



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 22, 2026 – 04:41 PM JST

PDB ID : 9VO5 / pdb\_00009vo5  
Title : X-ray structure of Clostridium perfringens pili CppB-D3D4D5-CppA covalent complex  
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Deposited on : 2025-07-01  
Resolution : 1.85 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](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 Phenix2.0  
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

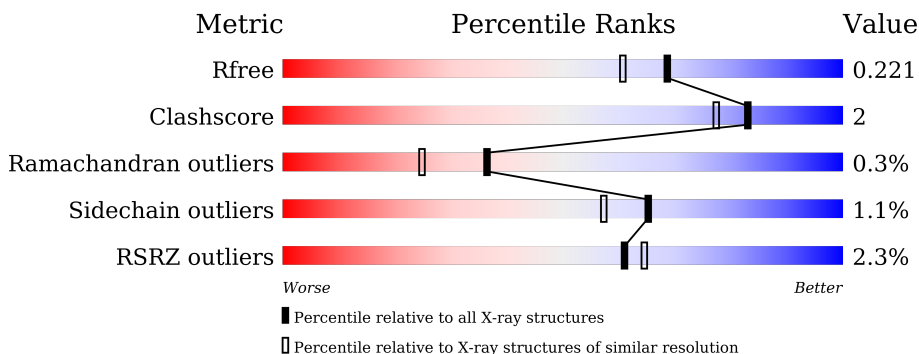
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	453	 92% 5% .
1	C	453	 90% 6% .
2	B	363	 93% 6% .
2	D	363	 87% 11% .

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14071 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 Probable surface protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	441	Total	C	N	O	S	0	0	0
			3419	2154	554	709	2			
1	C	439	Total	C	N	O	S	0	0	0
			3406	2147	552	705	2			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	MET	-	initiating methionine	UNP Q8XP10
A	476	HIS	-	expression tag	UNP Q8XP10
A	477	HIS	-	expression tag	UNP Q8XP10
A	478	HIS	-	expression tag	UNP Q8XP10
A	479	HIS	-	expression tag	UNP Q8XP10
A	480	HIS	-	expression tag	UNP Q8XP10
A	481	HIS	-	expression tag	UNP Q8XP10
C	29	MET	-	initiating methionine	UNP Q8XP10
C	476	HIS	-	expression tag	UNP Q8XP10
C	477	HIS	-	expression tag	UNP Q8XP10
C	478	HIS	-	expression tag	UNP Q8XP10
C	479	HIS	-	expression tag	UNP Q8XP10
C	480	HIS	-	expression tag	UNP Q8XP10
C	481	HIS	-	expression tag	UNP Q8XP10

- Molecule 2 is a protein called SpaA-like prealbumin fold domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	358	Total	C	N	O	S	0	0	0
			2845	1818	464	561	2			
2	D	356	Total	C	N	O	S	0	0	0
			2836	1813	462	559	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	326	MET	-	initiating methionine	UNP Q8XP11
D	326	MET	-	initiating methionine	UNP Q8XP11

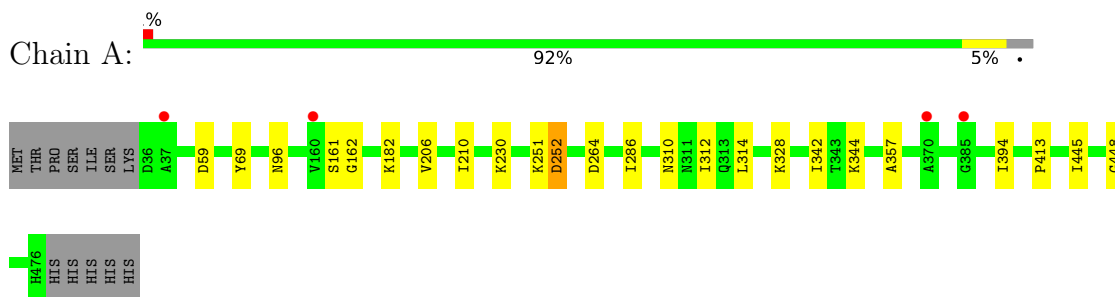
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	499	Total O 499 499	0	0
3	B	319	Total O 319 319	0	0
3	C	476	Total O 476 476	0	0
3	D	271	Total O 271 271	0	0

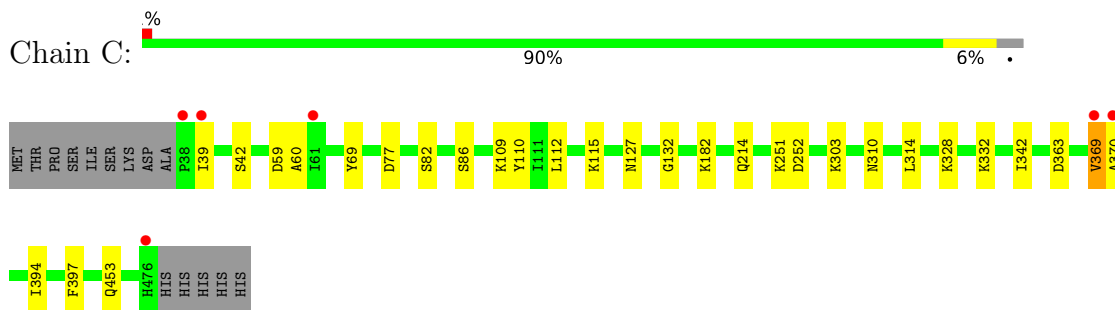
### 3 Residue-property plots [i](#)

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.

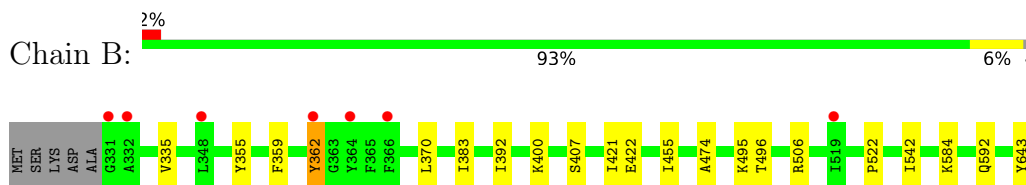
- Molecule 1: Probable surface protein



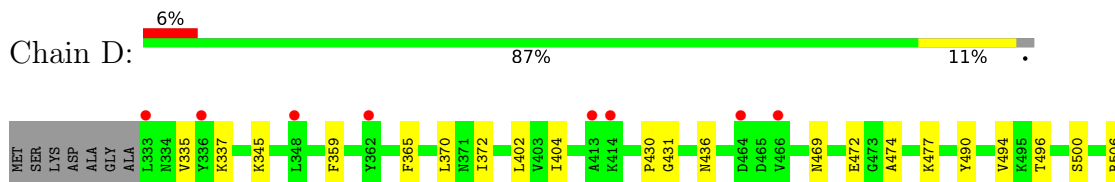
- Molecule 1: Probable surface protein



- Molecule 2: SpaA-like prealbumin fold domain-containing protein



- Molecule 2: SpaA-like prealbumin fold domain-containing protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.36Å 70.71Å 110.59Å 93.63° 107.20° 89.90°	Depositor
Resolution (Å)	48.36 – 1.85 48.36 – 1.85	Depositor EDS
% Data completeness (in resolution range)	95.6 (48.36-1.85) 95.6 (48.36-1.85)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.21 (at 1.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0430	Depositor
R, $R_{free}$	0.189 , 0.216 0.196 , 0.221	Depositor DCC
$R_{free}$ test set	7902 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.4	Xtrriage
Anisotropy	0.094	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 37.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14071	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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	0.44	0/3473	0.76	0/4697
1	C	0.43	0/3460	0.74	0/4678
2	B	0.44	0/2893	0.73	0/3905
2	D	0.44	0/2884	0.73	0/3893
All	All	0.44	0/12710	0.74	0/17173

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	3419	0	3363	12	0
1	C	3406	0	3355	16	0
2	B	2845	0	2886	17	0
2	D	2836	0	2878	21	0
3	A	499	0	0	0	0
3	B	319	0	0	0	0
3	C	476	0	0	0	0
3	D	271	0	0	0	0
All	All	14071	0	12482	61	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 2.

The worst 5 of 61 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)
2:D:666:LYS:HB2	2:D:673:TYR:CE1	2.15	0.79
2:B:359:PHE:HZ	2:B:370:LEU:HD21	1.59	0.68
1:A:206:VAL:HG21	1:A:312:ILE:HD13	1.76	0.68
2:B:359:PHE:CZ	2:B:370:LEU:HD21	2.28	0.67
2:D:359:PHE:CE2	2:D:370:LEU:HD21	2.32	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	439/453 (97%)	430 (98%)	7 (2%)	2 (0%)	24 13
1	C	437/453 (96%)	429 (98%)	7 (2%)	1 (0%)	43 31
2	B	356/363 (98%)	347 (98%)	9 (2%)	0	100 100
2	D	354/363 (98%)	341 (96%)	12 (3%)	1 (0%)	36 25
All	All	1586/1632 (97%)	1547 (98%)	35 (2%)	4 (0%)	36 25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	GLY
1	C	214	GLN
2	D	667	ASN
1	A	252	ASP

### 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	382/394 (97%)	380 (100%)	2 (0%)	81	77
1	C	381/394 (97%)	376 (99%)	5 (1%)	61	51
2	B	325/329 (99%)	323 (99%)	2 (1%)	78	73
2	D	325/329 (99%)	319 (98%)	6 (2%)	51	40
All	All	1413/1446 (98%)	1398 (99%)	15 (1%)	65	57

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	332	LYS
2	D	611	LYS
1	C	369	VAL
2	D	649	GLU
2	D	506	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	592	GLN
2	D	618	ASN
1	A	350	ASN
1	A	430	ASN
1	C	80	ASN

### 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 [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, 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	441/453 (97%)	-0.04	4 (0%) 81 84	17, 26, 46, 68	0
1	C	439/453 (96%)	-0.00	6 (1%) 73 77	17, 27, 51, 77	0
2	B	358/363 (98%)	0.25	7 (1%) 65 68	17, 33, 57, 88	0
2	D	356/363 (98%)	0.51	20 (5%) 30 33	21, 35, 70, 95	0
All	All	1594/1632 (97%)	0.16	37 (2%) 61 64	17, 30, 56, 95	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	38	PRO	4.7
2	D	413	ALA	4.0
1	C	39	ILE	4.0
2	B	366	PHE	3.9
2	D	662	ILE	3.3

### 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.