



Full wwPDB X-ray Structure Validation Report ⓘ

May 3, 2025 – 03:56 PM EDT

PDB ID : 3NCX / pdb_00003ncx
Title : Crystal structure of EHEC O157:H7 intimin mutant
Authors : Yi, Y.; Gao, F.; Gao, G.F.; Zou, Q.M.
Deposited on : 2010-06-06
Resolution : 2.60 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

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 : 4-5-2 with Phenix2.0rc1
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

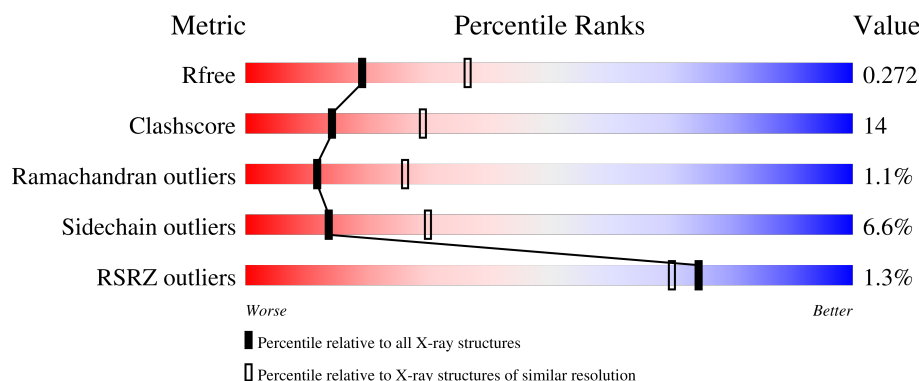
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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	189	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>• •</div> </div> </div>
1	B	189	<div> <div>2%</div> <div> <div></div> <div>61%</div> <div>31%</div> <div>5%</div> <div>•</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3126 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 Intimin adherence protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1449	916	235	293	5			
1	B	183	Total	C	N	O	S	0	0	0
			1414	895	230	284	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	746	MET	-	initiating methionine	UNP C6UYL6
A	916	TYR	ASN	engineered mutation	UNP C6UYL6
B	746	MET	-	initiating methionine	UNP C6UYL6
B	916	TYR	ASN	engineered mutation	UNP C6UYL6

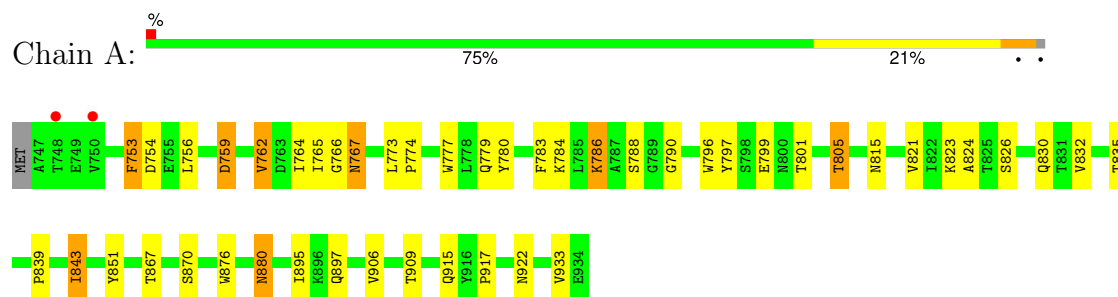
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	154	Total	O	0	0
			154	154		
2	B	109	Total	O	0	0
			109	109		

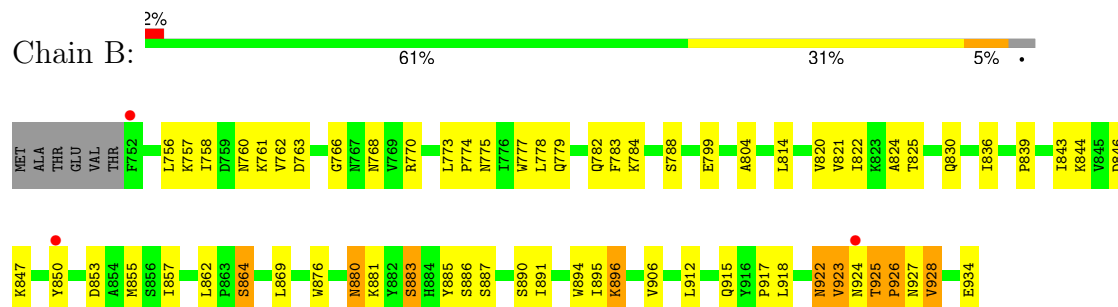
3 Residue-property plots

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: Intimin adherence protein



- Molecule 1: Intimin adherence protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	43.77Å 92.49Å 100.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.98 – 2.60 41.98 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (41.98-2.60) 99.6 (41.98-2.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	CNS, PHENIX (phenix.refine: 1.6.2_432)	Depositor
R, R_{free}	0.213 , 0.268 0.217 , 0.272	Depositor DCC
R_{free} test set	641 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.2	EDS
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3126	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical 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

5.1 Standard geometry

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	0.25	0/1479	0.65	0/2012
1	B	0.26	0/1444	0.70	0/1963
All	All	0.26	0/2923	0.67	0/3975

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

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	1449	0	1416	29	0
1	B	1414	0	1382	50	0
2	A	154	0	0	0	0
2	B	109	0	0	1	0
All	All	3126	0	2798	79	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 14.

All (79) 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:847:LYS:HD2	1:B:847:LYS:H	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:821:VAL:HG22	1:A:835:THR:HG22	1.60	0.83
1:B:850:TYR:HB3	1:B:924:ASN:HA	1.63	0.80
1:B:864:SER:HA	1:B:896:LYS:HB2	1.76	0.67
1:B:923:VAL:HG23	1:B:924:ASN:H	1.59	0.67
1:B:762:VAL:HG11	1:B:783:PHE:CD1	2.31	0.66
1:B:847:LYS:HD2	1:B:847:LYS:N	2.10	0.65
1:B:782:GLN:HE22	1:B:883:SER:N	1.98	0.62
1:B:761:LYS:HZ2	1:B:770:ARG:HD3	1.64	0.62
1:B:779:GLN:HE22	1:B:844:LYS:HG3	1.66	0.60
1:B:869:LEU:HB3	1:B:912:LEU:HD21	1.83	0.59
1:B:779:GLN:NE2	1:B:844:LYS:HG3	2.17	0.59
1:A:843:ILE:HD11	1:A:933:VAL:HG22	1.85	0.58
1:B:782:GLN:HE22	1:B:883:SER:H	1.52	0.58
1:B:773:LEU:HD12	1:B:774:PRO:HD2	1.85	0.57
1:A:765:ILE:HD11	1:A:784:LYS:HG2	1.88	0.56
1:B:855:MET:HA	1:B:862:LEU:HD11	1.87	0.55
1:A:773:LEU:HD12	1:A:774:PRO:HD2	1.89	0.55
1:B:822:ILE:HG12	1:B:836:ILE:HD13	1.89	0.54
1:B:777:TRP:CD2	1:B:814:LEU:HD13	2.43	0.54
1:B:925:THR:HG22	1:B:926:PRO:HB3	1.90	0.54
1:A:880:ASN:HD22	1:A:880:ASN:N	2.07	0.52
1:B:761:LYS:NZ	1:B:770:ARG:HD3	2.24	0.52
1:B:762:VAL:HG11	1:B:783:PHE:HD1	1.75	0.51
1:A:786:LYS:HE3	1:A:786:LYS:HA	1.93	0.51
1:A:767:ASN:C	1:A:767:ASN:HD22	2.19	0.50
1:A:826:SER:OG	1:A:830:GLN:HB2	2.12	0.50
1:B:766:GLY:HA2	1:B:881:LYS:HG2	1.94	0.49
1:B:846:ASP:HB3	1:B:847:LYS:HD2	1.94	0.49
1:B:926:PRO:O	1:B:928:VAL:HG12	2.11	0.49
1:B:766:GLY:HA3	1:B:876:TRP:O	2.12	0.49
1:B:768:ASN:HB2	2:B:206:HOH:O	2.12	0.49
1:B:763:ASP:HB3	1:B:784:LYS:HB2	1.95	0.48
1:B:894:TRP:NE1	1:B:928:VAL:HG22	2.28	0.48
1:B:915:GLN:O	1:B:917:PRO:HD3	2.14	0.48
1:A:796:TRP:CZ3	1:A:824:ALA:HB2	2.48	0.48
1:B:906:VAL:HG12	1:B:922:ASN:HA	1.96	0.47
1:B:906:VAL:HA	1:B:922:ASN:HA	1.95	0.47
1:A:756:LEU:HD12	1:A:788:SER:O	2.14	0.47
1:A:895:ILE:HD13	1:A:909:THR:HA	1.97	0.47
1:A:799:GLU:OE2	1:A:823:LYS:HE3	2.14	0.47
1:B:923:VAL:HG23	1:B:924:ASN:N	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:GLN:O	1:A:780:TYR:HB2	2.15	0.47
1:A:762:VAL:HG13	1:A:783:PHE:HB2	1.96	0.46
1:B:762:VAL:CG1	1:B:783:PHE:HB2	2.45	0.46
1:B:894:TRP:C	1:B:895:ILE:HD12	2.41	0.46
1:B:762:VAL:HG12	1:B:783:PHE:HB2	1.97	0.46
1:B:766:GLY:HA2	1:B:881:LYS:HB3	1.96	0.46
1:B:924:ASN:O	1:B:925:THR:HG23	2.16	0.46
1:B:853:ASP:O	1:B:857:ILE:HG13	2.15	0.46
1:B:756:LEU:HD12	1:B:788:SER:O	2.15	0.46
1:B:825:THR:HA	1:B:830:GLN:O	2.16	0.46
1:A:797:TYR:HE2	1:A:799:GLU:HG2	1.81	0.45
1:A:851:TYR:CZ	1:A:897:GLN:HG2	2.51	0.45
1:B:926:PRO:HB2	1:B:927:ASN:ND2	2.32	0.45
1:A:805:THR:HB	1:A:815:ASN:HD21	1.81	0.45
1:A:766:GLY:HA3	1:A:876:TRP:O	2.17	0.45
1:B:777:TRP:CD2	1:B:839:PRO:HG3	2.51	0.45
1:A:906:VAL:HG12	1:A:922:ASN:HD22	1.82	0.44
1:B:880:ASN:HA	1:B:885:TYR:HB2	1.99	0.44
1:B:777:TRP:CE3	1:B:814:LEU:HD13	2.53	0.43
1:A:762:VAL:HG12	1:A:764:ILE:HD12	1.99	0.43
1:A:851:TYR:OH	1:A:897:GLN:HG2	2.19	0.43
1:A:843:ILE:CD1	1:A:933:VAL:HG22	2.47	0.43
1:B:799:GLU:HG3	1:B:821:VAL:HB	2.00	0.43
1:B:804:ALA:HB3	1:B:820:VAL:HG11	2.01	0.42
1:B:762:VAL:HG12	1:B:763:ASP:N	2.33	0.42
1:A:801:THR:HG23	1:A:805:THR:OG1	2.19	0.42
1:B:880:ASN:O	1:B:886:SER:HA	2.20	0.42
1:A:867:THR:HA	1:A:870:SER:OG	2.19	0.41
1:A:753:PHE:HB3	1:A:790:GLY:O	2.20	0.41
1:A:764:ILE:HD12	1:A:764:ILE:N	2.35	0.41
1:A:777:TRP:CH2	1:A:839:PRO:HD3	2.55	0.41
1:B:890:SER:O	1:B:891:ILE:HD13	2.21	0.41
1:B:778:LEU:HD13	1:B:843:ILE:HD11	2.03	0.41
1:A:759:ASP:HB2	1:A:786:LYS:O	2.21	0.40
1:A:915:GLN:O	1:A:917:PRO:HD3	2.21	0.40
1:B:822:ILE:HG12	1:B:836:ILE:CD1	2.52	0.40
1:B:758:ILE:HD11	1:B:824:ALA:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
1	B	181/189 (96%)	159 (88%)	18 (10%)	4 (2%)	5	10
All	All	367/378 (97%)	337 (92%)	26 (7%)	4 (1%)	12	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	926	PRO
1	B	883	SER
1	B	864	SER
1	B	923	VAL

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 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	162/163 (99%)	152 (94%)	10 (6%)	15	33
1	B	158/163 (97%)	147 (93%)	11 (7%)	12	27
All	All	320/326 (98%)	299 (93%)	21 (7%)	14	30

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	753	PHE
1	A	754	ASP

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Mol	Chain	Res	Type
1	A	759	ASP
1	A	762	VAL
1	A	767	ASN
1	A	786	LYS
1	A	805	THR
1	A	832	VAL
1	A	843	ILE
1	A	880	ASN
1	B	757	LYS
1	B	760	ASN
1	B	775	ASN
1	B	880	ASN
1	B	887	SER
1	B	896	LYS
1	B	918	LEU
1	B	922	ASN
1	B	925	THR
1	B	928	VAL
1	B	934	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	760	ASN
1	A	767	ASN
1	A	779	GLN
1	A	815	ASN
1	A	880	ASN
1	A	897	GLN
1	A	915	GLN
1	A	922	ASN
1	A	924	ASN
1	A	927	ASN
1	B	779	GLN
1	B	782	GLN
1	B	866	GLN
1	B	880	ASN
1	B	897	GLN
1	B	927	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, 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	188/189 (99%)	-0.36	2 (1%) 77 74	13, 22, 38, 93	0
1	B	183/189 (96%)	0.05	3 (1%) 70 65	17, 33, 58, 66	0
All	All	371/378 (98%)	-0.16	5 (1%) 74 70	13, 27, 56, 93	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	924	ASN	3.7
1	A	750	VAL	2.8
1	B	752	PHE	2.6
1	A	748	THR	2.2
1	B	850	TYR	2.1

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.