



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 7, 2023 – 01:53 AM EST

PDB ID : 8FZZ
Title : Phocaeicola vulgatus type VI secretion system Ntox15 effector and immunity Tde2/Tdi2
Authors : Bosch, D.E.; Mougous, J.D.
Deposited on : 2023-01-30
Resolution : 2.68 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

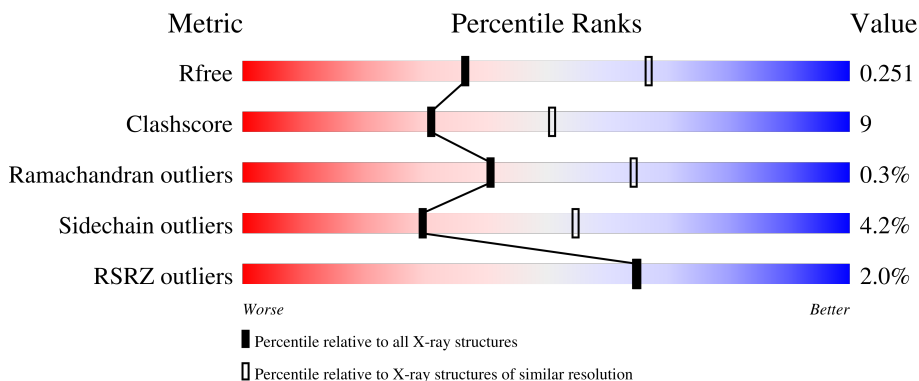
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.68 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	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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	201	 3% 49% 20% 30%
1	C	201	 2% 52% 18% 29%
2	B	202	 71% 24% 5%
2	D	202	 76% 19% 5%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5610 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 Ntox15 domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	141	1183	755	203	220	5	0	0	0
1	C	142	1206	770	211	220	5	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	162	MSE	-	initiating methionine	UNP R9H4Y9
A	163	GLY	-	expression tag	UNP R9H4Y9
A	164	SER	-	expression tag	UNP R9H4Y9
A	165	HIS	-	expression tag	UNP R9H4Y9
A	166	HIS	-	expression tag	UNP R9H4Y9
A	167	HIS	-	expression tag	UNP R9H4Y9
A	168	HIS	-	expression tag	UNP R9H4Y9
A	169	HIS	-	expression tag	UNP R9H4Y9
A	170	HIS	-	expression tag	UNP R9H4Y9
A	171	SER	-	expression tag	UNP R9H4Y9
A	172	GLN	-	expression tag	UNP R9H4Y9
A	173	ASP	-	expression tag	UNP R9H4Y9
C	162	MSE	-	initiating methionine	UNP R9H4Y9
C	163	GLY	-	expression tag	UNP R9H4Y9
C	164	SER	-	expression tag	UNP R9H4Y9
C	165	HIS	-	expression tag	UNP R9H4Y9
C	166	HIS	-	expression tag	UNP R9H4Y9
C	167	HIS	-	expression tag	UNP R9H4Y9
C	168	HIS	-	expression tag	UNP R9H4Y9
C	169	HIS	-	expression tag	UNP R9H4Y9
C	170	HIS	-	expression tag	UNP R9H4Y9
C	171	SER	-	expression tag	UNP R9H4Y9
C	172	GLN	-	expression tag	UNP R9H4Y9
C	173	ASP	-	expression tag	UNP R9H4Y9

- Molecule 2 is a protein called DUF1851 domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	196	1609	1050	243	304	4	8	0	0	0
2	D	196	1609	1050	243	304	4	8	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	197	HIS	-	expression tag	UNP R9H4T6
B	198	HIS	-	expression tag	UNP R9H4T6
B	199	HIS	-	expression tag	UNP R9H4T6
B	200	HIS	-	expression tag	UNP R9H4T6
B	201	HIS	-	expression tag	UNP R9H4T6
B	202	HIS	-	expression tag	UNP R9H4T6
D	197	HIS	-	expression tag	UNP R9H4T6
D	198	HIS	-	expression tag	UNP R9H4T6
D	199	HIS	-	expression tag	UNP R9H4T6
D	200	HIS	-	expression tag	UNP R9H4T6
D	201	HIS	-	expression tag	UNP R9H4T6
D	202	HIS	-	expression tag	UNP R9H4T6

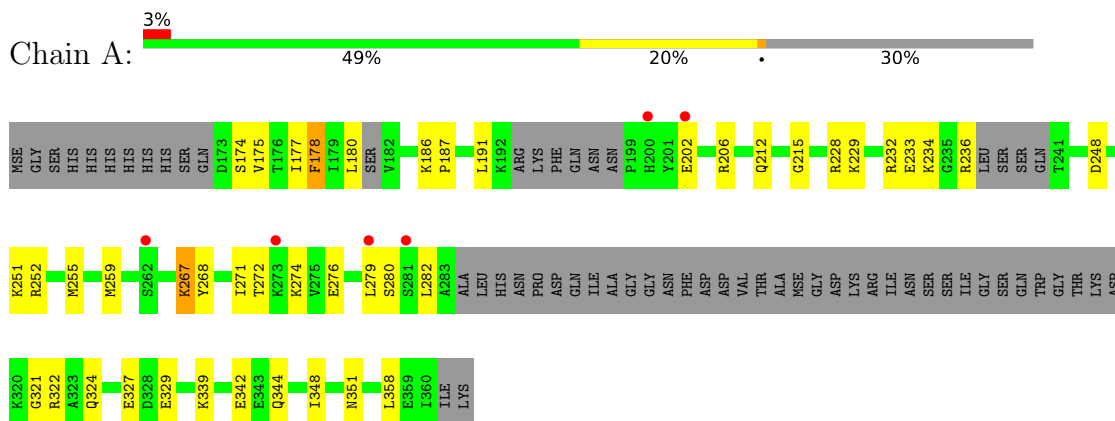
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	2	Total 2	O 2	0	0
3	D	1	Total 1	O 1	0	0

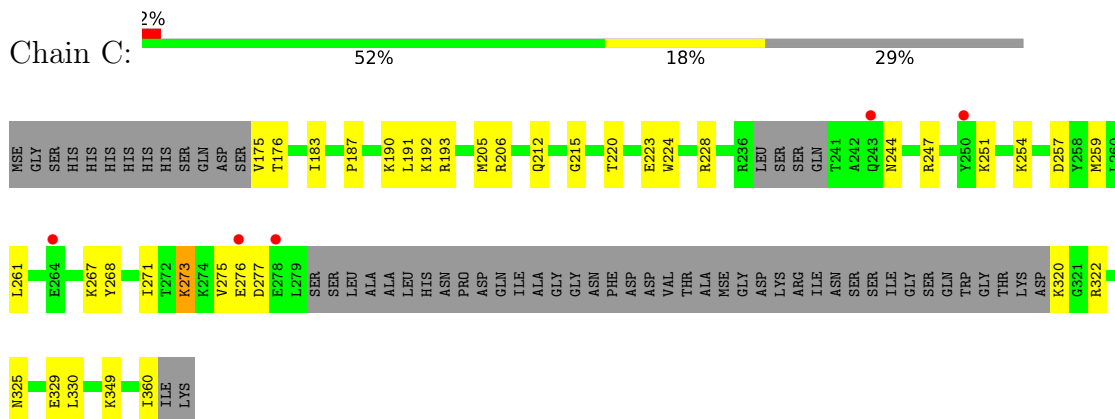
3 Residue-property plots [i](#)

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.

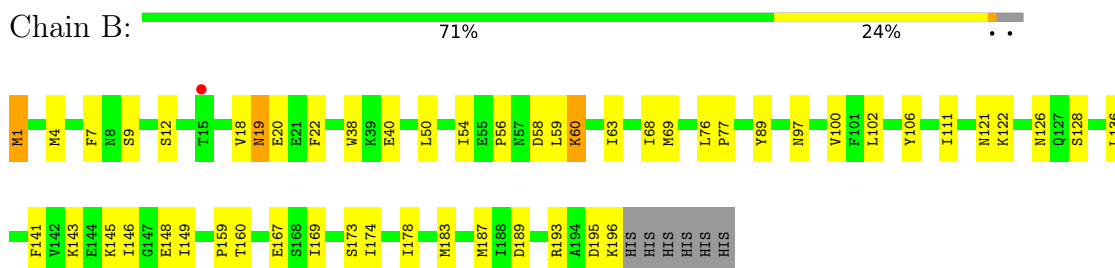
- Molecule 1: Ntox15 domain-containing protein



- Molecule 1: Ntox15 domain-containing protein



- Molecule 2: DUF1851 domain-containing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.31Å 84.77Å 175.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.04 – 2.68 39.04 – 2.68	Depositor EDS
% Data completeness (in resolution range)	92.1 (39.04-2.68) 92.1 (39.04-2.68)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.69Å)	Xtrriage
Refinement program	PHENIX v1.20.1	Depositor
R, R_{free}	0.185 , 0.251 0.186 , 0.251	Depositor DCC
R_{free} test set	1843 reflections (8.49%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtrriage
Anisotropy	0.031	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5610	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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	0.41	0/1194	0.59	0/1582
1	C	0.48	0/1220	0.63	0/1619
2	B	0.43	0/1641	0.58	0/2206
2	D	0.47	0/1641	0.60	0/2206
All	All	0.45	0/5696	0.60	0/7613

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	1183	0	1204	32	0
1	C	1206	0	1230	23	0
2	B	1609	0	1557	34	0
2	D	1609	0	1557	32	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
All	All	5610	0	5548	102	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 9.

The worst 5 of 102 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:B:183:MSE:HG2	2:B:187:MSE:HE3	1.64	0.79
2:B:4:MSE:HE3	2:B:121:ASN:HB3	1.63	0.79
2:D:169:ILE:HD13	2:D:172:ILE:HD12	1.71	0.71
1:A:180:LEU:HD13	1:A:348:ILE:HG21	1.74	0.69
2:B:195:ASP:O	2:B:196:LYS:HG3	1.94	0.67

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	131/201 (65%)	122 (93%)	9 (7%)	0	100	100
1	C	136/201 (68%)	132 (97%)	4 (3%)	0	100	100
2	B	194/202 (96%)	183 (94%)	11 (6%)	0	100	100
2	D	194/202 (96%)	185 (95%)	7 (4%)	2 (1%)	15	34
All	All	655/806 (81%)	622 (95%)	31 (5%)	2 (0%)	41	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	114	ASP
2	D	113	PRO

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	130/174 (75%)	123 (95%)	7 (5%)	22	44
1	C	132/174 (76%)	124 (94%)	8 (6%)	18	38
2	B	180/178 (101%)	173 (96%)	7 (4%)	32	58
2	D	180/178 (101%)	176 (98%)	4 (2%)	52	77
All	All	622/704 (88%)	596 (96%)	26 (4%)	30	55

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	193	ARG
1	C	254	LYS
2	D	128	SER
1	C	244	ASN
1	C	273	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	33	GLN
1	C	196	GLN
2	D	65	GLN
1	A	208	GLN
1	A	200	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 monosaccharides 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, 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	136/201 (67%)	0.32	6 (4%) 34 32	24, 40, 59, 69	0
1	C	137/201 (68%)	-0.01	5 (3%) 42 41	19, 31, 54, 87	0
2	B	188/202 (93%)	-0.22	1 (0%) 91 92	15, 31, 49, 59	0
2	D	188/202 (93%)	-0.38	1 (0%) 91 92	11, 21, 39, 59	0
All	All	649/806 (80%)	-0.11	13 (2%) 65 65	11, 30, 53, 87	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	GLU	3.3
1	A	200	HIS	2.9
1	C	278	GLU	2.9
2	B	15	THR	2.9
1	C	264	GLU	2.9

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 monosaccharides 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.