



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 10:09 pm BST

PDB ID : 1V6Y
Title : Crystal Structure Of chimeric Xylanase between Streptomyces Olivaceoviridis E-86 FXYN and Cellulomonas fimi Cex
Authors : Kaneko, S.; Ichinose, H.; Fujimoto, Z.; Kuno, A.; Yura, K.; Go, M.; Mizuno, H.; Kusakabe, I.; Kobayashi, H.
Deposited on : 2003-12-04
Resolution : 2.20 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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

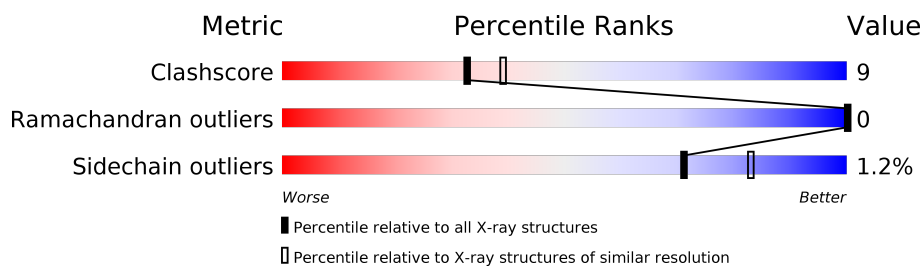
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	324	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2697 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 Beta-xylanase,Exoglucanase/xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	0	0	0
			2457	1535	445	464	13			


There are 9 discrepancies between the modelled and reference sequences:

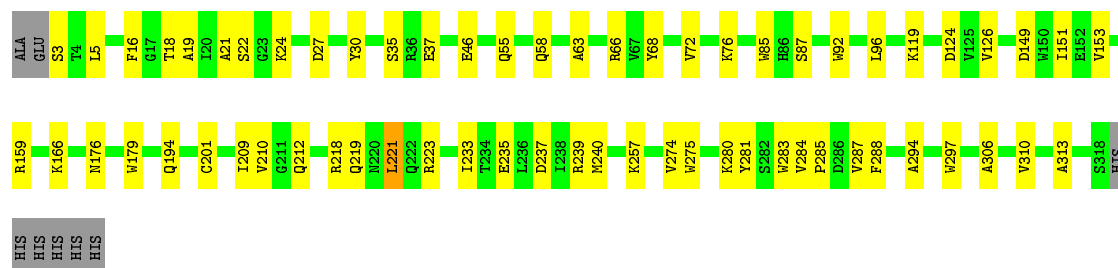
Chain	Residue	Modelled	Actual	Comment	Reference
A	316	SER	-	expression tag	UNP P07986
A	317	ARG	-	expression tag	UNP P07986
A	318	SER	-	expression tag	UNP P07986
A	319	HIS	-	expression tag	UNP P07986
A	320	HIS	-	expression tag	UNP P07986
A	321	HIS	-	expression tag	UNP P07986
A	322	HIS	-	expression tag	UNP P07986
A	323	HIS	-	expression tag	UNP P07986
A	324	HIS	-	expression tag	UNP P07986

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	240	Total	O	0	0
			240	240		

Note EDS was not executed.

- Chain A:  78% 19%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.48 Å 57.19 Å 106.67 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.67 – 2.20	Depositor
% Data completeness (in resolution range)	87.6 (28.67-2.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.153 , 0.198	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2697	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

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	0.30	0/2513	0.60	2/3406 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	124	ASP	N-CA-C	-5.27	96.78	111.00
1	A	233	ILE	N-CA-C	-5.24	96.86	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	2457	0	2354	42	0
2	A	240	0	0	7	0
All	All	2697	0	2354	42	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 9.

All (42) 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:209:ILE:HD11	1:A:239:ARG:NH2	2.05	0.70
1:A:35:SER:HA	1:A:76:LYS:HE2	1.73	0.70
1:A:27:ASP:HB3	1:A:30:TYR:HB3	1.79	0.62
1:A:280:LYS:HE3	1:A:281:TYR:CZ	2.38	0.58
1:A:55:GLN:HB2	1:A:58:GLN:HB2	1.85	0.58
1:A:284:VAL:HB	1:A:285:PRO:HD3	1.84	0.57
1:A:257:LYS:HG3	1:A:313:ALA:HB2	1.86	0.56
1:A:209:ILE:HB	1:A:212:GLN:HB2	1.87	0.56
1:A:176:ASN:HB3	1:A:179:TRP:CE2	2.41	0.55
1:A:21:ALA:HB3	1:A:24:LYS:HD3	1.89	0.55
1:A:126:VAL:HG11	1:A:151:ILE:CD1	2.37	0.54
1:A:85:TRP:CE2	1:A:87:SER:HB3	2.42	0.54
1:A:176:ASN:HB3	1:A:179:TRP:CD2	2.44	0.52
1:A:166:LYS:HD3	2:A:473:HOH:O	2.09	0.52
1:A:194:GLN:HG2	2:A:462:HOH:O	2.10	0.50
1:A:306:ALA:O	1:A:310:VAL:HG23	2.12	0.50
1:A:159:ARG:HD3	2:A:346:HOH:O	2.13	0.49
1:A:27:ASP:HA	2:A:416:HOH:O	2.14	0.48
1:A:68:TYR:CZ	1:A:119:LYS:HB3	2.49	0.47
1:A:92:TRP:O	1:A:96:LEU:HG	2.14	0.47
1:A:219:GLN:O	1:A:223:ARG:HG3	2.15	0.46
1:A:126:VAL:HG11	1:A:151:ILE:HD12	1.97	0.46
1:A:235:GLU:HG2	1:A:275:TRP:CE3	2.51	0.45
1:A:149:ASP:O	1:A:153:VAL:HG23	2.16	0.45
1:A:22:SER:HB2	1:A:66:ARG:HD2	1.99	0.44
1:A:287:VAL:HG23	1:A:288:PHE:CD2	2.52	0.44
1:A:219:GLN:CD	1:A:219:GLN:H	2.22	0.43
1:A:46:GLU:CD	1:A:46:GLU:H	2.21	0.43
1:A:210:VAL:HG23	1:A:239:ARG:O	2.19	0.43
1:A:18:THR:HA	1:A:274:VAL:O	2.18	0.42
1:A:46:GLU:HG3	1:A:63:ALA:HB1	2.01	0.42
1:A:218:ARG:NH2	2:A:436:HOH:O	2.52	0.42
1:A:5:LEU:HD13	1:A:16:PHE:CE2	2.54	0.42
1:A:221:LEU:HD13	2:A:402:HOH:O	2.21	0.41
1:A:68:TYR:CZ	1:A:72:VAL:HG21	2.55	0.41
1:A:209:ILE:CD1	1:A:239:ARG:CZ	2.98	0.41
1:A:37:GLU:HG3	1:A:297:TRP:CZ2	2.56	0.41
1:A:210:VAL:HG21	1:A:240:MET:HB3	2.03	0.41
1:A:237:ASP:HB2	1:A:294:ALA:HB1	2.01	0.40
1:A:218:ARG:CZ	1:A:219:GLN:HE21	2.34	0.40
1:A:19:ALA:HB2	1:A:275:TRP:CE3	2.56	0.40
1:A:3:SER:N	2:A:512:HOH:O	2.55	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	314/324 (97%)	308 (98%)	6 (2%)	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	250/257 (97%)	247 (99%)	3 (1%)	71	83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	201	CYS
1	A	221	LEU
1	A	283	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	173	ASN

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Mol	Chain	Res	Type
1	A	194	GLN
1	A	270	GLN

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 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.