



wwPDB EM Validation Summary Report ⓘ

May 24, 2026 – 02:07 AM JST

PDB ID : 9VEG / pdb_00009veg
EMDB ID : EMD-65007
Title : Structural basis for the assembly and translocation of the Vip1-Vip2 insecticidal binary toxin from *Bacillus thuringiensis*
Authors : Chen, P.; Zhao, T.
Deposited on : 2025-06-09
Resolution : 3.05 Å(reported)

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 : **FAILED**
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

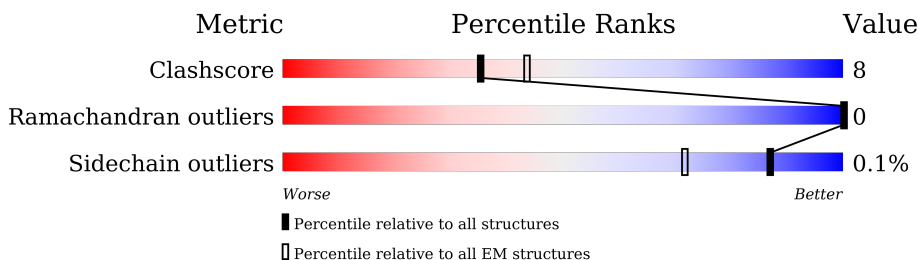
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 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
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	656	65% 13% 22%
1	B	656	65% 12% 23%
1	C	656	65% 12% 23%
1	F	656	60% 19% 22%
1	G	656	65% 13% 22%
2	H	400	74% 26%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 23058 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 Vip1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	511	Total	C	N	O	S	0	0
			3982	2486	662	824	10		
1	B	506	Total	C	N	O	S	0	0
			3947	2467	654	816	10		
1	C	504	Total	C	N	O	S	0	0
			3934	2460	652	812	10		
1	F	514	Total	C	N	O	S	0	0
			4004	2499	665	830	10		
1	G	512	Total	C	N	O	S	0	0
			3989	2491	663	825	10		

- Molecule 2 is a protein called Vip2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	400	Total	C	N	O	S	0	0
			3188	2018	532	626	12		

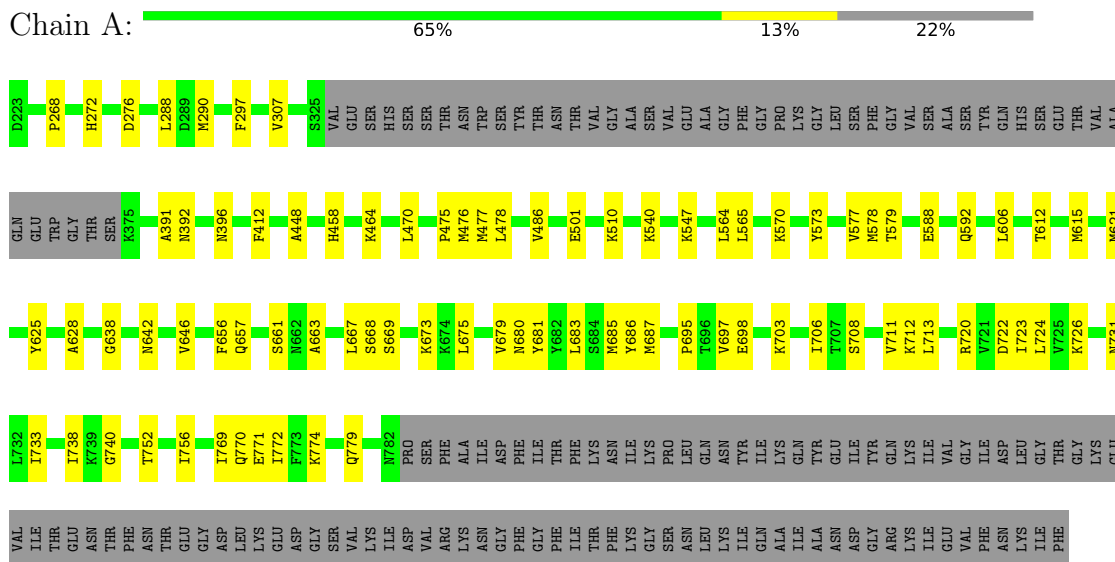
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	3	Total	Ca	0
			3	3	
3	B	3	Total	Ca	0
			3	3	
3	C	3	Total	Ca	0
			3	3	
3	F	2	Total	Ca	0
			2	2	
3	G	3	Total	Ca	0
			3	3	

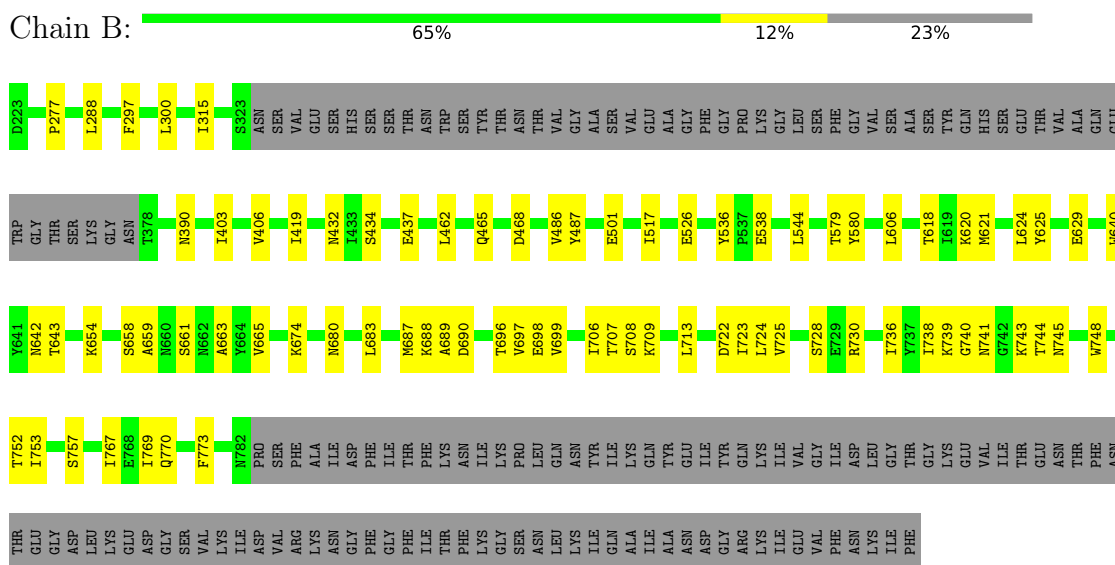
3 Residue-property plots

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: Vip1



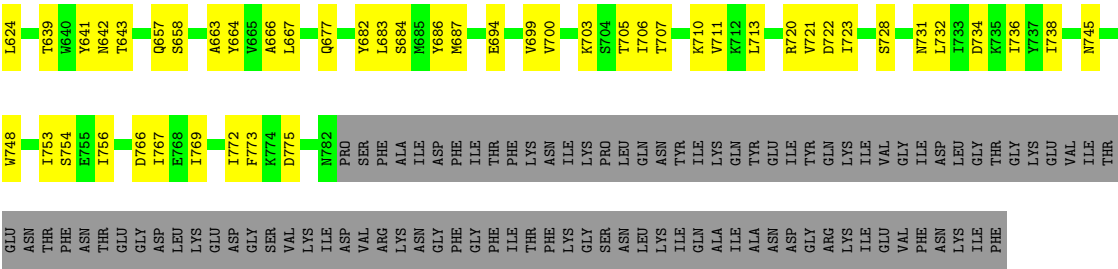
- Molecule 1: Vip1



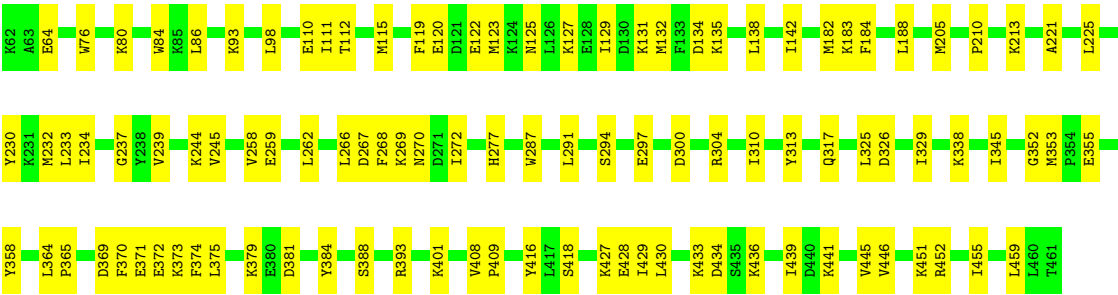
- Molecule 1: Vip1

23%





● Molecule 2: Vip2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107143	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.20	0/4051	0.36	0/5492
1	B	0.19	0/4016	0.35	0/5446
1	C	0.16	0/4003	0.35	0/5428
1	F	0.15	0/4073	0.35	0/5522
1	G	0.18	0/4058	0.36	0/5502
2	H	0.14	0/3241	0.34	0/4345
All	All	0.17	0/23442	0.35	0/31735

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	3982	0	3900	57	0
1	B	3947	0	3867	54	0
1	C	3934	0	3854	50	0
1	F	4004	0	3920	83	0
1	G	3989	0	3909	53	0
2	H	3188	0	3205	69	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	F	2	0	0	0	0
3	G	3	0	0	0	0
All	All	23058	0	22655	363	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 8.

The worst 5 of 363 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:H:86:LEU:CB	2:H:132:MET:HE2	1.81	1.10
2:H:86:LEU:HB3	2:H:132:MET:HE2	1.47	0.95
2:H:86:LEU:HB2	2:H:132:MET:HE2	1.48	0.94
1:B:624:LEU:HD12	1:B:753:ILE:HD11	1.50	0.91
2:H:86:LEU:HB3	2:H:132:MET:CE	2.00	0.90

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 PDB entries followed by that with respect to all EM entries.

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	507/656 (77%)	494 (97%)	13 (3%)	0	100	100
1	B	502/656 (76%)	487 (97%)	15 (3%)	0	100	100
1	C	500/656 (76%)	487 (97%)	13 (3%)	0	100	100
1	F	510/656 (78%)	487 (96%)	23 (4%)	0	100	100
1	G	508/656 (77%)	495 (97%)	13 (3%)	0	100	100
2	H	398/400 (100%)	386 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2925/3680 (80%)	2836 (97%)	89 (3%)	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 PDB entries followed by that with respect to all EM entries.

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	450/573 (78%)	450 (100%)	0	100	100
1	B	446/573 (78%)	446 (100%)	0	100	100
1	C	444/573 (78%)	444 (100%)	0	100	100
1	F	453/573 (79%)	452 (100%)	1 (0%)	87	87
1	G	451/573 (79%)	451 (100%)	0	100	100
2	H	351/351 (100%)	350 (100%)	1 (0%)	86	85
All	All	2595/3216 (81%)	2593 (100%)	2 (0%)	87	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	682	TYR
2	H	455	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	604	ASN
1	G	616	ASN
1	C	676	ASN
2	H	107	ASN
1	F	727	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](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.