



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 07:12 AM EDT

PDB ID : 2QV3  
Title : Crystal Structure of the Helicobacter pylori Vacuolating Toxin p55 Domain  
Authors : Gangwer, K.A.  
Deposited on : 2007-08-07  
Resolution : 2.40 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.

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 : 4.02b-467  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
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) : 2.37.1

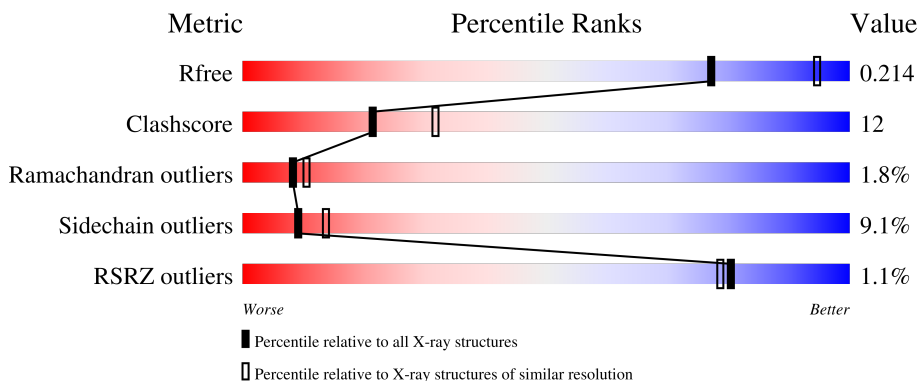
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	457	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3609 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 Vacuolating cytotoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	447	3403	2120	600	674	9	0	0	0

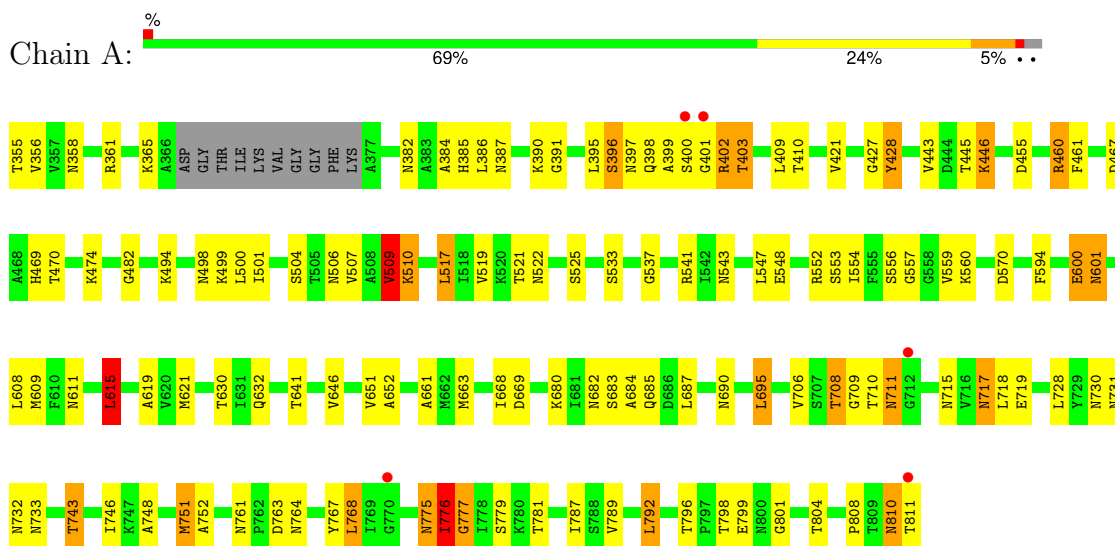
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	206	Total	O	0	0
			206	206		

### 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 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: Vacuolating cytotoxin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.61Å 56.61Å 256.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.03 – 2.40 49.02 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.8 (49.03-2.40) 96.8 (49.02-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.49 (at 2.39Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.181 , 0.222 0.174 , 0.214	Depositor DCC
$R_{free}$ test set	972 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.1	Xtrriage
Anisotropy	0.075	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 54.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.044 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3609	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% 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	1.09	2/3453 (0.1%)	1.05	10/4677 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	548	GLU	CD-OE2	6.81	1.33	1.25
1	A	652	ALA	CA-CB	5.00	1.62	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	517	LEU	CB-CG-CD2	7.94	124.50	111.00
1	A	460	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	509	VAL	CB-CA-C	-6.20	99.62	111.40
1	A	776	ILE	C-N-CA	-6.18	109.33	122.30
1	A	615	LEU	CA-CB-CG	5.82	128.70	115.30
1	A	467	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	669	ASP	CB-CG-OD2	5.58	123.33	118.30
1	A	455	ASP	CB-CG-OD2	5.55	123.30	118.30
1	A	608	LEU	CB-CG-CD1	5.13	119.73	111.00
1	A	608	LEU	CA-CB-CG	-5.12	103.53	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	396	SER	Peptide
1	A	711	ASN	Peptide
1	A	777	GLY	Peptide

## 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	3403	0	3360	81	0
2	A	206	0	0	7	0
All	All	3609	0	3360	81	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.

All (81) 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:395:LEU:CD2	1:A:401:GLY:HA2	1.62	1.27
1:A:395:LEU:HD21	1:A:401:GLY:CA	1.69	1.23
1:A:668:ILE:HD11	1:A:808:PRO:HB2	1.36	1.07
1:A:395:LEU:HD21	1:A:401:GLY:HA2	0.98	0.97
1:A:427:GLY:O	1:A:428:TYR:HB2	1.73	0.88
1:A:387:ASN:HB3	2:A:106:HOH:O	1.78	0.84
1:A:355:THR:HG23	1:A:384:ALA:HB3	1.62	0.81
1:A:395:LEU:HD23	1:A:396:SER:N	1.98	0.79
1:A:668:ILE:CD1	1:A:808:PRO:HB2	2.13	0.75
1:A:361:ARG:HB3	1:A:391:GLY:HA3	1.71	0.72
1:A:382:ASN:ND2	1:A:410:THR:OG1	2.22	0.72
1:A:507:VAL:HG12	1:A:509:VAL:HG22	1.69	0.72
1:A:421:VAL:HB	1:A:427:GLY:HA2	1.73	0.70
1:A:796:THR:HG22	2:A:206:HOH:O	1.92	0.68
1:A:382:ASN:ND2	1:A:410:THR:CB	2.58	0.67
1:A:382:ASN:HD22	1:A:410:THR:HB	1.59	0.67
1:A:690:ASN:OD1	1:A:792:LEU:HD12	1.96	0.66
1:A:395:LEU:HD23	1:A:401:GLY:HA2	1.68	0.66
1:A:460:ARG:HG2	1:A:461:PHE:CD1	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:ASN:HD22	1:A:410:THR:CB	2.13	0.62
1:A:355:THR:HG22	1:A:356:VAL:N	2.14	0.62
1:A:611:ASN:HA	1:A:632:GLN:HG2	1.81	0.61
1:A:395:LEU:CD2	1:A:401:GLY:CA	2.47	0.61
1:A:401:GLY:O	1:A:403:THR:N	2.34	0.61
1:A:777:GLY:HA2	2:A:102:HOH:O	2.02	0.59
1:A:798:THR:HB	1:A:801:GLY:CA	2.32	0.59
1:A:708:THR:C	1:A:710:THR:H	2.06	0.58
1:A:775:ASN:C	1:A:775:ASN:HD22	2.05	0.58
1:A:798:THR:HB	1:A:801:GLY:HA3	1.85	0.58
1:A:395:LEU:HD23	1:A:396:SER:H	1.69	0.57
1:A:684:ALA:HB1	1:A:728:LEU:HD23	1.87	0.57
1:A:398:GLN:HG2	1:A:402:ARG:HD2	1.86	0.56
1:A:385:HIS:HB3	2:A:78:HOH:O	2.05	0.56
1:A:519:VAL:HG21	1:A:559:VAL:CG2	2.36	0.56
1:A:594:PHE:CD1	1:A:621:MET:HG3	2.41	0.55
1:A:510:LYS:HD2	1:A:510:LYS:C	2.28	0.54
1:A:733:ASN:ND2	1:A:748:ALA:O	2.41	0.54
1:A:397:ASN:HB3	1:A:399:ALA:H	1.73	0.54
1:A:615:LEU:HD22	1:A:619:ALA:HB3	1.90	0.54
1:A:522:ASN:O	1:A:525:SER:HB2	2.08	0.53
1:A:668:ILE:HD11	1:A:808:PRO:CB	2.24	0.52
1:A:775:ASN:C	1:A:775:ASN:ND2	2.64	0.51
1:A:743:THR:HA	1:A:746:ILE:HD12	1.94	0.50
1:A:395:LEU:HD21	1:A:401:GLY:C	2.31	0.48
1:A:427:GLY:HA3	2:A:41:HOH:O	2.14	0.47
1:A:552:ARG:O	1:A:553:SER:HB2	2.14	0.47
1:A:733:ASN:HB3	1:A:752:ALA:HB2	1.97	0.47
1:A:356:VAL:HG22	1:A:385:HIS:HB2	1.96	0.47
1:A:661:ALA:HB1	1:A:663:MET:CE	2.44	0.47
1:A:506:ASN:ND2	1:A:533:SER:OG	2.43	0.47
1:A:641:THR:HG21	1:A:680:LYS:HD2	1.96	0.47
1:A:469:HIS:HD2	1:A:470:THR:OG1	1.98	0.46
1:A:781:THR:O	1:A:787:ILE:HA	2.15	0.46
1:A:541:ARG:NH1	1:A:570:ASP:OD2	2.49	0.46
1:A:600:GLU:H	1:A:600:GLU:CD	2.17	0.46
1:A:767:TYR:CE1	1:A:768:LEU:HD13	2.51	0.46
1:A:685:GLN:OE1	1:A:730:ASN:HA	2.16	0.46
1:A:731:ASN:O	1:A:732:ASN:HB2	2.15	0.46
1:A:521:THR:HA	1:A:557:GLY:HA3	1.97	0.45
1:A:615:LEU:HD22	1:A:619:ALA:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:LYS:HE3	1:A:537:GLY:HA3	1.99	0.45
1:A:796:THR:CG2	2:A:206:HOH:O	2.56	0.45
1:A:398:GLN:HG2	1:A:402:ARG:CD	2.47	0.45
1:A:751:MET:HE3	1:A:751:MET:HA	1.99	0.44
1:A:717:ASN:ND2	1:A:719:GLU:OE2	2.51	0.44
1:A:761:ASN:O	1:A:764:ASN:HB2	2.19	0.43
1:A:601:ASN:HD22	1:A:601:ASN:HA	1.67	0.43
1:A:445:THR:O	1:A:446:LYS:HB2	2.18	0.43
1:A:776:ILE:HD12	1:A:776:ILE:HA	1.89	0.43
1:A:651:VAL:HG21	1:A:695:LEU:HD12	2.01	0.43
1:A:682:ASN:O	1:A:683:SER:HB2	2.20	0.42
1:A:541:ARG:HH11	1:A:543:ASN:ND2	2.17	0.42
1:A:460:ARG:NH2	2:A:131:HOH:O	2.52	0.42
1:A:609:MET:HG2	1:A:630:THR:HB	2.02	0.42
1:A:409:LEU:HA	1:A:443:VAL:HB	2.02	0.42
1:A:767:TYR:CD1	1:A:799:GLU:HA	2.55	0.42
1:A:482:GLY:HA2	1:A:504:SER:HB3	2.02	0.41
1:A:499:LYS:HD3	1:A:501:ILE:HD11	2.01	0.41
1:A:554:ILE:HD12	1:A:556:SER:HB3	2.03	0.40
1:A:708:THR:C	1:A:710:THR:N	2.72	0.40
1:A:810:ASN:CG	1:A:811:THR:H	2.24	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	443/457 (97%)	409 (92%)	26 (6%)	8 (2%)	<b>8</b> <b>10</b>

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	428	TYR
1	A	402	ARG
1	A	709	GLY
1	A	474	LYS
1	A	708	THR
1	A	711	ASN
1	A	810	ASN
1	A	403	THR

### 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	374/381 (98%)	340 (91%)	34 (9%)	<b>9</b> <b>14</b>

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	358	ASN
1	A	365	LYS
1	A	386	LEU
1	A	390	LYS
1	A	400	SER
1	A	446	LYS
1	A	494	LYS
1	A	498	ASN
1	A	500	LEU
1	A	509	VAL
1	A	510	LYS
1	A	517	LEU
1	A	547	LEU
1	A	560	LYS
1	A	600	GLU
1	A	601	ASN
1	A	615	LEU
1	A	646	VAL
1	A	687	LEU

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Mol	Chain	Res	Type
1	A	695	LEU
1	A	706	VAL
1	A	715	ASN
1	A	717	ASN
1	A	718	LEU
1	A	743	THR
1	A	751	MET
1	A	763	ASP
1	A	768	LEU
1	A	775	ASN
1	A	776	ILE
1	A	779	SER
1	A	789	VAL
1	A	792	LEU
1	A	804	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	382	ASN
1	A	398	GLN
1	A	422	ASN
1	A	453	ASN
1	A	469	HIS
1	A	472	ASN
1	A	496	ASN
1	A	506	ASN
1	A	601	ASN
1	A	715	ASN
1	A	717	ASN
1	A	733	ASN
1	A	764	ASN
1	A	775	ASN

### 5.3.3 RNA

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, 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	447/457 (97%)	-0.24	5 (1%) 80 79	36, 48, 68, 87	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	811	THR	4.4
1	A	401	GLY	2.7
1	A	712	GLY	2.6
1	A	770	GLY	2.3
1	A	400	SER	2.2

### 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.