

Full wwPDB X-ray Structure Validation Report (i)

Nov 21, 2023 – 05:22 PM JST

PDB ID	:	7W44
Title	:	Complex structure of a leaf-branch compost cutinase variant LCC ICCG_RIP
Authors	:	Niu, D.; Zeng, W.; Huang, J.W.; Chen, C.C.; Liu, W.D.; Guo, R.T.
Deposited on		
Resolution	:	1.85 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 (i) 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 (1)) were used in the production of this report:

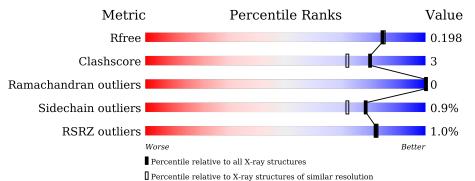
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.85 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 <=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	А	269	90%	6% •
1	В	269	2% 90%	5% • •



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4532 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 Leaf-branch compost cutinase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	257	Total	С	Ν	Ο	S	0	2	0
			1951	1225	351	368	7			
1	В	257	Total	С	Ν	Ο	S	0	9	0
	I B	201	1953	1226	352	368	7	0		0

Chain	Residue	Modelled	Actual	Comment	Reference
А	35	MET	-	initiating methionine	UNP G9BY57
А	59	ARG	ALA	conflict	UNP G9BY57
А	63	ILE	VAL	conflict	UNP G9BY57
А	127	GLY	TYR	conflict	UNP G9BY57
А	238	CYS	ASP	conflict	UNP G9BY57
А	243	ILE	PHE	conflict	UNP G9BY57
А	248	PRO	ASN	conflict	UNP G9BY57
А	283	CYS	SER	conflict	UNP G9BY57
А	294	ALA	-	expression tag	UNP G9BY57
А	295	GLY	-	expression tag	UNP G9BY57
А	296	ALA	-	expression tag	UNP G9BY57
А	297	GLY	-	expression tag	UNP G9BY57
А	298	ALA	-	expression tag	UNP G9BY57
А	299	GLY	-	expression tag	UNP G9BY57
А	300	ALA	-	expression tag	UNP G9BY57
А	301	GLY	-	expression tag	UNP G9BY57
А	302	ALA	-	expression tag	UNP G9BY57
А	303	GLY	-	expression tag	UNP G9BY57
В	35	MET	-	initiating methionine	UNP G9BY57
В	59	ARG	ALA	conflict	UNP G9BY57
В	63	ILE	VAL	conflict	UNP G9BY57
В	127	GLY	TYR	conflict	UNP G9BY57
В	238	CYS	ASP	conflict	UNP G9BY57
В	243	ILE	PHE	conflict	UNP G9BY57
В	248	PRO	ASN	conflict	UNP G9BY57

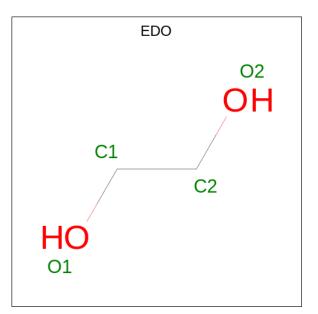
There are 36 discrepancies between the modelled and reference sequences:

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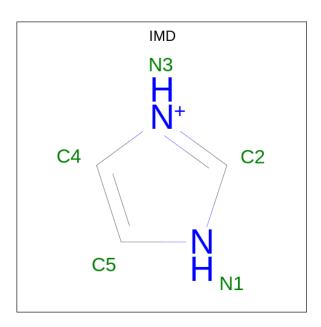
Continued from previous page								
Chain	Residue	Modelled	Actual	Comment	Reference			
В	283	CYS	SER	conflict	UNP G9BY57			
В	294	ALA	-	expression tag	UNP G9BY57			
В	295	GLY	-	expression tag	UNP G9BY57			
В	296	ALA	-	expression tag	UNP G9BY57			
В	297	GLY	-	expression tag	UNP G9BY57			
В	298	ALA	-	expression tag	UNP G9BY57			
В	299	GLY	-	expression tag	UNP G9BY57			
В	300	ALA	-	expression tag	UNP G9BY57			
В	301	GLY	-	expression tag	UNP G9BY57			
В	302	ALA	-	expression tag	UNP G9BY57			
В	303	GLY	-	expression tag	UNP G9BY57			

• Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{N} \\ 5 & 3 & 2 \end{array}$; 1	0	0

• Molecule 4 is water.

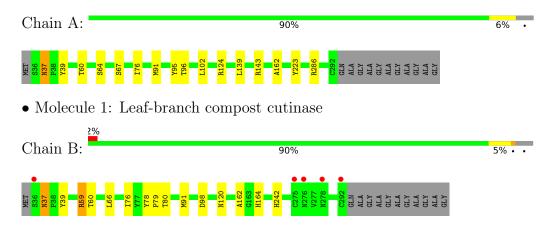
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	340	Total O 340 340	0	0
4	В	275	Total O 275 275	0	0



3 Residue-property plots (i)

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: Leaf-branch compost cutinase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	64.57Å 153.27Å 118.24Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.94 - 1.85	Depositor
Resolution (A)	24.69 - 1.85	EDS
% Data completeness	99.0 (24.94-1.85)	Depositor
(in resolution range)	99.0 (24.69-1.85)	EDS
R _{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.44 (at 1.85 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
D D.	0.151 , 0.187	Depositor
R, R_{free}	0.164 , 0.198	DCC
R_{free} test set	2483 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.5	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , 54.2	EDS
L-test for $twinning^2$	$ < L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4532	wwPDB-VP
Average B, all atoms $(Å^2)$	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.30% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: IMD, EDO

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.74	0/2008	0.87	0/2748	
1	В	0.72	0/2010	0.86	0/2753	
All	All	0.73	0/4018	0.87	0/5501	

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 (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	А	1951	0	1909	12	0
1	В	1953	0	1910	8	0
2	А	4	0	6	2	0
2	В	4	0	6	0	0
3	В	5	0	5	1	0
4	А	340	0	0	0	0
4	В	275	0	0	2	0
All	All	4532	0	3836	21	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 3.



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:286:ARG:HA	2:A:401:EDO:H21	1.83	0.59
1:A:64:SER:OG	1:A:67:SER:HB3	2.08	0.54
3:B:401:IMD:H2	4:B:510:HOH:O	2.07	0.54
1:B:98:ASP:HB2	1:B:120:ASN:OD1	2.09	0.53
1:A:91:MET:HA	1:A:162:ALA:O	2.09	0.52
1:B:59:ARG:HG3	1:B:80:THR:HB	1.90	0.52
1:B:91:MET:HA	1:B:162:ALA:O	2.08	0.52
1:A:91:MET:HE2	1:A:102:LEU:HD13	1.93	0.50
1:A:286:ARG:CA	2:A:401:EDO:H21	2.45	0.47
1:A:37:ASN:ND2	1:A:39:TYR:H	2.13	0.46
1:A:96:THR:HA	1:A:124:ARG:HB3	1.98	0.46
1:A:139:LEU:O	1:A:143:ARG:HG3	2.16	0.44
1:B:60:THR:HA	1:B:76:ILE:O	2.18	0.43
1:A:95:TYR:CD2	1:A:96:THR:HG23	2.53	0.43
1:B:164:HIS:HE1	1:B:242:HIS:O	2.02	0.43
1:A:223:TYR:CD1	1:A:223:TYR:C	2.92	0.42
1:B:164:HIS:HD2	4:B:580:HOH:O	2.01	0.42
1:A:60:THR:HA	1:A:76:ILE:O	2.19	0.42
1:B:37:ASN:ND2	1:B:39:TYR:H	2.18	0.41
1:B:78:TYR:HA	1:B:79:PRO:HD3	1.89	0.41
1:A:37:ASN:C	1:A:37:ASN:HD22	2.24	0.40

All (21) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Perce	ntiles
1	А	257/269~(96%)	253~(98%)	4 (2%)	0	100	100
1	В	257/269~(96%)	253~(98%)	4 (2%)	0	100	100
All	All	514/538~(96%)	506~(98%)	8 (2%)	0	100	100



There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	213/213~(100%)	212 (100%)	1 (0%)	88 86
1	В	213/213~(100%)	210~(99%)	3 (1%)	67 55
All	All	426/426 (100%)	422~(99%)	4 (1%)	78 72

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	37	ASN
1	В	37	ASN
1	В	59	ARG
1	В	66	LEU

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such side chains are listed below:

Mol	Chain	Res	Type
1	А	37	ASN
1	А	164	HIS
1	А	266	ASN
1	В	37	ASN
1	В	164	HIS
1	В	224	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	B	ond leng	gths	B	ond ang	gles
IVIOI	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	EDO	А	401	-	3,3,3	0.07	0	$2,\!2,\!2$	0.26	0
3	IMD	В	401	-	3,5,5	0.90	0	4,5,5	0.76	0
2	EDO	В	402	-	3,3,3	0.18	0	$2,\!2,\!2$	0.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	А	401	-	-	0/1/1/1	-
3	IMD	В	401	-	-	-	0/1/1/1
2	EDO	В	402	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	402	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	401	EDO	2	0
3	В	401	IMD	1	0

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	А	257/269~(95%)	-0.47	0 100 100	9, 14, 22, 45	0
1	В	257/269~(95%)	-0.30	5 (1%) 66 66	10, 14, 27, 61	0
All	All	514/538~(95%)	-0.38	5 (0%) 82 82	9, 14, 25, 61	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	276	ASN	4.9
1	В	36	SER	4.2
1	В	292	CYS	3.7
1	В	275	CYS	2.7
1	В	278	ASN	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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	IMD	В	401	5/5	0.78	0.20	$19,\!20,\!23,\!25$	0
2	EDO	А	401	4/4	0.81	0.14	31,37,38,40	0
2	EDO	В	402	4/4	0.89	0.17	31,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.

