



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 6, 2024 – 01:19 AM EDT

PDB ID : 2P3Y  
Title : Crystal structure of VPA0735 from *Vibrio parahaemolyticus*. NorthEast Structural Genomics target VpR109  
Authors : Seetharaman, J.; Neely, H.; Forouhar, F.; Wang, D.; Fang, Y.; Cunningham, K.; Ma, L.-C.; Xia, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2007-03-10  
Resolution : 1.80 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>.

---

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

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

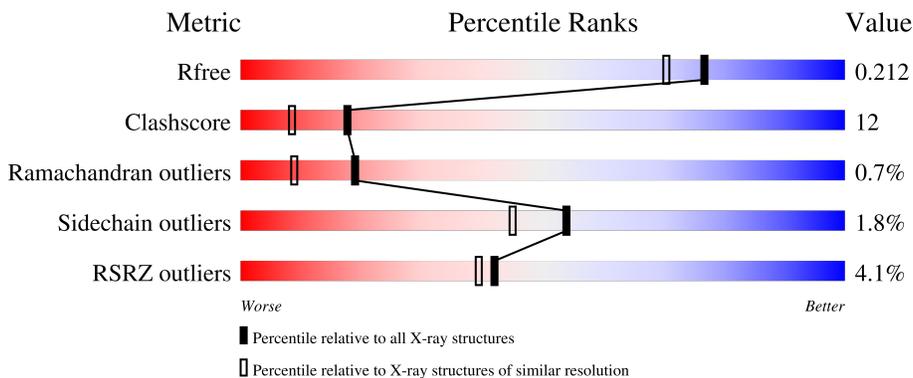
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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	491	 4% 71% 21% • 6%
1	B	491	 3% 75% 18% • 6%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8142 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 Hypothetical protein VPA0735.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	461	3726	2387	625	700	14	0	0	0
1	B	461	3726	2387	625	700	14	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q87I71
A	13	MSE	MET	modified residue	UNP Q87I71
A	45	MSE	MET	modified residue	UNP Q87I71
A	48	MSE	MET	modified residue	UNP Q87I71
A	52	MSE	MET	modified residue	UNP Q87I71
A	71	MSE	MET	modified residue	UNP Q87I71
A	88	MSE	MET	modified residue	UNP Q87I71
A	131	MSE	MET	modified residue	UNP Q87I71
A	134	MSE	MET	modified residue	UNP Q87I71
A	135	MSE	MET	modified residue	UNP Q87I71
A	263	MSE	MET	modified residue	UNP Q87I71
A	297	MSE	MET	modified residue	UNP Q87I71
A	352	MSE	MET	modified residue	UNP Q87I71
A	407	MSE	MET	modified residue	UNP Q87I71
A	469	MSE	MET	modified residue	UNP Q87I71
A	476	MSE	MET	modified residue	UNP Q87I71
A	484	LEU	-	cloning artifact	UNP Q87I71
A	485	GLU	-	cloning artifact	UNP Q87I71
A	486	HIS	-	cloning artifact	UNP Q87I71
A	487	HIS	-	cloning artifact	UNP Q87I71
A	488	HIS	-	cloning artifact	UNP Q87I71
A	489	HIS	-	cloning artifact	UNP Q87I71
A	490	HIS	-	cloning artifact	UNP Q87I71
A	491	HIS	-	cloning artifact	UNP Q87I71
B	1	MSE	MET	modified residue	UNP Q87I71

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	13	MSE	MET	modified residue	UNP Q87I71
B	45	MSE	MET	modified residue	UNP Q87I71
B	48	MSE	MET	modified residue	UNP Q87I71
B	52	MSE	MET	modified residue	UNP Q87I71
B	71	MSE	MET	modified residue	UNP Q87I71
B	88	MSE	MET	modified residue	UNP Q87I71
B	131	MSE	MET	modified residue	UNP Q87I71
B	134	MSE	MET	modified residue	UNP Q87I71
B	135	MSE	MET	modified residue	UNP Q87I71
B	263	MSE	MET	modified residue	UNP Q87I71
B	297	MSE	MET	modified residue	UNP Q87I71
B	352	MSE	MET	modified residue	UNP Q87I71
B	407	MSE	MET	modified residue	UNP Q87I71
B	469	MSE	MET	modified residue	UNP Q87I71
B	476	MSE	MET	modified residue	UNP Q87I71
B	484	LEU	-	cloning artifact	UNP Q87I71
B	485	GLU	-	cloning artifact	UNP Q87I71
B	486	HIS	-	cloning artifact	UNP Q87I71
B	487	HIS	-	cloning artifact	UNP Q87I71
B	488	HIS	-	cloning artifact	UNP Q87I71
B	489	HIS	-	cloning artifact	UNP Q87I71
B	490	HIS	-	cloning artifact	UNP Q87I71
B	491	HIS	-	cloning artifact	UNP Q87I71

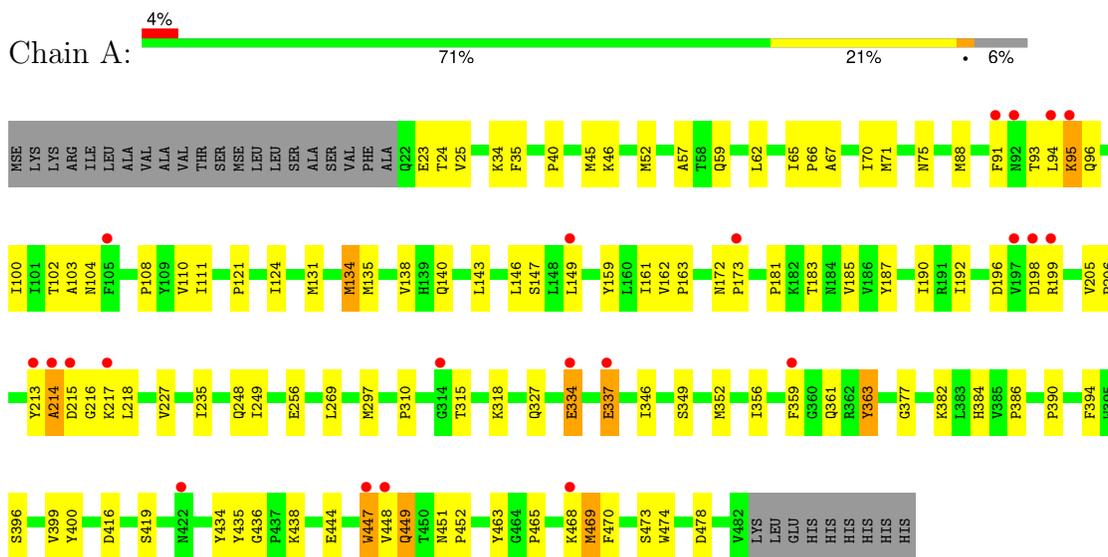
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	326	Total O 326 326	0	0
2	B	364	Total O 364 364	0	0

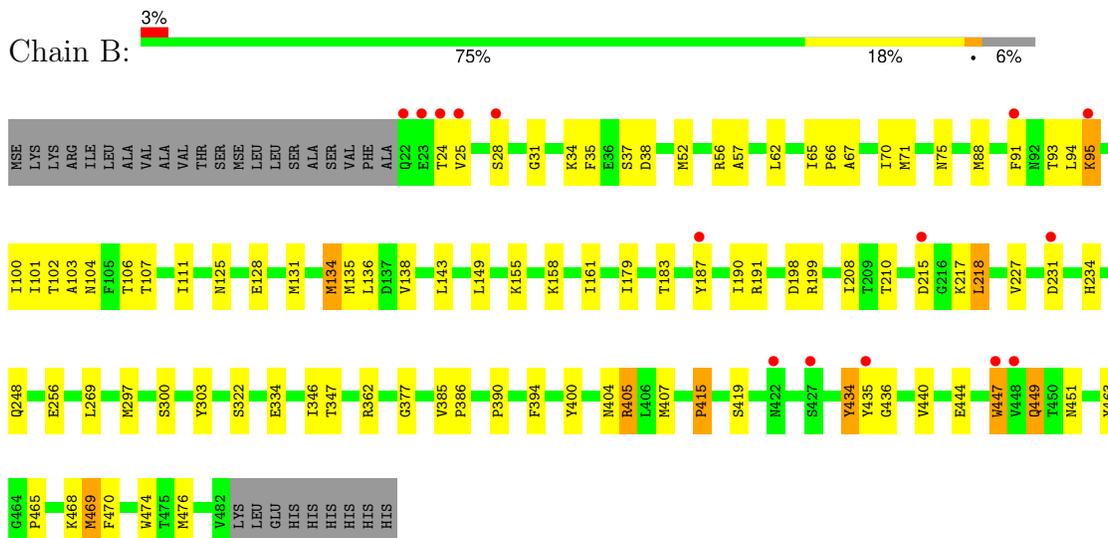
### 3 Residue-property plots [i](#)

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: Hypothetical protein VPA0735



- Molecule 1: Hypothetical protein VPA0735



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.76Å 64.25Å 78.52Å 84.81° 89.14° 76.47°	Depositor
Resolution (Å)	35.70 – 1.80 35.70 – 1.80	Depositor EDS
% Data completeness (in resolution range)	80.7 (35.70-1.80) 86.0 (35.70-1.80)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	0.02	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.39 (at 1.79Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.204 , 0.234 0.217 , 0.212	Depositor DCC
$R_{free}$ test set	4409 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.3	Xtrriage
Anisotropy	0.665	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8142	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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	0.43	0/3812	0.60	0/5149
1	B	0.46	1/3812 (0.0%)	0.66	3/5149 (0.1%)
All	All	0.45	1/7624 (0.0%)	0.63	3/10298 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	334	GLU	CD-OE1	-5.46	1.19	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	435	TYR	N-CA-CB	-13.17	86.89	110.60
1	B	435	TYR	N-CA-C	-8.07	89.21	111.00
1	B	434	TYR	N-CA-C	-5.14	97.11	111.00

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	3726	0	3651	102	0
1	B	3726	0	3651	88	0
2	A	326	0	0	7	0
2	B	364	0	0	4	0
All	All	8142	0	7302	180	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 12.

The worst 5 of 180 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:134:MSE:O	1:B:134:MSE:HE2	1.52	1.07
1:A:45:MSE:HE1	1:B:303:TYR:HB2	1.37	1.04
1:A:45:MSE:HE2	1:B:300:SER:HA	1.40	1.00
1:B:407:MSE:HE3	1:B:415:PRO:HG3	1.42	0.97
1:A:124:ILE:HD12	1:A:135:MSE:HE2	1.49	0.95

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	459/491 (94%)	444 (97%)	11 (2%)	4 (1%)	14	5
1	B	459/491 (94%)	444 (97%)	13 (3%)	2 (0%)	30	19
All	All	918/982 (94%)	888 (97%)	24 (3%)	6 (1%)	19	9

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	ALA
1	A	334	GLU
1	A	449	GLN
1	B	449	GLN
1	A	215	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	406/416 (98%)	399 (98%)	7 (2%)	56	47
1	B	406/416 (98%)	398 (98%)	8 (2%)	50	40
All	All	812/832 (98%)	797 (98%)	15 (2%)	54	45

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

Mol	Chain	Res	Type
1	B	95	LYS
1	B	447	TRP
1	B	134	MSE
1	B	469	MSE
1	B	405	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	278	ASN
1	B	451	ASN
1	B	404	ASN
1	A	422	ASN
1	B	207	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	447/491 (91%)	0.39	22 (4%) 36 33	11, 21, 32, 43	0
1	B	447/491 (91%)	0.15	15 (3%) 48 46	9, 18, 30, 49	0
All	All	894/982 (91%)	0.27	37 (4%) 42 39	9, 19, 31, 49	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	448	VAL	6.5
1	A	215	ASP	5.8
1	B	447	TRP	4.7
1	A	447	TRP	4.7
1	A	214	ALA	4.2

### 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.