



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 01:48 AM UTC

PDB ID : 2VZS / pdb_00002vzs
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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

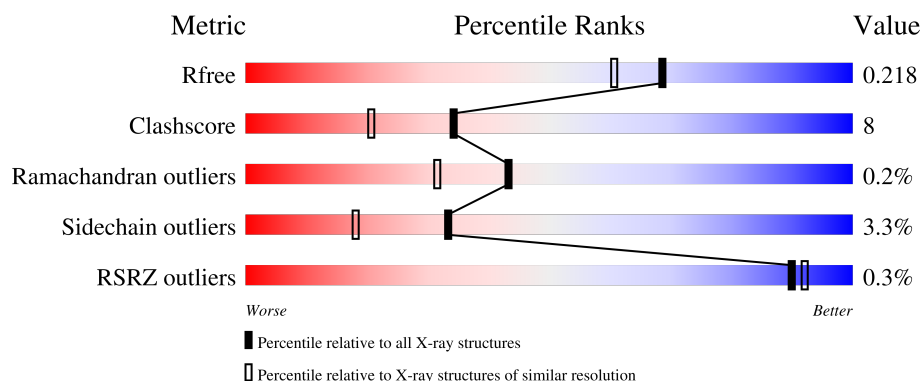
1 Overall quality at a glance

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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (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 $\leq 5\%$. 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	
1	B	1032	

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
4	GOL	B	1904	-	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			

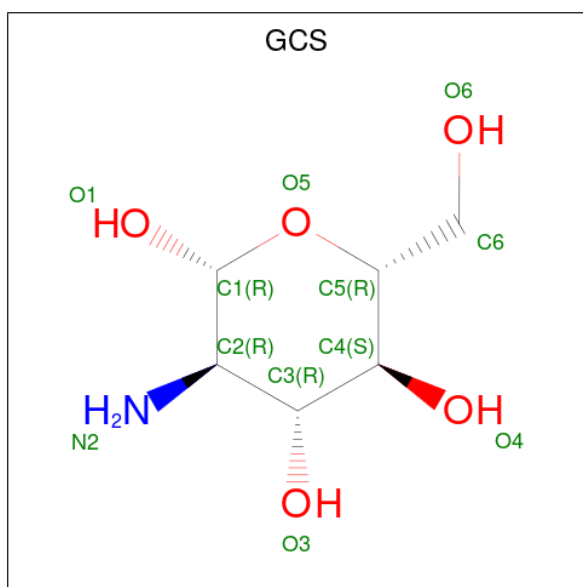
There are 2 discrepancies between the modelled and reference sequences:

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 (CCD ID: 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 (CCD ID: GCS) (formula: C₆H₁₃NO₅).



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 (CCD ID: GOL) (formula: $C_3H_8O_3$).



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		

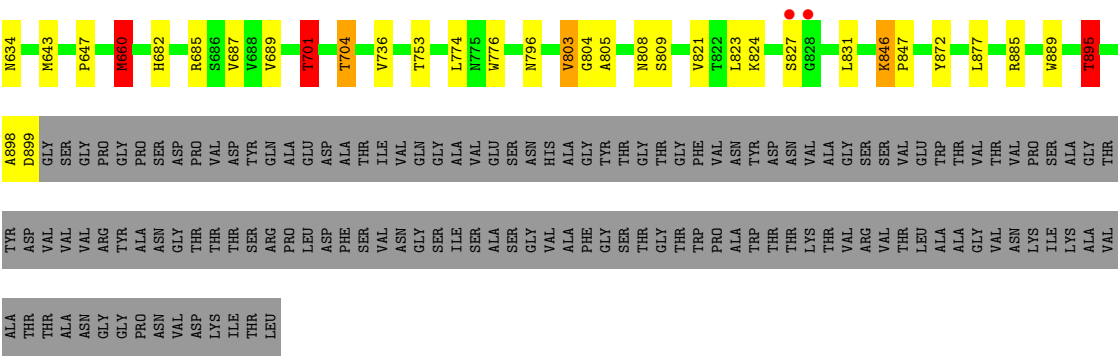
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

- 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, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 ²)	19.9	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	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 ²)	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.*

¹Intensities estimated from amplitudes.

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.

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: 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	1.05	5/6715 (0.1%)	1.03	26/9163 (0.3%)
1	B	1.06	6/6715 (0.1%)	1.08	32/9163 (0.3%)
All	All	1.05	11/13430 (0.1%)	1.05	58/18326 (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

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	468	SER	CA-C	8.85	1.57	1.52
1	A	430	GLU	CB-CG	7.53	1.75	1.52
1	B	335	ARG	CD-NE	-7.40	1.35	1.46
1	B	454	ARG	CD-NE	-6.88	1.36	1.46
1	A	898	ALA	C-N	-6.18	1.24	1.33

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	597	TYR	N-CA-C	16.58	132.60	112.38
1	A	597	TYR	N-CA-C	15.25	130.99	112.38
1	B	335	ARG	NE-CZ-NH2	-14.65	106.01	119.20
1	B	454	ARG	NE-CZ-NH2	-14.19	106.43	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	LYS	N-CA-C	-13.86	96.50	113.41

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	103	0
1	B	6552	0	6328	93	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	41	1
5	B	871	0	0	45	1
All	All	14981	0	12705	196	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 8.

The worst 5 of 196 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:512:MET:HE1	5:A:2516:HOH:O	1.15	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:643:MET:HE3	5:B:2625:HOH:O	1.10	1.27
1:B:483:ALA:HB3	5:B:2492:HOH:O	1.30	1.24
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%)	43	31
1	B	856/1032 (83%)	833 (97%)	21 (2%)	2 (0%)	43	31
All	All	1712/2064 (83%)	1671 (98%)	37 (2%)	4 (0%)	43	31

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%)	678 (97%)	24 (3%)	32	17
All	All	1404/1668 (84%)	1357 (97%)	47 (3%)	33	18

5 of 47 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	247	LEU
1	B	608	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	808	ASN
1	B	894	GLN
1	B	276	GLN
1	B	796	ASN
1	B	212	ASN

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	0.81	0	5,5,5	0.77	0
3	GCS	B	1903	-	12,12,12	1.31	1 (8%)	16,17,17	2.08	2 (12%)
4	GOL	B	1904	-	5,5,5	0.82	0	5,5,5	1.94	3 (60%)
3	GCS	A	1902	-	12,12,12	1.05	1 (8%)	16,17,17	1.99	4 (25%)
4	GOL	A	1903	-	5,5,5	0.78	0	5,5,5	0.28	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
4	GOL	B	1902	-	-	0/4/4/4	-
3	GCS	B	1903	-	-	0/2/22/22	0/1/1/1
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	-

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 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1903	GCS	O1-C1-O5	-6.09	92.33	110.41
3	B	1903	GCS	O5-C1-C2	5.10	115.47	109.51
3	A	1902	GCS	O1-C1-O5	-4.27	97.72	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1902	GCS	O5-C1-C2	4.23	114.44	109.51
3	A	1902	GCS	O5-C5-C4	-3.05	104.20	109.70

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	B	1903	GCS	1	0
3	A	1902	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, 95th 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 ²)	Q<0.9
1	A	858/1032 (83%)	-0.49	3 (0%)	90 92	11, 19, 28, 42	1 (0%)
1	B	858/1032 (83%)	-0.46	2 (0%)	91 93	11, 19, 29, 43	0
All	All	1716/2064 (83%)	-0.48	5 (0%)	90 92	11, 19, 28, 43	1 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	VAL	2.7
1	A	45	GLY	2.4
1	A	48	ALA	2.2
1	B	828	GLY	2.1
1	B	827	SER	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 oligosaccharides 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, 95th 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($\text{\AA}^2$)	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
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.