



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 04:56 AM BST

PDB ID : 2XBD  
Title : INTERNAL XYLAN BINDING DOMAIN FROM CELLULOMONAS FIMI  
XYLANASE D, NMR, MINIMIZED AVERAGE STRUCTURE  
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Deposited on : 1998-10-27

This is a Full wwPDB NMR 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  
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

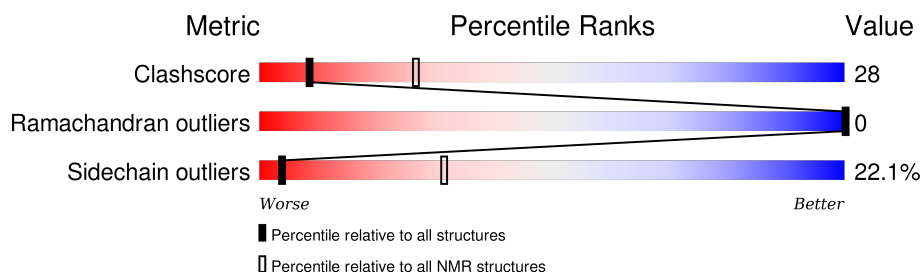
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 57%.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	87	

## 2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1192 atoms, of which 577 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called XYLANASE D.

Mol	Chain	Residues	Atoms						Trace
1	A	87	Total	C	H	N	O	S	0
			1192	368	577	110	134	3	

## 4 Residue-property plots

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: XYLANASE D

Chain A: 



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *HYBRID DISTANCE GEOMETRY/ SIMULATED ANNEALING*.

Of the 50 calculated structures, 1 were deposited, based on the following criterion: *MINIMIZED AVERAGE STRUCTURE, CALCULATED FROM 38 LOWEST ENERGY STRUCTURES*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	3.1
MSI FELIX	structure solution	97.0

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 4241
Number of chemical shift lists	1
Total number of shifts	632
Number of shifts mapped to atoms	632
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	57%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality [i](#)

### 6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

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	Planarity
1	A	0	3
All	All	0	3

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	262	ARG	Sidechain
1	A	255	ARG	Sidechain
1	A	302	ARG	Sidechain

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	615	577	574	33
All	All	615	577	574	33

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 28.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:275:TRP:CZ3	1:A:277:VAL:HG23	0.80	2.11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:275:TRP:CE3	1:A:277:VAL:HG23	0.80	2.12
1:A:247:THR:O	1:A:247:THR:HG22	0.68	1.88
1:A:267:TYR:CE2	1:A:328:ALA:HB2	0.66	2.26
1:A:275:TRP:CZ3	1:A:277:VAL:CG2	0.63	2.80
1:A:265:VAL:HG11	1:A:267:TYR:CE1	0.63	2.28
1:A:253:ALA:HB2	1:A:267:TYR:CE2	0.56	2.36
1:A:267:TYR:CD2	1:A:328:ALA:HB2	0.55	2.36
1:A:251:VAL:HG13	1:A:269:VAL:CG2	0.53	2.32
1:A:291:TRP:O	1:A:292:ASN:CB	0.52	2.58
1:A:277:VAL:HG11	1:A:313:PHE:HZ	0.52	1.64
1:A:250:SER:O	1:A:269:VAL:HG13	0.52	2.04
1:A:265:VAL:CG1	1:A:267:TYR:CE1	0.50	2.94
1:A:267:TYR:CD2	1:A:328:ALA:CB	0.50	2.95
1:A:247:THR:CG2	1:A:247:THR:O	0.48	2.60
1:A:291:TRP:CZ2	1:A:314:GLY:HA3	0.48	2.44
1:A:267:TYR:CE2	1:A:328:ALA:CB	0.48	2.97
1:A:291:TRP:CE2	1:A:314:GLY:HA3	0.46	2.46
1:A:289:ALA:HB3	1:A:316:THR:CB	0.46	2.41
1:A:287:ILE:HD12	1:A:295:VAL:HG11	0.46	1.88
1:A:285:GLN:NE2	1:A:322:SER:HB3	0.45	2.27
1:A:291:TRP:O	1:A:292:ASN:HB2	0.44	2.12
1:A:267:TYR:OH	1:A:326:PRO:O	0.44	2.32
1:A:263:PHE:CZ	1:A:317:VAL:HB	0.44	2.48
1:A:253:ALA:HB2	1:A:267:TYR:CD2	0.43	2.49
1:A:289:ALA:HB3	1:A:316:THR:HB	0.42	1.91
1:A:277:VAL:HG11	1:A:313:PHE:CZ	0.42	2.48
1:A:250:SER:O	1:A:269:VAL:HG22	0.41	2.15
1:A:281:LEU:HD22	1:A:285:GLN:OE1	0.41	2.15
1:A:275:TRP:HB2	1:A:330:CYS:SG	0.41	2.55
1:A:292:ASN:HB3	1:A:313:PHE:CB	0.41	2.46
1:A:289:ALA:HB3	1:A:316:THR:OG1	0.40	2.16
1:A:292:ASN:HB3	1:A:313:PHE:CA	0.40	2.47

## 6.3 Torsion angles ⓘ

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	85/87 (98%)	73 (86%)	12 (14%)	0 (0%)	100	100
All	All	85/87 (98%)	73 (86%)	12 (14%)	0 (0%)	100	100

There are no Ramachandran outliers.

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	68/68 (100%)	53 (78%)	15 (22%)	4	31
All	All	68/68 (100%)	53 (78%)	15 (22%)	4	31

All 15 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	288	GLN
1	A	292	ASN
1	A	309	SER
1	A	324	THR
1	A	270	SER
1	A	333	SER
1	A	325	THR
1	A	302	ARG
1	A	298	SER
1	A	323	SER
1	A	251	VAL
1	A	252	THR
1	A	284	SER
1	A	250	SER
1	A	254	THR

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 57% for the well-defined parts and 57% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 4241

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	632
Number of shifts mapped to atoms	632
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

#### 7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	—
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	84	$-0.77 \pm 0.68$	None needed (imprecise)

#### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 57%, i.e. 511 atoms were assigned a chemical shift out of a possible 899. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	256/431 (59%)	172/172 (100%)	0/174 (0%)	84/85 (99%)
Sidechain	220/406 (54%)	207/234 (88%)	0/152 (0%)	13/20 (65%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	35/62 (56%)	32/32 (100%)	0/27 (0%)	3/3 (100%)
Overall	511/899 (57%)	411/438 (94%)	0/353 (0%)	100/108 (93%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 57%, i.e. 511 atoms were assigned a chemical shift out of a possible 899. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	256/431 (59%)	172/172 (100%)	0/174 (0%)	84/85 (99%)
Sidechain	220/406 (54%)	207/234 (88%)	0/152 (0%)	13/20 (65%)
Aromatic	35/62 (56%)	32/32 (100%)	0/27 (0%)	3/3 (100%)
Overall	511/899 (57%)	411/438 (94%)	0/353 (0%)	100/108 (93%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	267	TYR	HB2	0.87	4.76 – 1.06	-5.5

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

