



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:40 am BST

PDB ID : 4NCD  
Title : Crystal Structure of Class 5 Fimbriae Chaperone CfaA  
Authors : Bao, R.; Xia, D.  
Deposited on : 2013-10-24  
Resolution : 2.04 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.

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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) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

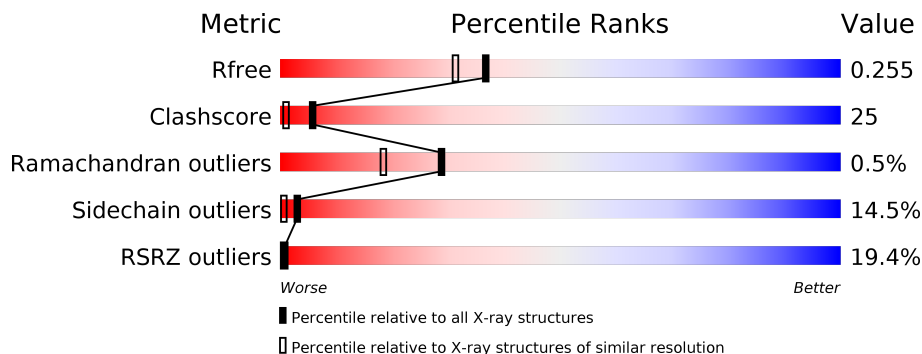
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.04 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))
$R_{free}$	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 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	246	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1818 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 Gram-negative pili assembly chaperone, N-terminal domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	211	1698	1093	283	319	3	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	LEU	-	EXPRESSION TAG	UNP N4NNE0
A	221	GLU	-	EXPRESSION TAG	UNP N4NNE0
A	222	HIS	-	EXPRESSION TAG	UNP N4NNE0
A	223	HIS	-	EXPRESSION TAG	UNP N4NNE0
A	224	HIS	-	EXPRESSION TAG	UNP N4NNE0
A	225	HIS	-	EXPRESSION TAG	UNP N4NNE0
A	226	HIS	-	EXPRESSION TAG	UNP N4NNE0
A	227	HIS	-	EXPRESSION TAG	UNP N4NNE0

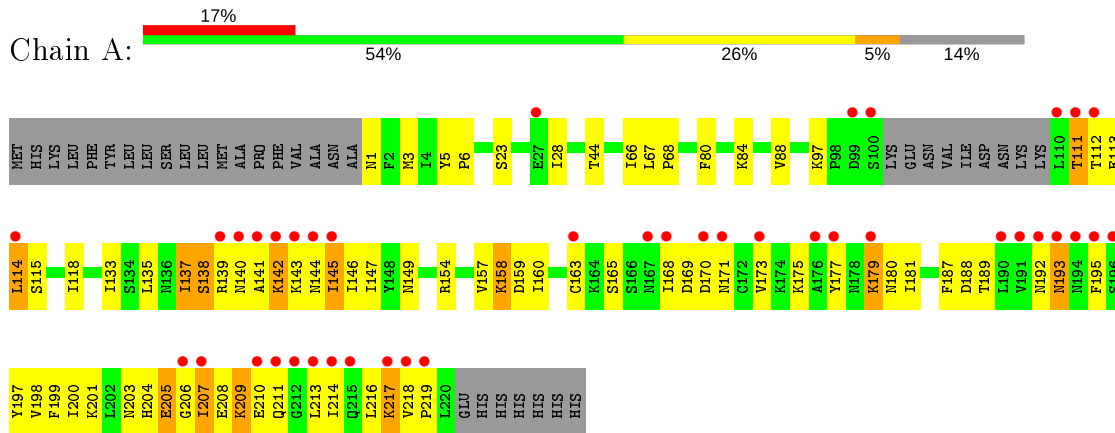
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	120	120	120	0	0

### 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.

- Molecule 1: Gram-negative pili assembly chaperone, N-terminal domain protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.61Å 28.58Å 90.72Å 90.00° 118.89° 90.00°	Depositor
Resolution (Å)	39.72 – 2.04 39.71 – 2.04	Depositor EDS
% Data completeness (in resolution range)	96.7 (39.72-2.04) 91.0 (39.71-2.04)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.21 (at 2.03Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.217 , 0.256 0.218 , 0.255	Depositor DCC
$R_{free}$ test set	1474 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.4	Xtrriage
Anisotropy	0.146	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 61.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	1818	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.40% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [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	0.56	1/1729 (0.1%)	0.64	1/2336 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219	PRO	N-CD	5.14	1.55	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	218	VAL	C-N-CD	5.75	140.47	128.40

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	1698	0	1743	87	0
2	A	120	0	0	5	0
All	All	1818	0	1743	87	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 25.

All (87) 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:206:GLY:O	1:A:207:ILE:HG22	1.11	1.25
1:A:201:LYS:NZ	1:A:211:GLN:HE21	1.42	1.15
1:A:199:PHE:CD2	1:A:214:ILE:HG22	1.84	1.12
1:A:206:GLY:O	1:A:207:ILE:CG2	2.01	1.08
1:A:114:LEU:HD12	1:A:115:SER:N	1.68	1.08
1:A:142:LYS:HD3	1:A:142:LYS:H	1.02	1.08
1:A:137:ILE:HD12	1:A:138:SER:H	1.15	1.07
1:A:201:LYS:HD2	1:A:211:GLN:NE2	1.72	1.04
1:A:142:LYS:N	1:A:142:LYS:HD3	1.74	1.02
1:A:154:ARG:NH2	1:A:205:GLU:OE1	1.93	1.02
1:A:199:PHE:CE2	1:A:214:ILE:CG2	2.43	1.02
1:A:199:PHE:CE2	1:A:214:ILE:HG22	1.97	0.99
1:A:142:LYS:O	1:A:144:ASN:HB2	1.63	0.97
1:A:179:LYS:HD2	1:A:180:ASN:O	1.67	0.94
1:A:201:LYS:CD	1:A:211:GLN:NE2	2.30	0.94
1:A:142:LYS:H	1:A:142:LYS:CD	1.80	0.94
1:A:137:ILE:HD12	1:A:138:SER:N	1.82	0.92
1:A:201:LYS:HZ2	1:A:211:GLN:HE21	1.10	0.92
1:A:145:ILE:HG21	1:A:217:LYS:HE2	1.51	0.92
1:A:142:LYS:N	1:A:142:LYS:CD	2.30	0.91
1:A:201:LYS:HD2	1:A:211:GLN:HE22	1.36	0.89
1:A:139:ARG:HH21	1:A:139:ARG:HG2	1.39	0.88
1:A:199:PHE:CE2	1:A:214:ILE:HG21	2.13	0.82
1:A:114:LEU:HD12	1:A:115:SER:H	1.43	0.81
1:A:199:PHE:HE2	1:A:214:ILE:HG21	1.46	0.80
1:A:118:ILE:O	2:A:387:HOH:O	1.99	0.80
1:A:207:ILE:O	1:A:209:LYS:HE3	1.84	0.78
1:A:142:LYS:HG2	1:A:144:ASN:HD22	1.47	0.78
1:A:201:LYS:NZ	1:A:211:GLN:NE2	2.28	0.78
1:A:142:LYS:HG2	1:A:144:ASN:ND2	2.01	0.75
1:A:201:LYS:HZ2	1:A:211:GLN:NE2	1.87	0.71
1:A:145:ILE:HG21	1:A:217:LYS:CE	2.23	0.69
1:A:68:PRO:HG3	2:A:417:HOH:O	1.92	0.68
1:A:201:LYS:CE	1:A:211:GLN:HE21	2.07	0.68
1:A:80:PHE:O	2:A:308:HOH:O	2.13	0.67
1:A:179:LYS:CD	1:A:180:ASN:O	2.45	0.65
1:A:214:ILE:HG13	1:A:214:ILE:O	1.97	0.64
1:A:135:LEU:HD12	1:A:213:LEU:CD2	2.29	0.64
1:A:208:GLU:HA	1:A:208:GLU:OE1	1.97	0.63
1:A:139:ARG:NH2	1:A:139:ARG:HG2	2.12	0.61
1:A:111:THR:HG22	1:A:112:THR:N	2.15	0.61
1:A:135:LEU:HD12	1:A:213:LEU:HD23	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ASN:H	1:A:192:ASN:HA	1.66	0.60
1:A:197:TYR:OH	1:A:216:LEU:HD12	2.02	0.59
1:A:207:ILE:O	1:A:209:LYS:CE	2.51	0.59
1:A:211:GLN:HA	1:A:211:GLN:OE1	2.04	0.58
1:A:137:ILE:HD13	1:A:147:ILE:HD13	1.87	0.57
1:A:146:ILE:HD13	1:A:188:ASP:HA	1.87	0.57
1:A:199:PHE:HE2	1:A:214:ILE:CG2	2.02	0.56
1:A:201:LYS:HZ3	1:A:211:GLN:HE21	1.43	0.56
1:A:175:LYS:HB3	1:A:177:TYR:CE1	2.41	0.55
1:A:142:LYS:O	1:A:143:LYS:C	2.45	0.55
1:A:142:LYS:O	1:A:144:ASN:CB	2.48	0.55
1:A:66:ILE:O	1:A:68:PRO:HD3	2.07	0.54
1:A:199:PHE:HD2	1:A:214:ILE:HG22	1.63	0.53
1:A:179:LYS:HD2	1:A:180:ASN:C	2.27	0.53
1:A:139:ARG:HB2	1:A:143:LYS:HA	1.90	0.53
1:A:157:VAL:O	1:A:177:TYR:O	2.27	0.53
1:A:140:ASN:CB	1:A:142:LYS:O	2.58	0.52
1:A:139:ARG:HH21	1:A:139:ARG:CG	2.14	0.52
1:A:84:LYS:HD3	2:A:416:HOH:O	2.09	0.52
1:A:149:ASN:ND2	1:A:181:ILE:O	2.40	0.52
1:A:139:ARG:NH2	1:A:139:ARG:CG	2.73	0.51
1:A:217:LYS:NZ	1:A:217:LYS:CB	2.72	0.51
1:A:201:LYS:CE	1:A:211:GLN:NE2	2.70	0.50
1:A:138:SER:HB2	2:A:394:HOH:O	2.11	0.50
1:A:146:ILE:CD1	1:A:188:ASP:HA	2.42	0.50
1:A:193:ASN:OD1	1:A:193:ASN:N	2.45	0.49
1:A:140:ASN:HB2	1:A:142:LYS:O	2.14	0.48
1:A:139:ARG:HD2	1:A:143:LYS:HG3	1.96	0.47
1:A:177:TYR:CD2	1:A:187:PHE:HE2	2.32	0.47
1:A:206:GLY:O	1:A:207:ILE:CB	2.62	0.47
1:A:175:LYS:CB	1:A:177:TYR:CE1	2.99	0.45
1:A:158:LYS:HG3	1:A:203:ASN:OD1	2.15	0.45
1:A:23:SER:HB2	1:A:67:LEU:HG	1.99	0.45
1:A:145:ILE:O	1:A:189:THR:HG23	2.17	0.45
1:A:168:ILE:O	1:A:169:ASP:HB3	2.18	0.44
1:A:142:LYS:HD2	1:A:142:LYS:N	2.29	0.43
1:A:143:LYS:HE2	1:A:217:LYS:HD2	2.00	0.43
1:A:160:ILE:HG12	1:A:200:ILE:HD13	2.00	0.43
1:A:141:ALA:HB3	1:A:142:LYS:CD	2.49	0.43
1:A:163:CYS:O	1:A:195:PHE:HB3	2.20	0.42
1:A:143:LYS:CE	1:A:217:LYS:HD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ILE:HD11	1:A:145:ILE:HB	2.03	0.41
1:A:179:LYS:HD3	1:A:180:ASN:N	2.36	0.40
1:A:5:TYR:CG	1:A:6:PRO:HA	2.56	0.40
1:A:195:PHE:HB2	1:A:217:LYS:HZ1	1.86	0.40

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	207/246 (84%)	201 (97%)	5 (2%)	1 (0%)	29 18

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	207	ILE

### 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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	193/226 (85%)	165 (86%)	28 (14%)	3 1

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ASN
1	A	3	MET
1	A	28	ILE
1	A	44	THR
1	A	88	VAL
1	A	97	LYS
1	A	111	THR
1	A	113	GLU
1	A	114	LEU
1	A	133	ILE
1	A	137	ILE
1	A	138	SER
1	A	142	LYS
1	A	145	ILE
1	A	158	LYS
1	A	159	ASP
1	A	165	SER
1	A	170	ASP
1	A	171	ASN
1	A	173	VAL
1	A	179	LYS
1	A	193	ASN
1	A	198	VAL
1	A	204	HIS
1	A	205	GLU
1	A	209	LYS
1	A	210	GLU
1	A	217	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	211	GLN

### 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

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	211/246 (85%)	0.85	41 (19%) <b>1</b> <b>0</b>	17, 45, 86, 97	2 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	110	LEU	10.3
1	A	191	VAL	6.6
1	A	112	THR	6.5
1	A	171	ASN	5.8
1	A	145	ILE	5.2
1	A	168	ILE	5.0
1	A	218	VAL	4.9
1	A	192	ASN	4.7
1	A	219	PRO	4.7
1	A	207	ILE	4.6
1	A	176	ALA	4.2
1	A	177	TYR	4.1
1	A	141	ALA	3.8
1	A	206	GLY	3.8
1	A	139	ARG	3.7
1	A	142	LYS	3.6
1	A	99	ASP	3.5
1	A	173	VAL	3.4
1	A	194	ASN	3.4
1	A	27	GLU	3.2
1	A	210	GLU	3.1
1	A	214	ILE	3.1
1	A	213	LEU	3.1
1	A	167	ASN	3.0
1	A	144	ASN	2.7
1	A	100	SER	2.6
1	A	114	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	217	LYS	2.5
1	A	193	ASN	2.5
1	A	215	GLN	2.5
1	A	170	ASP	2.5
1	A	163	CYS	2.5
1	A	140	ASN	2.4
1	A	143	LYS	2.4
1	A	196	SER	2.4
1	A	195	PHE	2.4
1	A	211	GLN	2.2
1	A	111	THR	2.2
1	A	179	LYS	2.1
1	A	212	GLY	2.1
1	A	190	LEU	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 carbohydrates 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.