



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1QE3  
Title : PNB ESTERASE  
Authors : Spiller, B.; Gershenson, A.; Arnold, F.; Stevens, R.  
Deposited on : 1999-07-12  
Resolution : 1.50 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](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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

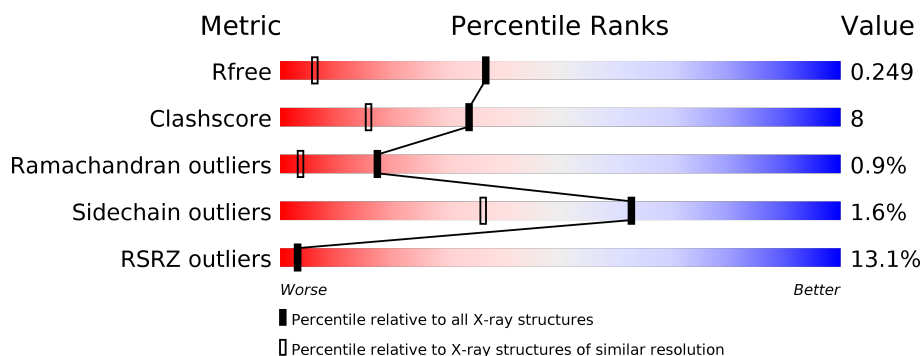
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 on 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	489	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4001 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 PARA-NITROBENZYL ESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3643	2340	598	695	10			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

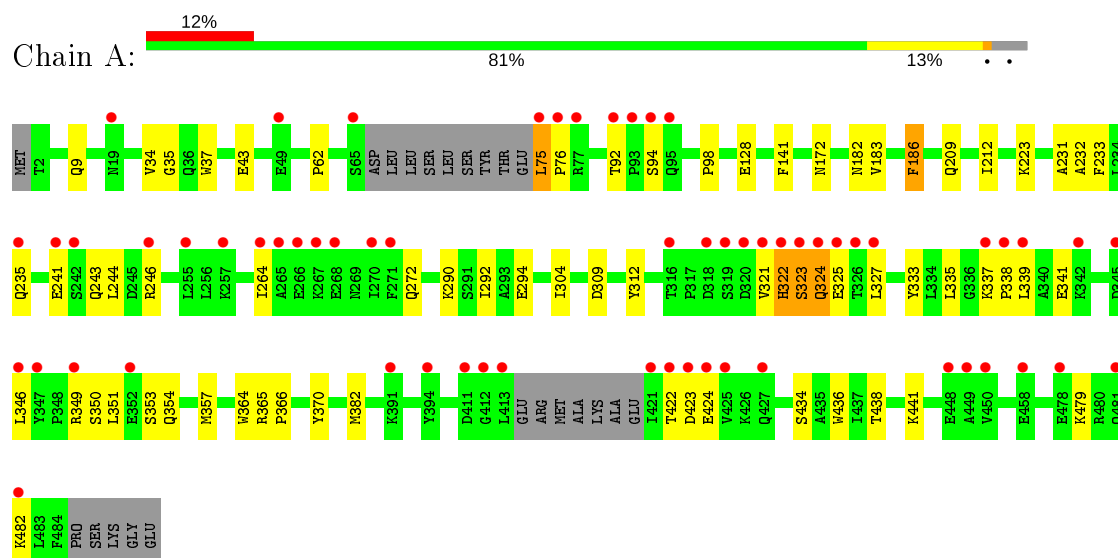
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	352	Total 352	O 352	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: PARA-NITROBENZYL ESTERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.24Å 80.71Å 99.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.50 21.19 – 1.50	Depositor EDS
% Data completeness (in resolution range)	83.7 (25.00-1.50) 92.3 (21.19-1.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 1.49Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.220 , 0.240 0.231 , 0.249	Depositor DCC
$R_{free}$ test set	8113 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.5	Xtriage
Anisotropy	0.602	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4001	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 5.99% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4

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	0.31	0/3744	0.60	0/5104

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	3643	0	3533	61	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
4	A	352	0	0	2	0
All	All	4001	0	3533	61	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 8.

All (61) 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:324:GLN:HA	1:A:327:LEU:HB3	1.65	0.79
1:A:322:HIS:CD2	1:A:350:SER:H	2.04	0.74
1:A:183:VAL:H	1:A:209:GLN:NE2	1.86	0.74
1:A:75:LEU:N	1:A:76:PRO:HD2	2.04	0.73
1:A:322:HIS:HD2	1:A:350:SER:H	1.38	0.70
1:A:9:GLN:HE21	1:A:172:ASN:HD21	1.39	0.69
1:A:34:VAL:HG23	4:A:825:HOH:O	1.95	0.67
1:A:183:VAL:H	1:A:209:GLN:HE21	1.42	0.65
1:A:422:THR:HG22	1:A:423:ASP:H	1.61	0.63
1:A:231:ALA:O	1:A:235:GLN:HG3	1.97	0.63
1:A:422:THR:HG22	1:A:423:ASP:N	2.14	0.62
1:A:272:GLN:HG3	1:A:333:TYR:CZ	2.35	0.62
1:A:244:LEU:HD22	1:A:244:LEU:H	1.66	0.61
1:A:75:LEU:N	1:A:76:PRO:CD	2.64	0.60
1:A:353:SER:O	1:A:357:MET:HG3	2.02	0.60
1:A:92:THR:HG21	1:A:128:GLU:OE1	2.03	0.59
1:A:321:VAL:HA	1:A:354:GLN:HE22	1.66	0.59
1:A:323:SER:N	1:A:349:ARG:HH12	2.03	0.57
1:A:365:ARG:HB3	1:A:366:PRO:HD3	1.89	0.55
1:A:292:ILE:HG13	1:A:370:TYR:CZ	2.42	0.54
1:A:337:LYS:N	1:A:338:PRO:HD2	2.22	0.54
1:A:324:GLN:CA	1:A:327:LEU:HB3	2.37	0.53
1:A:322:HIS:CE1	1:A:327:LEU:HD13	2.43	0.53
1:A:9:GLN:NE2	1:A:172:ASN:HD21	2.06	0.53
1:A:264:ILE:HG22	1:A:264:ILE:O	2.09	0.53
1:A:34:VAL:HG22	1:A:35:GLY:N	2.25	0.52
1:A:75:LEU:HD22	1:A:76:PRO:N	2.25	0.52
1:A:346:LEU:HD21	1:A:482:LYS:HD3	1.92	0.51
1:A:243:GLN:HB3	1:A:246:ARG:HD3	1.93	0.50
1:A:92:THR:HG22	1:A:94:SER:H	1.76	0.50
1:A:322:HIS:CE1	1:A:354:GLN:HB3	2.46	0.50
1:A:364:TRP:CE3	1:A:479:LYS:HE3	2.47	0.49
1:A:244:LEU:N	1:A:244:LEU:HD22	2.29	0.48
1:A:75:LEU:HD13	1:A:75:LEU:N	2.29	0.48
1:A:346:LEU:HD21	1:A:482:LYS:CD	2.44	0.47
1:A:37:TRP:CZ3	1:A:43:GLU:HG3	2.49	0.47
1:A:62:PRO:HB2	1:A:141:PHE:CE1	2.50	0.47
1:A:186:PHE:CB	1:A:212:ILE:HB	2.46	0.46
1:A:223:LYS:HE2	4:A:833:HOH:O	2.16	0.46
1:A:98:PRO:HG2	1:A:441:LYS:HG2	1.97	0.46
1:A:322:HIS:ND1	1:A:327:LEU:HD22	2.31	0.45
1:A:323:SER:N	1:A:349:ARG:NH1	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:ALA:HA	1:A:235:GLN:HE21	1.82	0.43
1:A:322:HIS:HD2	1:A:350:SER:N	2.11	0.43
1:A:75:LEU:HD13	1:A:76:PRO:HD3	2.00	0.43
1:A:422:THR:CG2	1:A:423:ASP:H	2.31	0.43
1:A:339:LEU:HD23	1:A:339:LEU:O	2.19	0.43
1:A:322:HIS:HB3	1:A:323:SER:H	1.37	0.43
1:A:337:LYS:O	1:A:341:GLU:HG3	2.19	0.43
1:A:322:HIS:O	1:A:323:SER:HB2	2.19	0.42
1:A:290:LYS:NZ	1:A:294:GLU:HG3	2.33	0.42
1:A:186:PHE:HB2	1:A:212:ILE:HB	2.02	0.42
1:A:309:ASP:HB3	1:A:312:TYR:CD1	2.55	0.42
1:A:349:ARG:O	1:A:350:SER:HB3	2.20	0.42
1:A:327:LEU:CD1	1:A:357:MET:SD	3.08	0.41
1:A:434:SER:O	1:A:438:THR:HG23	2.20	0.41
1:A:351:LEU:HA	1:A:354:GLN:NE2	2.35	0.41
1:A:422:THR:CG2	1:A:423:ASP:N	2.82	0.41
1:A:304:ILE:O	1:A:382:MET:HA	2.20	0.41
1:A:241:GLU:O	1:A:244:LEU:CD2	2.70	0.40
1:A:335:LEU:HD22	1:A:339:LEU:HD13	2.04	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	Percentiles
1	A	461/489 (94%)	441 (96%)	16 (4%)	4 (1%)	17 3

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	323	SER
1	A	324	GLN

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Mol	Chain	Res	Type
1	A	322	HIS
1	A	325	GLU

### 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	A	384/403 (95%)	378 (98%)	6 (2%)	62 36

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

Mol	Chain	Res	Type
1	A	75	LEU
1	A	182	ASN
1	A	186	PHE
1	A	233	PHE
1	A	424	GLU
1	A	436	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	19	ASN
1	A	182	ASN
1	A	209	GLN
1	A	235	GLN
1	A	322	HIS
1	A	354	GLN
1	A	456	HIS

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z  > 2$
2	SO4	A	490	-	4,4,4	0.16	0	6,6,6	0.13	0

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 ⓘ

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	467/489 (95%)	0.90	61 (13%) 3 3	11, 17, 31, 42	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	322	HIS	11.7
1	A	75	LEU	10.9
1	A	421	ILE	9.7
1	A	270	ILE	8.4
1	A	320	ASP	6.9
1	A	321	VAL	6.8
1	A	325	GLU	6.7
1	A	267	LYS	6.4
1	A	264	ILE	5.9
1	A	65	SER	5.4
1	A	327	LEU	5.3
1	A	235	GLN	5.3
1	A	93	PRO	5.2
1	A	422	THR	5.2
1	A	266	GLU	5.2
1	A	394	TYR	5.1
1	A	326	THR	4.8
1	A	412	GLY	4.6
1	A	318	ASP	4.6
1	A	316	THR	4.5
1	A	346	LEU	4.3
1	A	449	ALA	3.9
1	A	19	ASN	3.9
1	A	319	SER	3.9
1	A	424	GLU	3.8
1	A	413	LEU	3.6
1	A	92	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	411	ASP	3.5
1	A	265	ALA	3.5
1	A	448	GLU	3.3
1	A	345	ASP	3.2
1	A	94	SER	3.2
1	A	352	GLU	3.2
1	A	268	GLU	3.1
1	A	77	ARG	3.1
1	A	337	LYS	3.1
1	A	241	GLU	3.0
1	A	76	PRO	3.0
1	A	257	LYS	2.8
1	A	339	LEU	2.8
1	A	95	GLN	2.6
1	A	481	GLN	2.6
1	A	242	SER	2.6
1	A	423	ASP	2.5
1	A	342	LYS	2.4
1	A	482	LYS	2.4
1	A	478	GLU	2.4
1	A	324	GLN	2.4
1	A	347	TYR	2.4
1	A	349	ARG	2.4
1	A	49	GLU	2.3
1	A	391	LYS	2.3
1	A	323	SER	2.3
1	A	246	ARG	2.2
1	A	458	GLU	2.2
1	A	427	GLN	2.2
1	A	271	PHE	2.1
1	A	425	VAL	2.1
1	A	255	LEU	2.1
1	A	450	VAL	2.0
1	A	338	PRO	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	490	5/5	0.87	0.27	59,59,59,59	0
3	ZN	A	500	1/1	0.99	0.05	17,17,17,17	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.