

# Full wwPDB X-ray Structure Validation Report (i)

Dec 19, 2021 – 06:04 am GMT

PDB ID : 7078

Title: Structure of the PL6 family chondroitinase B from Pseudopedobacter saltans,

Pedsa3807

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Deposited on : 2021-04-13

Resolution : 1.58 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467 Xtriage (Phenix) : 1.13

EDS : 2.24

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

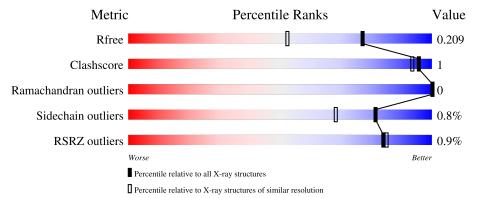
Validation Pipeline (wwPDB-VP) : 2.24

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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	A	492	97%	•			
1	В	492	95%	5%			



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8525 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 Polysaccharide lyase from Pseudopedobacter saltans, Pedsa3807.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	491	Total 3798	C 2409	N 661	O 719	S 9	0	0	0
1	В	492	Total 3819	C 2421	- '	O 726	S 9	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	GLY	-	expression tag	UNP F0S763
В	15	GLY	-	expression tag	UNP F0S763

• Molecule 2 is water.

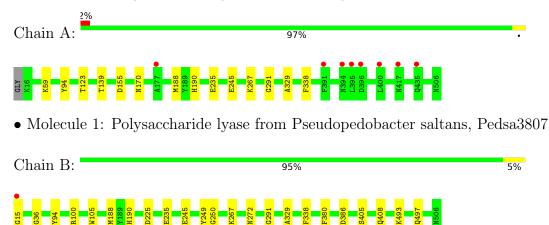
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	422	Total O 422 422	0	0
2	В	486	Total O 486 486	0	0



# 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: Polysaccharide lyase from Pseudopedobacter saltans, Pedsa3807





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	78.33Å 87.45Å 148.49Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.35 - 1.58	Depositor
resolution (A)	58.35 - 1.58	EDS
% Data completeness	96.0 (58.35-1.58)	Depositor
(in resolution range)	96.0 (58.35-1.58)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.23 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
P.P.	0.178 , 0.210	Depositor
$R, R_{free}$	0.178 , 0.209	DCC
$R_{free}$ test set	6756 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.3	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$  <  L  > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8525	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	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 43.11 % 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 1.8504e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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		
WIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.73	0/3881	0.81	0/5269	
1	В	0.74	0/3902	0.82	0/5295	
All	All	0.73	0/7783	0.82	0/10564	

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	A	3798	0	3594	6	0
1	В	3819	0	3621	10	0
2	A	422	0	0	1	0
2	В	486	0	0	0	0
All	All	8525	0	7215	16	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 1.

All (16) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	$egin{aligned} & \operatorname{Clash} \ & \operatorname{overlap}\ (\begin{subarray}{c} \begin{subarray}{c} \$	
1:B:493:LYS:O	1:B:497:GLN:HG3	1.96	0.65	

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Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:A:59:LYS:HB2	2:A:939:HOH:O	2.09	0.52
1:A:139:THR:HG22	1:A:170:ASN:HB2	1.96	0.47
1:B:15:GLY:HA2	1:B:36:GLY:O	2.14	0.47
1:A:245:GLU:HA	1:A:267:LYS:O	2.16	0.46
1:A:291:GLY:O	1:A:329:ALA:HA	2.15	0.46
1:B:100:ARG:HD2	1:B:105:TRP:CE2	2.52	0.45
1:A:188:MET:HB3	1:A:190:HIS:CD2	2.54	0.43
1:B:386:ASP:OD1	1:B:408:GLN:OE1	2.37	0.42
1:A:123:THR:HA	1:A:155:ASP:O	2.19	0.42
1:B:245:GLU:HA	1:B:267:LYS:O	2.19	0.42
1:B:291:GLY:O	1:B:329:ALA:HA	2.19	0.41
1:B:380:PHE:O	1:B:405:SER:HA	2.21	0.40
1:B:250:GLY:HA2	1:B:272:ASN:O	2.20	0.40
1:B:225:ASP:HA	1:B:249:TYR:O	2.22	0.40
1:B:188:MET:HB3	1:B:190:HIS:CD2	2.56	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	Perce	entiles
1	A	489/492~(99%)	475 (97%)	14 (3%)	0	100	100
1	В	$490/492\ (100\%)$	480 (98%)	10 (2%)	0	100	100
All	All	979/984 (100%)	955 (98%)	24 (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 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	$390/422 \ (92\%)$	387 (99%)	3 (1%)	81 68
1	В	394/422 (93%)	391 (99%)	3 (1%)	81 68
All	All	784/844 (93%)	778 (99%)	6 (1%)	81 68

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	TYR
1	A	235	GLU
1	A	338	PHE
1	В	94	TYR
1	В	235	GLU
1	В	338	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	435	GLN
1	В	402	ASN
1	В	408	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)

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,  $95^{th}$  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	<RSRZ $>$	$\# \mathbf{RSRZ} >$	2	$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	491/492 (99%)	-0.07	8 (1%) 72	74	14, 23, 39, 48	0
1	В	$492/492 \ (100\%)$	-0.31	1 (0%) 95	94	14, 21, 34, 48	1 (0%)
All	All	983/984 (99%)	-0.19	9 (0%) 84	85	14, 22, 36, 48	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	391	PHE	3.2
1	A	400	LEU	3.1
1	В	15	GLY	2.9
1	A	394	ASN	2.5
1	A	417	ASN	2.4
1	A	177	ALA	2.3
1	A	435	GLN	2.2
1	A	395	LEU	2.2
1	A	396	ASP	2.0

### 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.

