



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 3, 2024 – 01:07 am GMT

PDB ID : 2VZS  
Title : Chitosan Product complex of Amycolatopsis orientalis exo-chitosanase CsxA  
Authors : Lammerts van Bueren, A.; Ghinet, M.G.; Gregg, K.; Fleury, A.; Brzezinski, R.; Boraston, A.B.  
Deposited on : 2008-08-05  
Resolution : 1.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

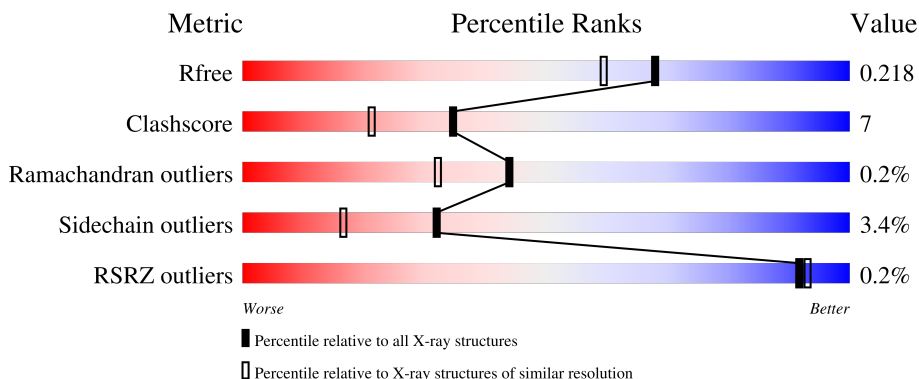
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	3097 (1.86-1.86)
Clashscore	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)
RSRZ outliers	164620	3097 (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  $\geq 3$ , 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  $\leq 5\%$ . 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	1032	 72% 9% 17%
1	B	1032	 73% 9% 17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CD	A	1899	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14981 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 EXO-BETA-D-GLUCOSAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	858	Total	C	N	O	S	4	0	1
			6552	4115	1133	1287	17			
1	B	858	Total	C	N	O	S	0	0	1
			6552	4115	1133	1287	17			

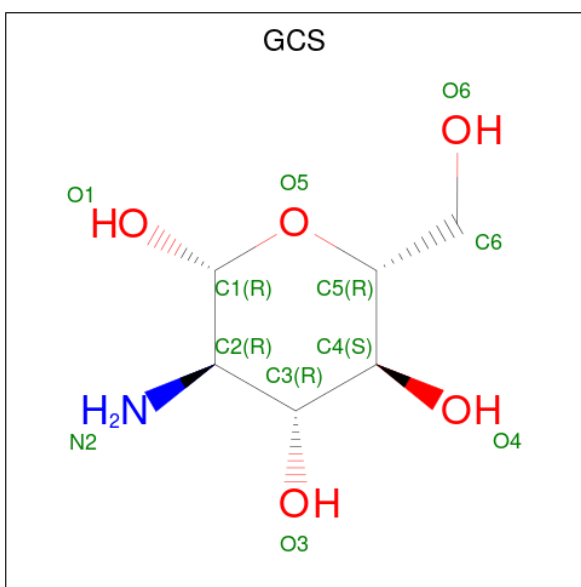
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	750	ASN	TRP	conflict	UNP Q56F26
B	750	ASN	TRP	conflict	UNP Q56F26

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cd	0	0
			3	3		
2	B	3	Total	Cd	0	0
			3	3		

- Molecule 3 is 2-amino-2-deoxy-beta-D-glucopyranose (three-letter code: GCS) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	6	1	5		
3	B	1	Total	C	N	O	0	0
			12	6	1	5		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

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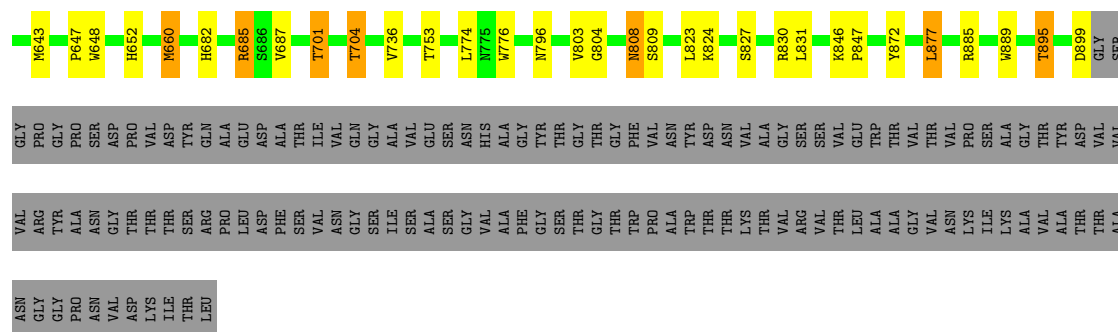
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	958	Total	O	0	0
			958	958		
5	B	871	Total	O	0	0
			871	871		







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.54Å 121.81Å 91.84Å 90.00° 90.42° 90.00°	Depositor
Resolution (Å)	40.00 – 1.85 40.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-1.85) 99.8 (40.00-1.85)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.173 , 0.220 0.172 , 0.218	Depositor DCC
$R_{free}$ test set	8098 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 47.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14981	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GCS, GOL, CD

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	0.90	1/6715 (0.0%)	0.97	23/9163 (0.3%)
1	B	0.90	2/6715 (0.0%)	1.04	25/9163 (0.3%)
All	All	0.90	3/13430 (0.0%)	1.00	48/18326 (0.3%)

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 outliers	#Planarity outliers
1	A	0	3
1	B	0	3
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	430	GLU	CB-CG	12.05	1.75	1.52
1	B	335	ARG	CD-NE	-6.21	1.35	1.46
1	B	454	ARG	CD-NE	-5.79	1.36	1.46

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	335	ARG	NE-CZ-NH2	-28.58	106.01	120.30
1	B	454	ARG	NE-CZ-NH2	-27.75	106.43	120.30
1	A	335	ARG	NE-CZ-NH2	-26.63	106.99	120.30
1	A	335	ARG	NE-CZ-NH1	21.46	131.03	120.30
1	B	454	ARG	NE-CZ-NH1	21.35	130.98	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	468	SER	Peptide
1	A	596	ARG	Peptide
1	A	98	GLY	Peptide
1	B	468	SER	Peptide
1	B	98	GLY	Peptide

## 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	6552	0	6328	100	0
1	B	6552	0	6328	92	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	12	0	13	1	0
3	B	12	0	13	1	0
4	A	6	0	8	0	0
4	B	12	0	15	0	0
5	A	958	0	0	40	1
5	B	871	0	0	45	1
All	All	14981	0	12705	192	1

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 7.

The worst 5 of 192 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:B:643:MET:CE	5:B:2625:HOH:O	1.81	1.26
1:B:483:ALA:HB3	5:B:2492:HOH:O	1.30	1.24
1:A:512:MET:HE1	5:A:2516:HOH:O	1.39	1.18
1:B:753:THR:HB	5:B:2719:HOH:O	1.39	1.18
1:A:846:LYS:HG2	5:A:2389:HOH:O	1.41	1.16

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:2020:HOH:O	5:B:2658:HOH:O[1_655]	2.00	0.20

## 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	856/1032 (83%)	838 (98%)	16 (2%)	2 (0%)	44 32
1	B	856/1032 (83%)	833 (97%)	21 (2%)	2 (0%)	44 32
All	All	1712/2064 (83%)	1671 (98%)	37 (2%)	4 (0%)	44 32

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	469	ASP
1	A	202	ILE
1	B	202	ILE
1	B	205	ALA

### 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	702/834 (84%)	679 (97%)	23 (3%)	33 18
1	B	702/834 (84%)	677 (96%)	25 (4%)	30 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1404/1668 (84%)	1356 (97%)	48 (3%)	32 16

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	144	LEU
1	B	337	VAL
1	B	211	GLN
1	B	236	GLN
1	B	608	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	194	ASN
1	B	348	GLN
1	B	299	ASN
1	B	352	ASN
1	A	682	HIS

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 for Mogul analysis.

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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	B	1902	-	5,5,5	0.77	0	5,5,5	0.73	0
4	GOL	B	1904	-	5,5,5	0.80	0	5,5,5	1.83	2 (40%)
3	GCS	A	1902	-	12,12,12	1.05	1 (8%)	16,17,17	1.98	4 (25%)
4	GOL	A	1903	-	5,5,5	0.74	0	5,5,5	0.29	0
3	GCS	B	1903	-	12,12,12	1.31	1 (8%)	16,17,17	2.07	2 (12%)

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
4	GOL	B	1902	-	-	0/4/4/4	-
4	GOL	B	1904	-	-	3/4/4/4	-
3	GCS	A	1902	-	-	0/2/22/22	0/1/1/1
4	GOL	A	1903	-	-	0/4/4/4	-
3	GCS	B	1903	-	-	0/2/22/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1903	GCS	C1-C2	3.28	1.56	1.52
3	A	1902	GCS	C1-C2	2.01	1.55	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1903	GCS	O1-C1-O5	-6.01	92.33	110.38
3	B	1903	GCS	O5-C1-C2	5.10	115.47	109.51
3	A	1902	GCS	O5-C1-C2	4.23	114.44	109.51
3	A	1902	GCS	O1-C1-O5	-4.22	97.72	110.38
3	A	1902	GCS	O5-C5-C4	-3.02	104.20	109.69

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1904	GOL	O1-C1-C2-C3
4	B	1904	GOL	O1-C1-C2-O2
4	B	1904	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1902	GCS	1	0
3	B	1903	GCS	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	858/1032 (83%)	-0.59	3 (0%) 90 92	11, 19, 28, 42	1 (0%)
1	B	858/1032 (83%)	-0.56	0 100 100	11, 19, 29, 43	0
All	All	1716/2064 (83%)	-0.57	3 (0%) 92 93	11, 19, 28, 43	1 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	VAL	2.5
1	A	45	GLY	2.2
1	A	48	ALA	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 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<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	CD	A	1899	1/1	0.64	0.45	237,237,237,237	0
2	CD	A	1901	1/1	0.83	0.28	120,120,120,120	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	1903	6/6	0.93	0.07	21,22,24,25	0
4	GOL	B	1902	6/6	0.93	0.12	20,24,24,25	0
4	GOL	B	1904	6/6	0.94	0.07	20,20,23,24	0
2	CD	B	1901	1/1	0.95	0.24	76,76,76,76	0
3	GCS	B	1903	12/12	0.97	0.04	14,16,20,24	0
3	GCS	A	1902	12/12	0.97	0.04	16,18,20,25	0
2	CD	A	1900	1/1	0.99	0.15	37,37,37,37	0
2	CD	B	1899	1/1	1.00	0.01	18,18,18,18	0
2	CD	B	1900	1/1	1.00	0.01	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.