



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:09 AM UTC

PDB ID : 3GTN / pdb_00003gtn
Title : Crystal Structure of XynC from Bacillus subtilis 168
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Deposited on : 2009-03-27
Resolution : 2.68 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
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

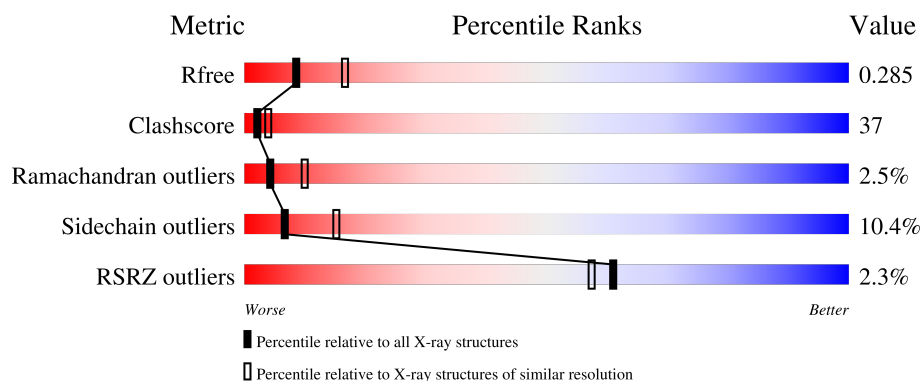
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.68 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	401	2% 42% 46% 8% ..
1	B	401	2% 35% 52% 11% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6306 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 Glucuronoxylanase xynC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3158	1997	564	588	9			
1	B	394	Total	C	N	O	S	0	0	0
			3148	1991	561	587	9			

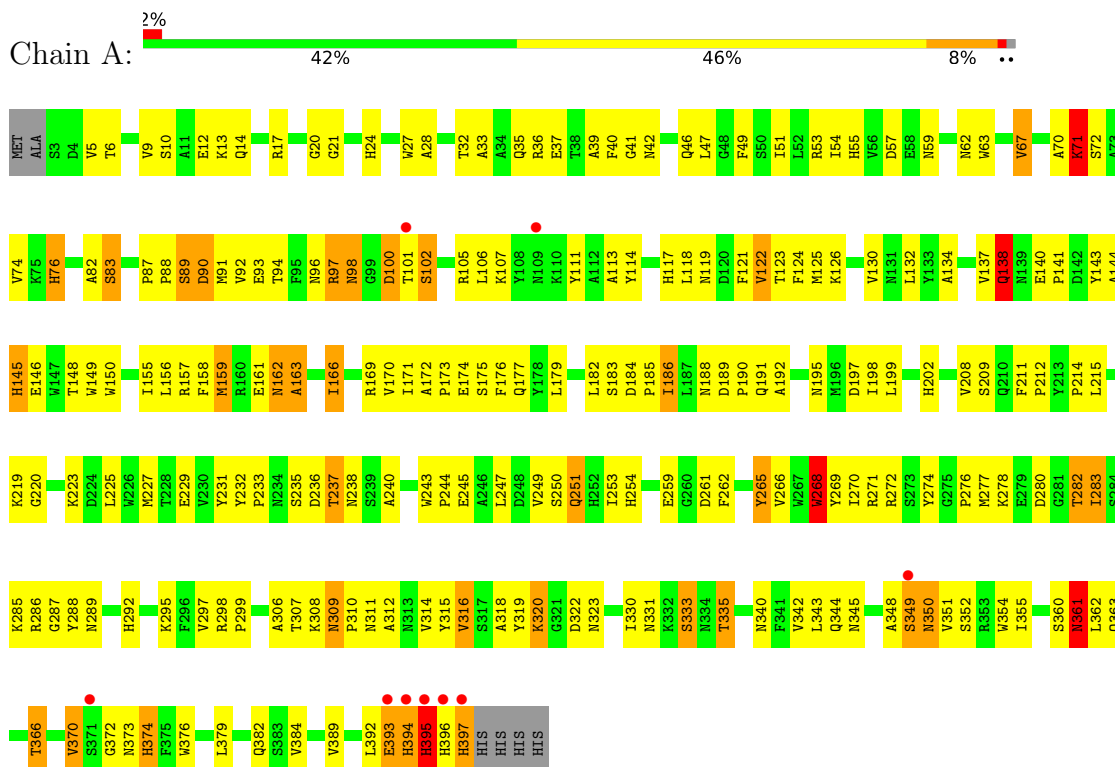
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q45070
A	392	LEU	-	expression tag	UNP Q45070
A	393	GLU	-	expression tag	UNP Q45070
A	394	HIS	-	expression tag	UNP Q45070
A	395	HIS	-	expression tag	UNP Q45070
A	396	HIS	-	expression tag	UNP Q45070
A	397	HIS	-	expression tag	UNP Q45070
A	398	HIS	-	expression tag	UNP Q45070
A	399	HIS	-	expression tag	UNP Q45070
A	400	HIS	-	expression tag	UNP Q45070
A	401	HIS	-	expression tag	UNP Q45070
B	1	MET	-	initiating methionine	UNP Q45070
B	392	LEU	-	expression tag	UNP Q45070
B	393	GLU	-	expression tag	UNP Q45070
B	394	HIS	-	expression tag	UNP Q45070
B	395	HIS	-	expression tag	UNP Q45070
B	396	HIS	-	expression tag	UNP Q45070
B	397	HIS	-	expression tag	UNP Q45070
B	398	HIS	-	expression tag	UNP Q45070
B	399	HIS	-	expression tag	UNP Q45070
B	400	HIS	-	expression tag	UNP Q45070
B	401	HIS	-	expression tag	UNP Q45070

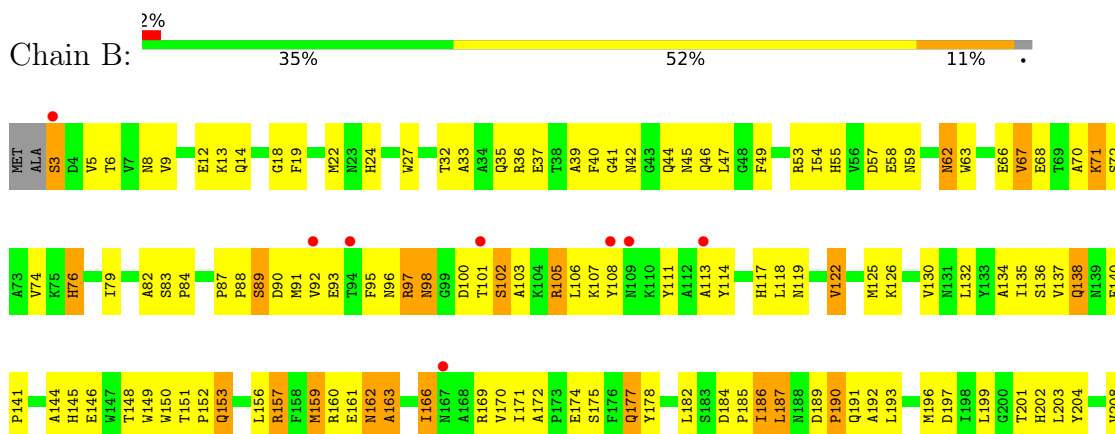
3 Residue-property plots

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: Glucuronoxylanase xynC



• Molecule 1: Glucuronoxylanase xynC



S209	Q210	F211	P212	Y213	P214	L215		A221	G222	K223	D224	L225	W226	M227	T228	E229	V230	Y231	Y232	P233	N234	S235	D236	T237	N238	S239	D240	R241	W242	P243	E244	A245	L246	L247	D248	V249	S250	Q251	H252	I253	H254	N255	A256	M257	V258	E259	G260	D261	F262	Q263	A264	Y265	V266	W267	W268	Y269	I270	R271	R272
	P276	M277	K278	E279	D280	G281	T282	I283	S284	K285	R286	G287	Y288	N289	M290	A291	H292		K295	F296	V297		V302	R303	I304	D305	A306	T307	K308	N309	P310	N311	A312	N313	V314	Y315	V316	S317	A318	Y319	K320	G321	D322	N323	K324	V325		I330	N331	K332	S333	N334	T335		Q339	N340	F341	V342	L343
Q344	N345		A348	S349	N350	V351	S352	R353	W354	I355		S358	S359	S360	N361	L362	Q363		T366		V370	S371	G372	N373	H374	F375	W376	A377	H378	L379	P380	A381	Q382	S383	V384	T385	T386	F387	V388	V389	H390	R391	L392	E393	H394	H395	H396	HIS	HIS	HIS	HIS	HIS							

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.34Å 82.11Å 96.65Å 90.00° 104.70° 90.00°	Depositor
Resolution (Å)	33.33 – 2.68 33.33 – 2.68	Depositor EDS
% Data completeness (in resolution range)	95.7 (33.33-2.68) 95.6 (33.33-2.68)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.236 , 0.287 0.238 , 0.285	Depositor DCC
R_{free} test set	1281 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6306	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.97% 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](#)

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	1.02	8/3249 (0.2%)	1.17	20/4425 (0.5%)
1	B	1.03	15/3238 (0.5%)	1.25	33/4410 (0.7%)
All	All	1.02	23/6487 (0.4%)	1.21	53/8835 (0.6%)

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	153	GLN	CD-NE2	-7.33	1.17	1.33
1	A	13	LYS	CA-C	-6.46	1.50	1.53
1	B	13	LYS	CA-C	-6.40	1.50	1.53
1	A	138	GLN	CD-NE2	-6.24	1.20	1.33
1	B	62	ASN	CG-OD1	6.23	1.35	1.23

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	VAL	N-CA-C	8.26	118.31	110.30
1	B	187	LEU	N-CA-C	-7.10	103.59	111.82
1	B	249	VAL	N-CA-C	-6.84	103.64	110.62
1	B	117	HIS	CB-CG-CD2	-6.82	122.34	131.20
1	B	394	HIS	CB-CG-CD2	-6.73	122.45	131.20

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	3158	0	3003	203	1
1	B	3148	0	2996	256	1
All	All	6306	0	5999	459	2

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 37.

The worst 5 of 459 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:137:VAL:HG21	1:A:159:MET:HE1	1.30	1.13
1:A:138:GLN:HG2	1:A:150:TRP:NE1	1.63	1.12
1:B:134:ALA:HB1	1:B:171:ILE:CD1	1.83	1.08
1:B:394:HIS:O	1:B:394:HIS:ND1	1.89	1.05
1:B:288:TYR:CE2	1:B:361:ASN:ND2	2.23	1.05

All (2) 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)
1:B:37:GLU:OE2	1:B:209:SER:OG[2_546]	1.98	0.22
1:A:37:GLU:OE2	1:A:209:SER:OG[2_555]	2.18	0.02

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	393/401 (98%)	353 (90%)	31 (8%)	9 (2%)	5	11
1	B	392/401 (98%)	337 (86%)	44 (11%)	11 (3%)	4	8
All	All	785/802 (98%)	690 (88%)	75 (10%)	20 (2%)	4	10

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	TRP
1	B	166	ILE
1	B	268	TRP
1	B	394	HIS
1	A	71	LYS

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	336/341 (98%)	297 (88%)	39 (12%)	5	12
1	B	335/341 (98%)	304 (91%)	31 (9%)	8	19
All	All	671/682 (98%)	601 (90%)	70 (10%)	7	15

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	320	LYS
1	B	335	THR
1	B	374	HIS
1	A	335	THR
1	A	333	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	340	ASN
1	B	138	GLN
1	B	340	ASN
1	B	210	GLN
1	A	210	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 oligosaccharides 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, 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	395/401 (98%)	0.25	9 (2%) 61 57	13, 25, 41, 66	0
1	B	394/401 (98%)	0.23	9 (2%) 61 57	13, 25, 40, 50	0
All	All	789/802 (98%)	0.24	18 (2%) 61 57	13, 25, 41, 66	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	92	VAL	3.4
1	B	370	VAL	3.1
1	A	396	HIS	3.0
1	B	101	THR	2.9
1	A	371	SER	2.8

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.