



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:50 AM UTC

PDB ID : 1BVN / pdb_00001bvn
Title : PIG PANCREATIC ALPHA-AMYLASE IN COMPLEX WITH THE PROTEINACEOUS INHIBITOR TENDAMISTAT
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Deposited on : 1998-09-16
Resolution : 2.50 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

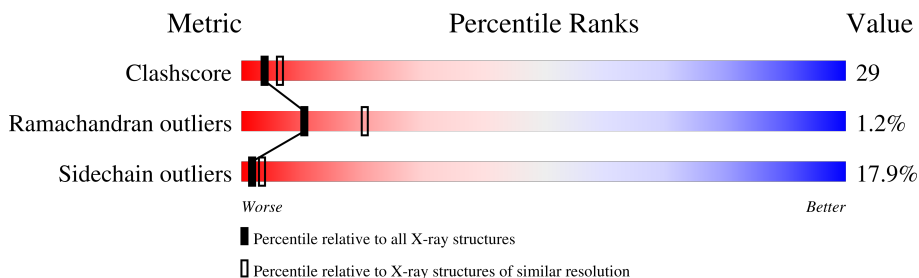
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	P	496	
2	T	74	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4606 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 PROTEIN (ALPHA-AMYLASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	496	Total	C	N	O	S	0	0	0
			3907	2467	689	730	21			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	12	ASP	SER	conflict	UNP P00690
P	49	VAL	ILE	conflict	UNP P00690
P	196	LEU	ILE	conflict	UNP P00690
P	243	SER	GLN	conflict	UNP P00690
P	310	SER	ALA	conflict	UNP P00690
P	404	GLN	GLU	conflict	UNP P00690
P	451	ASN	ASP	conflict	UNP P00690
P	484	GLN	GLU	conflict	UNP P00690

- Molecule 2 is a protein called PROTEIN (TENDAMISTAT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	71	Total	C	N	O	S	0	0	0
			536	333	90	109	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	829	GLU	GLN	conflict	UNP P01092

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total	Ca	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	1	Total 1	Cl 1	0	0

- Molecule 5 is water.

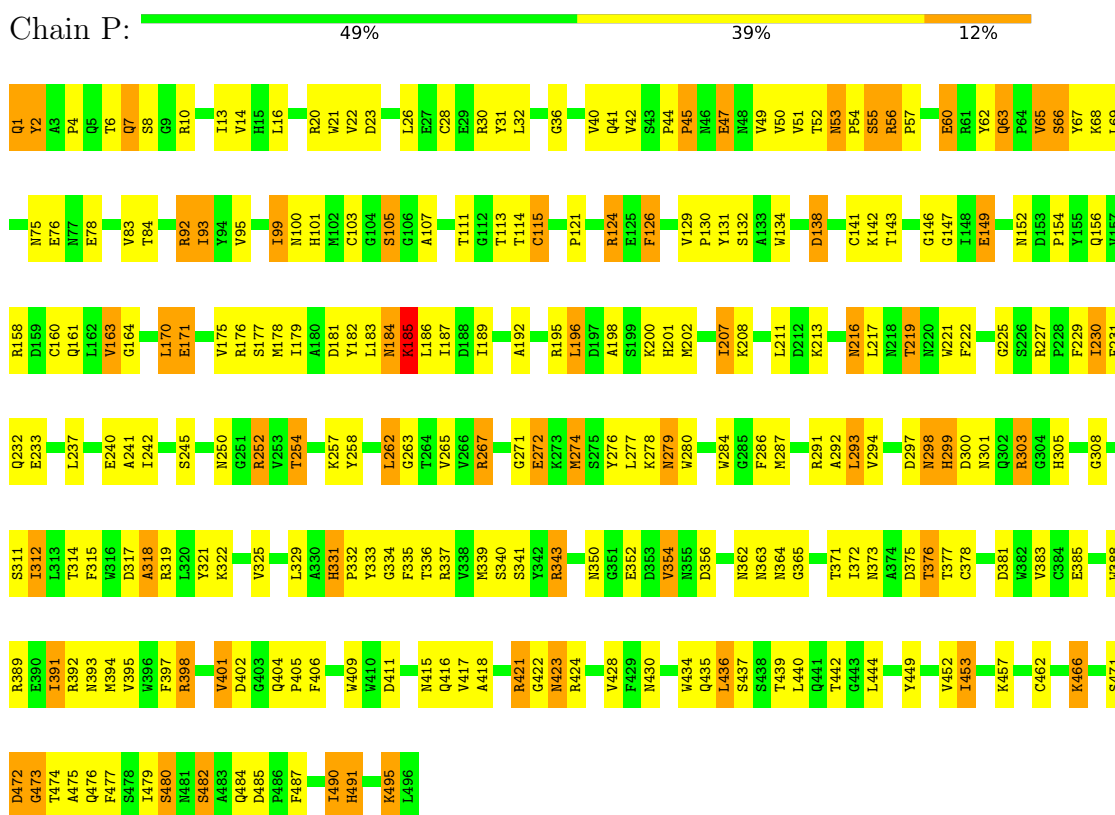
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	P	144	Total 144	O 144	0	0
5	T	17	Total 17	O 17	0	0

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN (ALPHA-AMYLASE)



• Molecule 2: PROTEIN (TENDAMISTAT)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	77.70Å 77.70Å 359.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.40 – 2.50	Depositor
% Data completeness (in resolution range)	73.7 (29.40-2.50)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.185	Depositor
R, R_{free}	0.166 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4606	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	P	0.49	0/4017	1.07	25/5459 (0.5%)
2	T	0.48	0/548	0.97	1/748 (0.1%)
All	All	0.49	0/4565	1.06	26/6207 (0.4%)

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	P	0	2

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	P	473	GLY	N-CA-C	-10.62	99.71	115.00
1	P	185	LYS	N-CA-C	-8.95	99.15	112.04
1	P	216	ASN	N-CA-C	-8.30	99.35	110.55
1	P	76	GLU	N-CA-C	7.19	119.12	111.28
1	P	293	LEU	N-CA-C	-7.11	97.14	108.73

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	P	2	TYR	Sidechain
1	P	53	ASN	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	P	3907	0	3684	216	0
2	T	536	0	497	40	0
3	P	1	0	0	0	0
4	P	1	0	0	0	0
5	P	144	0	0	5	0
5	T	17	0	0	1	0
All	All	4606	0	4181	247	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 29.

The worst 5 of 247 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:P:143:THR:HG23	1:P:146:GLY:H	1.34	0.92
1:P:423:ASN:HD22	1:P:423:ASN:H	1.13	0.91
1:P:99:ILE:HD11	1:P:196:LEU:HD21	1.53	0.91
1:P:401:VAL:HG11	1:P:421:ARG:HB2	1.53	0.91
1:P:301:ASN:HB3	1:P:312:ILE:HG12	1.50	0.90

There are no symmetry-related clashes.

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	P	494/496 (100%)	440 (89%)	47 (10%)	7 (1%)	9 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	T	69/74 (93%)	65 (94%)	4 (6%)	0	100	100
All	All	563/570 (99%)	505 (90%)	51 (9%)	7 (1%)	10	20

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	280	TRP
1	P	55	SER
1	P	111	THR
1	P	271	GLY
1	P	318	ALA

5.3.2 Protein sidechains ⓘ

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	P	413/413 (100%)	339 (82%)	74 (18%)	2	3
2	T	57/60 (95%)	47 (82%)	10 (18%)	2	3
All	All	470/473 (99%)	386 (82%)	84 (18%)	2	3

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	421	ARG
1	P	484	GLN
1	P	434	TRP
1	P	462	CYS
2	T	821	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	362	ASN
1	P	408	ASN

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Mol	Chain	Res	Type
1	P	423	ASN
1	P	373	ASN
1	P	220	ASN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.