



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:19 PM GMT

PDB ID : 3WVF
Title : Crystal structure of YidC from Escherichia coli
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Deposited on : 2014-05-20
Resolution : 3.20 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

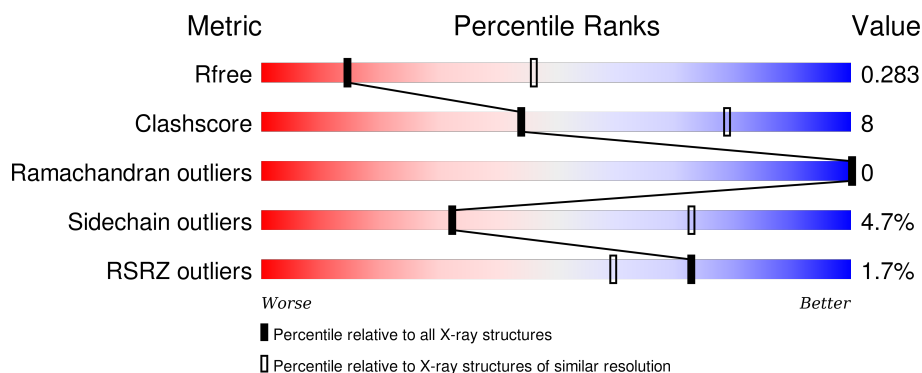
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	551	
1	B	551	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6943 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 Membrane protein insertase YidC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3513	2290	566	640	17			
1	B	445	Total	C	N	O	S	0	0	0
			3430	2236	554	624	16			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	541	LEU	-	EXPRESSION TAG	UNP Q1R4M9
A	542	GLU	-	EXPRESSION TAG	UNP Q1R4M9
A	543	SER	-	EXPRESSION TAG	UNP Q1R4M9
A	544	SER	-	EXPRESSION TAG	UNP Q1R4M9
A	545	GLY	-	EXPRESSION TAG	UNP Q1R4M9
A	546	GLU	-	EXPRESSION TAG	UNP Q1R4M9
A	547	ASN	-	EXPRESSION TAG	UNP Q1R4M9
A	548	LEU	-	EXPRESSION TAG	UNP Q1R4M9
A	549	TYR	-	EXPRESSION TAG	UNP Q1R4M9
A	550	PHE	-	EXPRESSION TAG	UNP Q1R4M9
A	551	GLN	-	EXPRESSION TAG	UNP Q1R4M9
B	541	LEU	-	EXPRESSION TAG	UNP Q1R4M9
B	542	GLU	-	EXPRESSION TAG	UNP Q1R4M9
B	543	SER	-	EXPRESSION TAG	UNP Q1R4M9
B	544	SER	-	EXPRESSION TAG	UNP Q1R4M9
B	545	GLY	-	EXPRESSION TAG	UNP Q1R4M9
B	546	GLU	-	EXPRESSION TAG	UNP Q1R4M9
B	547	ASN	-	EXPRESSION TAG	UNP Q1R4M9
B	548	LEU	-	EXPRESSION TAG	UNP Q1R4M9
B	549	TYR	-	EXPRESSION TAG	UNP Q1R4M9
B	550	PHE	-	EXPRESSION TAG	UNP Q1R4M9
B	551	GLN	-	EXPRESSION TAG	UNP Q1R4M9

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.73Å 76.01Å 91.32Å 78.08° 82.45° 77.55°	Depositor
Resolution (Å)	33.88 – 3.20 39.56 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.3 (33.88-3.20) 85.8 (39.56-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 3.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.221 , 0.277 0.229 , 0.283	Depositor DCC
R_{free} test set	1651 reflections (10.03%)	DCC
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.523	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 16486 reflections	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6943	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.40 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5339e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.26	0/3607	0.44	0/4915
1	B	0.23	0/3522	0.42	0/4807
All	All	0.24	0/7129	0.43	0/9722

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	3513	0	3447	55	0
1	B	3430	0	3333	55	0
All	All	6943	0	6780	110	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.

All (110) 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:69:ASP:HB3	1:A:83:LEU:HB2	1.71	0.72
1:B:366:ARG:HG2	1:B:523:VAL:HG11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ARG:HD3	1:A:129:PRO:HD2	1.76	0.66
1:B:69:ASP:HB3	1:B:83:LEU:HB2	1.78	0.65
1:B:112:SER:HG	1:B:178:TYR:HH	1.43	0.65
1:A:468:PRO:HG2	1:A:507:LEU:HD23	1.79	0.65
1:A:99:LEU:HD11	1:A:260:PHE:HB3	1.78	0.64
1:B:166:VAL:HB	1:B:175:ASN:HB2	1.79	0.63
1:B:351:VAL:HG13	1:B:353:ASN:H	1.64	0.63
1:A:166:VAL:HG13	1:A:175:ASN:HB2	1.82	0.62
1:B:343:LEU:HG	1:B:361:ILE:HD11	1.82	0.62
1:B:90:GLU:HG3	1:B:93:SER:HB2	1.82	0.61
1:B:116:GLY:O	1:B:122:ASN:ND2	2.31	0.61
1:B:475:MET:O	1:B:479:GLN:NE2	2.34	0.60
1:A:379:SER:HA	1:A:417:VAL:HG12	1.83	0.60
1:B:131:TYR:HB3	1:B:151:MET:HB2	1.84	0.60
1:A:200:ILE:O	1:A:219:ARG:NH1	2.31	0.60
1:A:390:ILE:HA	1:A:393:MET:HG3	1.85	0.59
1:A:358:ILE:O	1:A:362:THR:OG1	2.20	0.58
1:B:520:SER:O	1:B:523:VAL:HG12	2.05	0.57
1:A:433:PHE:HD2	1:A:517:TYR:HE2	1.51	0.57
1:A:355:GLY:HA3	1:A:451:PHE:CD1	2.41	0.55
1:B:521:ASN:O	1:B:524:THR:HG22	2.07	0.55
1:A:77:GLY:HA3	1:A:163:LYS:HE2	1.89	0.55
1:A:115:THR:OG1	1:A:116:GLY:N	2.40	0.55
1:A:226:PRO:HD2	1:A:248:SER:HB2	1.88	0.54
1:A:405:SER:O	1:A:409:MET:HB2	2.08	0.54
1:A:353:ASN:OD1	1:A:354:TRP:N	2.42	0.53
1:B:500:VAL:O	1:B:503:THR:HG22	2.09	0.52
1:B:317:MET:HG2	1:B:324:LEU:HG	1.91	0.52
1:B:85:PRO:HA	1:B:96:PRO:HB3	1.91	0.52
1:A:361:ILE:O	1:A:365:VAL:HG23	2.10	0.51
1:B:450:PRO:HA	1:B:456:HIS:HA	1.93	0.51
1:A:382:LYS:HZ2	1:A:386:LEU:HG	1.76	0.50
1:B:88:PRO:O	1:B:447:ARG:NH2	2.40	0.50
1:B:359:ILE:HG12	1:B:519:VAL:HG21	1.94	0.50
1:A:116:GLY:O	1:A:122:ASN:ND2	2.37	0.50
1:B:259:TYR:HA	1:B:444:VAL:HG22	1.93	0.50
1:B:508:TRP:CE3	1:B:508:TRP:HA	2.46	0.49
1:A:382:LYS:NZ	1:A:386:LEU:HG	2.28	0.49
1:B:443:SER:HB2	1:B:446:LEU:HD12	1.95	0.49
1:B:141:ALA:O	1:B:169:ARG:NH2	2.45	0.49
1:A:407:GLU:HA	1:A:410:ALA:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:ILE:O	1:A:473:VAL:HG23	2.14	0.48
1:B:269:ASP:N	1:B:269:ASP:OD1	2.47	0.48
1:A:266:PRO:HB3	1:A:288:TYR:CE2	2.48	0.48
1:A:83:LEU:HD23	1:A:96:PRO:HG2	1.95	0.48
1:A:141:ALA:O	1:A:169:ARG:NH2	2.47	0.48
1:A:90:GLU:HG2	1:A:93:SER:HB2	1.96	0.48
1:B:115:THR:OG1	1:B:116:GLY:N	2.47	0.47
1:A:355:GLY:HA3	1:A:451:PHE:HD1	1.79	0.47
1:B:99:LEU:HD23	1:B:309:VAL:HG23	1.96	0.47
1:A:522:LEU:O	1:A:526:ILE:HG12	2.15	0.47
1:A:379:SER:HA	1:A:417:VAL:CG1	2.45	0.47
1:B:347:ILE:HD13	1:B:361:ILE:HD13	1.96	0.47
1:A:409:MET:O	1:A:413:LYS:HG2	2.16	0.46
1:A:370:TYR:HA	1:A:373:THR:HG22	1.96	0.46
1:B:458:LEU:HA	1:B:511:SER:HB3	1.98	0.46
1:B:192:THR:HG21	1:B:303:MET:HB3	1.99	0.45
1:B:361:ILE:HA	1:B:361:ILE:HD12	1.72	0.45
1:A:162:THR:HB	1:A:179:ASN:HB3	1.97	0.45
1:B:390:ILE:HD11	1:B:411:LEU:HD23	1.99	0.45
1:B:314:GLN:HG2	1:B:328:VAL:HG21	1.98	0.45
1:B:430:MET:HB2	1:B:431:PRO:HD3	1.99	0.45
1:A:100:LEU:HD21	1:A:262:THR:HG21	1.98	0.45
1:A:343:LEU:O	1:A:347:ILE:HG13	2.17	0.44
1:B:358:ILE:O	1:B:361:ILE:HG22	2.17	0.44
1:B:508:TRP:HA	1:B:508:TRP:HE3	1.81	0.44
1:B:259:TYR:HB3	1:B:444:VAL:HG13	2.00	0.44
1:B:149:VAL:HB	1:B:165:PHE:HB2	2.00	0.44
1:A:163:LYS:NZ	1:A:178:TYR:OH	2.51	0.44
1:B:155:ASP:OD1	1:B:159:ASN:N	2.50	0.44
1:B:266:PRO:HB3	1:B:288:TYR:CE2	2.53	0.44
1:A:106:PHE:HZ	1:A:198:GLN:HE21	1.66	0.44
1:A:131:TYR:HB3	1:A:151:MET:HB2	1.98	0.44
1:B:318:ALA:HB2	1:B:325:ASP:HB3	2.00	0.43
1:A:387:GLN:N	1:A:388:PRO:HD2	2.33	0.43
1:B:402:GLN:O	1:B:405:SER:OG	2.37	0.43
1:A:358:ILE:O	1:A:361:ILE:HG22	2.19	0.43
1:A:365:VAL:O	1:A:369:MET:HB2	2.19	0.43
1:A:396:ARG:HD3	1:A:397:LEU:HD22	2.01	0.43
1:A:428:ILE:O	1:A:431:PRO:HD2	2.19	0.43
1:B:162:THR:HB	1:B:179:ASN:HB2	2.01	0.43
1:B:312:GLU:H	1:B:444:VAL:HG21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:451:PHE:HB2	1:B:458:LEU:HD21	2.01	0.42
1:A:199:SER:O	1:A:219:ARG:NH2	2.45	0.42
1:B:317:MET:HE3	1:B:325:ASP:HA	2.01	0.42
1:A:87:TYR:HA	1:A:88:PRO:HD3	1.93	0.42
1:B:335:PHE:CD2	1:B:336:ILE:HG13	2.55	0.42
1:A:85:PRO:HA	1:A:96:PRO:HB3	2.01	0.42
1:B:57:GLN:H	1:B:75:ARG:HD2	1.85	0.42
1:B:338:GLN:HB3	1:B:339:PRO:HD3	2.02	0.42
1:B:353:ASN:HB3	1:B:356:PHE:HB2	2.01	0.41
1:A:462:ASP:OD1	1:A:466:ILE:N	2.51	0.41
1:A:119:GLY:HA2	1:A:120:PRO:HD3	1.95	0.41
1:B:355:GLY:HA3	1:B:451:PHE:CD2	2.54	0.41
1:B:356:PHE:O	1:B:360:ILE:HG13	2.20	0.41
1:A:354:TRP:O	1:A:358:ILE:HG13	2.20	0.41
1:B:451:PHE:HB3	1:B:455:ILE:HB	2.02	0.41
1:B:121:ASP:OD1	1:B:128:ARG:NE	2.54	0.41
1:A:355:GLY:O	1:A:359:ILE:HG13	2.20	0.41
1:B:336:ILE:O	1:B:340:LEU:HB2	2.20	0.41
1:B:501:ILE:H	1:B:501:ILE:HG12	1.59	0.41
1:A:259:TYR:HA	1:A:444:VAL:HG22	2.03	0.41
1:A:524:THR:O	1:A:527:GLN:HB3	2.21	0.41
1:A:122:ASN:HA	1:A:123:PRO:HD3	1.95	0.40
1:B:291:GLN:HA	1:B:292:PRO:HD3	1.93	0.40
1:A:503:THR:O	1:A:507:LEU:HG	2.21	0.40
1:A:152:THR:HG22	1:A:162:THR:HG23	2.02	0.40
1:A:67:VAL:O	1:A:85:PRO:HD2	2.22	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	442/551 (80%)	424 (96%)	18 (4%)	0	100	100
1	B	439/551 (80%)	421 (96%)	18 (4%)	0	100	100
All	All	881/1102 (80%)	845 (96%)	36 (4%)	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 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	370/471 (79%)	349 (94%)	21 (6%)	25	67
1	B	354/471 (75%)	341 (96%)	13 (4%)	41	79
All	All	724/942 (77%)	690 (95%)	34 (5%)	32	73

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

Mol	Chain	Res	Type
1	A	103	SER
1	A	128	ARG
1	A	249	LYS
1	A	325	ASP
1	A	332	TRP
1	A	334	TRP
1	A	350	PHE
1	A	369	MET
1	A	374	LYS
1	A	377	TYR
1	A	400	ASP
1	A	411	LEU
1	A	417	VAL
1	A	430	MET
1	A	436	LEU
1	A	461	GLN
1	A	470	LEU
1	A	471	MET

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Mol	Chain	Res	Type
1	A	476	PHE
1	A	497	PHE
1	A	527	GLN
1	B	338	GLN
1	B	345	LYS
1	B	353	ASN
1	B	361	ILE
1	B	372	LEU
1	B	390	ILE
1	B	456	HIS
1	B	466	ILE
1	B	477	PHE
1	B	479	GLN
1	B	501	ILE
1	B	504	VAL
1	B	524	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
1	A	198	GLN
1	A	296	GLN
1	A	323	HIS
1	A	448	GLN
1	B	177	ASN
1	B	299	GLN
1	B	338	GLN
1	B	353	ASN
1	B	456	HIS
1	B	479	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	448/551 (81%)	-0.26	9 (2%) 68 54	8, 29, 61, 81	0
1	B	445/551 (80%)	-0.22	6 (1%) 79 67	9, 34, 66, 81	0
All	All	893/1102 (81%)	-0.24	15 (1%) 73 60	8, 31, 64, 81	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	479	GLN	4.2
1	B	478	ILE	3.8
1	A	418	ASN	2.8
1	A	377	TYR	2.8
1	A	376	GLN	2.8
1	B	423	CYS	2.5
1	A	423	CYS	2.5
1	A	381	ALA	2.4
1	A	419	PRO	2.4
1	A	374	LYS	2.4
1	B	527	GLN	2.4
1	A	379	SER	2.4
1	B	476	PHE	2.2
1	B	418	ASN	2.2
1	A	371	PRO	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 carbohydrates 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.