0/2584	0.35	0/3486
All	All	0.28	0/5168	0.47	0/6972

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	2519	0	2516	20	0
1	B	2519	0	2516	16	0
2	A	53	0	0	0	0
2	B	63	0	0	0	0
All	All	5154	0	5032	36	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.

All (36) 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:B:24:SER:HB3	1:B:43:VAL:HG12	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:VAL:HG21	1:A:320:PHE:CE2	2.25	0.71
1:A:87:LEU:HD23	1:A:89:MET:HE2	1.79	0.63
1:A:44:ASP:HB3	1:A:47:LYS:HG2	1.79	0.62
1:B:260:ASP:HB3	1:B:263:GLU:HG2	1.86	0.57
1:A:23:PHE:O	1:A:43:VAL:HG23	2.04	0.57
1:A:75:VAL:HG21	1:A:320:PHE:CZ	2.40	0.57
1:B:102:GLU:HG3	1:B:149:LEU:HD23	1.90	0.53
1:A:43:VAL:CG1	1:A:87:LEU:HB3	2.41	0.51
1:A:43:VAL:HG12	1:A:87:LEU:HB3	1.93	0.51
1:B:101:PHE:CE1	1:B:303:LYS:HE3	2.46	0.50
1:B:238:ASN:HD21	1:B:240:ARG:NH1	2.10	0.49
1:A:94:MET:HG3	1:A:320:PHE:CE2	2.48	0.48
1:B:101:PHE:CE1	1:B:299:ASN:HB3	2.50	0.47
1:A:51:SER:HB3	1:A:54:LEU:HB2	1.96	0.47
1:A:224:GLU:O	1:A:228:GLU:HG2	2.14	0.47
1:B:56:THR:HG22	1:B:60:LYS:HE2	1.96	0.46
1:A:113:TYR:OH	1:A:212:LEU:O	2.30	0.45
1:A:94:MET:HG3	1:A:320:PHE:HE2	1.83	0.44
1:A:42:ILE:HG22	1:A:86:MET:HE3	2.00	0.44
1:A:63:ALA:O	1:A:67[B]:HIS:HB2	2.18	0.44
1:B:124:GLN:HB2	1:B:158:VAL:CG2	2.47	0.44
1:B:75:VAL:HG21	1:B:320:PHE:CZ	2.53	0.43
1:B:23:PHE:CD1	1:B:48:PHE:HA	2.53	0.43
1:A:99:LEU:HD11	1:A:121:TYR:CD2	2.54	0.42
1:B:43:VAL:HG22	1:B:87:LEU:HB3	2.01	0.42
1:B:11:VAL:HG13	1:B:12:TYR:CD2	2.54	0.42
1:A:101:PHE:CE1	1:A:299:ASN:HB3	2.54	0.42
1:A:184:HIS:HA	1:A:226:LEU:HD21	2.02	0.42
1:B:94:MET:HG3	1:B:320:PHE:HE2	1.85	0.42
1:A:228:GLU:O	1:A:232:LYS:HG3	2.19	0.41
1:B:299:ASN:HA	1:B:302:ARG:HD3	2.02	0.41
1:A:92:GLU:HG3	1:A:94:MET:HE3	2.03	0.41
1:A:316:LYS:C	1:A:318:ASN:N	2.78	0.40
1:B:94:MET:HG3	1:B:320:PHE:CE2	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	311/338 (92%)	300 (96%)	11 (4%)	0	100	100
1	B	311/338 (92%)	299 (96%)	12 (4%)	0	100	100
All	All	622/676 (92%)	599 (96%)	23 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	273/289 (94%)	271 (99%)	2 (1%)	81	90
1	B	273/289 (94%)	272 (100%)	1 (0%)	89	95
All	All	546/578 (94%)	543 (100%)	3 (0%)	84	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	GLU
1	A	158	VAL
1	B	179	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	36	GLN
1	A	184	HIS
1	B	145	HIS
1	B	238	ASN
1	B	272	ASN
1	B	315	HIS

### 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 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	314/338 (92%)	0.92	36 (11%) 11 9	30, 56, 96, 131	1 (0%)
1	B	314/338 (92%)	1.02	46 (14%) 7 6	28, 56, 101, 127	1 (0%)
All	All	628/676 (92%)	0.97	82 (13%) 8 7	28, 56, 99, 131	2 (0%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	23	PHE	4.5
1	B	304	LEU	4.1
1	B	22	PRO	4.1
1	A	323	ASP	4.0
1	A	110	GLY	4.0
1	B	111	PHE	4.0
1	B	318	ASN	3.9
1	B	53	GLY	3.7
1	B	50	SER	3.6
1	B	222	THR	3.5
1	B	323	ASP	3.4
1	B	325	PRO	3.3
1	B	52	PRO	3.2
1	A	222	THR	3.2
1	B	326	GLU	3.1
1	A	95	ASP	3.0
1	A	304	LEU	3.0
1	A	155	SER	3.0
1	A	215	GLY	2.9
1	A	316	LYS	2.9
1	B	314	SER	2.9
1	A	326	GLU	2.9
1	B	221	GLY	2.9
1	A	318	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	283	ALA	2.9
1	B	316	LYS	2.8
1	A	11	VAL	2.8
1	B	59	LEU	2.7
1	A	100	CYS	2.7
1	A	282	TYR	2.7
1	B	315	HIS	2.7
1	A	62	GLU	2.7
1	B	62	GLU	2.7
1	B	54	LEU	2.6
1	B	313	SER	2.6
1	B	68	MET	2.6
1	A	154	ASN	2.6
1	A	291	THR	2.6
1	A	96	GLY	2.6
1	B	263	GLU	2.5
1	A	220	TYR	2.5
1	A	286	ILE	2.5
1	B	5	ASP	2.5
1	A	99	LEU	2.5
1	A	153	GLU	2.5
1	B	227	PHE	2.5
1	B	7	LEU	2.5
1	B	67[A]	HIS	2.5
1	A	152	LYS	2.4
1	B	6	VAL	2.4
1	A	36	GLN	2.4
1	A	22	PRO	2.4
1	B	48	PHE	2.4
1	B	320	PHE	2.4
1	A	5	ASP	2.4
1	B	57	GLU	2.4
1	B	301	ARG	2.4
1	B	322	GLY	2.4
1	B	83	SER	2.3
1	B	55	SER	2.3
1	B	96	GLY	2.3
1	A	313	SER	2.3
1	B	286	ILE	2.3
1	A	101	PHE	2.2
1	A	34	THR	2.2
1	B	249	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	314	SER	2.2
1	A	53	GLY	2.2
1	B	224	GLU	2.2
1	B	63	ALA	2.1
1	B	223	LYS	2.1
1	A	57	GLU	2.1
1	B	153	GLU	2.1
1	B	290	GLU	2.1
1	B	110	GLY	2.1
1	B	155	SER	2.1
1	B	225	ARG	2.1
1	A	148	LEU	2.1
1	A	223	LYS	2.1
1	A	248	SER	2.0
1	B	248	SER	2.0
1	A	83	SER	2.0

## 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.