

# wwPDB X-ray Structure Validation Summary Report (i)

Nov 13, 2023 – 03:10 pm GMT

PDB ID	:	7QOP
Title	:	A mutant of the nitrile hydratase from Geobacillus pallidus having enhanced
		thermostability
Authors	:	Van Wyk, J.C.; Cowan, D.A.; Danson, M.J.; Tsekoa, T.L.; Sayed, M.F.; Sewell,
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Deposited on		
Resolution	:	1.80  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 (i) 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 (i)) were used in the production of this report:

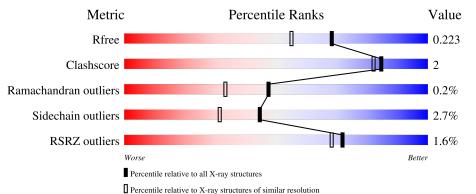
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793(1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 <=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	А	207	% • 88%	9%	••		
2	В	229	87%	11%	••		



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3845 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 Nitrile hydratase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	202	Total 1639	C 1041	N 285	O 306	${ m S} 7$	2	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	47	SER	ILE	engineered mutation	UNP Q84FS5

• Molecule 2 is a protein called Nitrile hydratase subunit beta.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	В	227	Total	С	Ν	Ο	$\mathbf{S}$	0	1	0
	D	221	1862	1198	313	343	8	0	1	0

• Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Co 1 1	0	0

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Mg 1 1	0	0

• Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total Cl 1 1	0	0

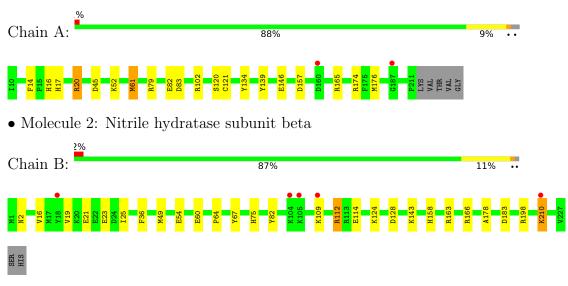
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	160	Total O 160 160	0	0
6	В	181	Total O 181 181	0	0



# 3 Residue-property plots (i)

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: Nitrile hydratase



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	106.50Å $106.50$ Å $83.01$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	75.31 - 1.80	Depositor
Resolution (A)	31.29 - 1.80	EDS
% Data completeness	98.7 (75.31-1.80)	Depositor
(in resolution range)	98.7 (31.29-1.80)	EDS
R <sub>merge</sub>	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$6.06 (at 1.80 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
D D.	0.178 , $0.217$	Depositor
$R, R_{free}$	0.183 , $0.223$	DCC
$R_{free}$ test set	2221 reflections $(5.03\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	21.2	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34,42.1	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.52, < L^2>=0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3845	wwPDB-VP
Average B, all atoms $(Å^2)$	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: CO, CSD, MG, 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	Bo	Bond lengths		ond angles
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	1.34	7/1668~(0.4%)	1.08	9/2268~(0.4%)
2	В	1.31	5/1915~(0.3%)	1.07	4/2588~(0.2%)
All	All	1.32	12/3583~(0.3%)	1.07	13/4856~(0.3%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	82[A]	GLU	CD-OE1	-15.92	1.08	1.25
1	А	82[B]	GLU	CD-OE1	-15.92	1.08	1.25
2	В	54	GLU	CD-OE1	6.70	1.33	1.25
1	А	139	TYR	CE2-CZ	6.55	1.47	1.38
2	В	21	GLU	CD-OE2	6.11	1.32	1.25

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	176	MET	CG-SD-CE	-9.79	84.54	100.20
1	А	165	ARG	NE-CZ-NH1	-7.42	116.59	120.30
1	А	157	ASP	CB-CG-OD2	7.26	124.83	118.30
1	А	45	ASP	CB-CG-OD1	6.87	124.48	118.30
2	В	49	MET	CG-SD-CE	6.72	110.95	100.20

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1639	0	1610	7	0
2	В	1862	0	1816	9	0
3	А	1	0	0	0	0
4	А	1	0	0	0	0
5	А	1	0	0	0	0
6	А	160	0	0	1	1
6	В	181	0	0	4	1
All	All	3845	0	3426	16	1

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.

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 2.

The worst 5 of 16 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:20:ARG:HD2	6:B:363:HOH:O	1.70	0.89
2:B:2:ASN:HD21	2:B:166:ARG:HH12	1.24	0.82
1:A:61:MET:HE3	1:A:61:MET:H	1.56	0.71
2:B:75:HIS:HD2	6:B:460:HOH:O	1.82	0.62
1:A:79:ARG:NE	6:A:402:HOH:O	2.31	0.59

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)
6:A:511:HOH:O	6:B:405:HOH:O[7_558]	2.19	0.01

### 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	Perce	ntiles
1	А	199/207~(96%)	194 (98%)	4 (2%)	1 (0%)	29	15
2	В	226/229 (99%)	220 (97%)	6 (3%)	0	100	100
All	All	425/436~(98%)	414 (97%)	10 (2%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	А	120	SER	

#### 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	А	178/181~(98%)	177~(99%)	1 (1%)	86 84
2	В	195/196~(100%)	186 (95%)	9~(5%)	27 13
All	All	373/377~(99%)	363~(97%)	10 (3%)	44 31

 $5~{\rm of}~10$  residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
2	В	143	LYS
2	В	183	ASP
2	В	210	LYS
2	В	64	PRO
2	В	109	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	В	192	ASN
2	В	158	HIS
2	В	75	HIS
2	В	29	HIS
2	В	152	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)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	Dec	Link	B	ond leng	gths	В	ond ang	gles
INIOI	туре	Chain	$\operatorname{Res}$		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
1	CSD	А	119	1	3,7,8	1.27	0	1,8,10	0.19	0
1	CSD	А	121	3,1	3,7,8	1.34	0	1,8,10	0.64	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
1	CSD	А	119	1	-	0/2/6/8	-
1	CSD	А	121	3,1	-	0/2/6/8	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	А	121	CSD	1	0



#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 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 (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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	200/207~(96%)	-0.20	2 (1%) 82 80	12, 20, 35, 46	3(1%)
2	В	227/229 (99%)	-0.22	5 (2%) 62 57	12, 19, 36, 46	2 (0%)
All	All	427/436~(97%)	-0.21	7 (1%) 72 68	12, 20, 36, 46	5 (1%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	104	LYS	3.8
2	В	210	LYS	3.6
1	А	187	GLY	2.7
2	В	109	LYS	2.3
2	В	18	TYR	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
1	CSD	А	119	8/9	0.98	0.11	$13,\!15,\!16,\!16$	0
1	CSD	А	121	8/9	0.98	0.09	14,15,18,32	0

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



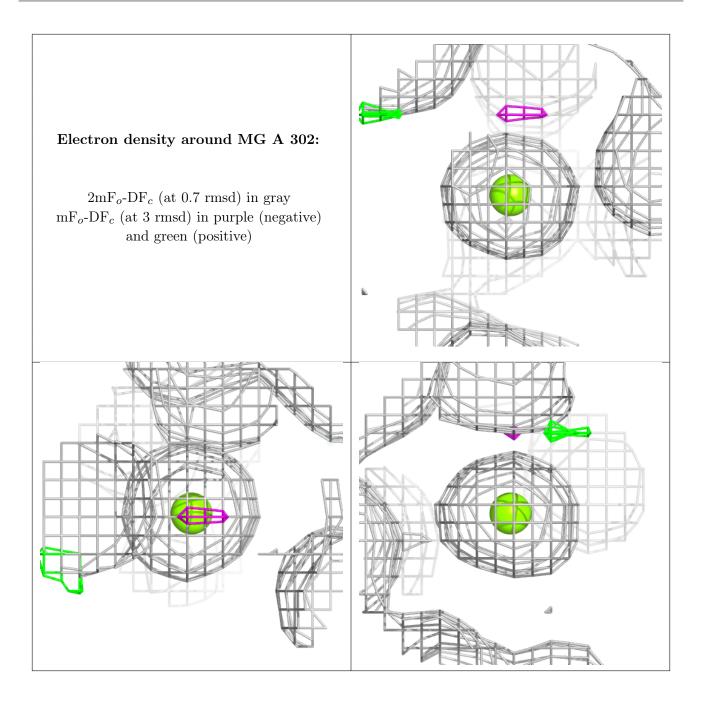
### 6.4 Ligands (i)

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,  $95^{th}$  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.

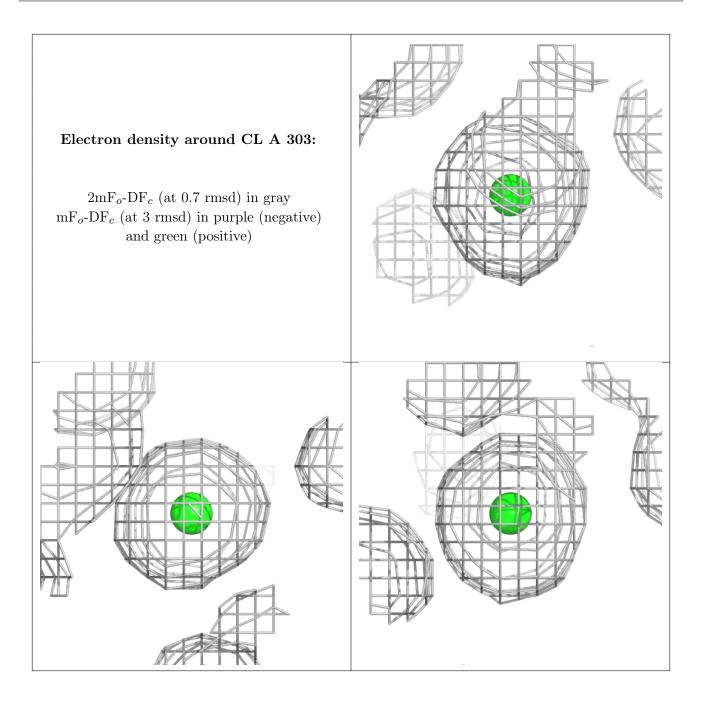
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
4	MG	А	302	1/1	0.99	0.07	22,22,22,22	0
5	CL	А	303	1/1	0.99	0.05	19,19,19,19	0
3	CO	А	301	1/1	1.00	0.06	$15,\!15,\!15,\!15$	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

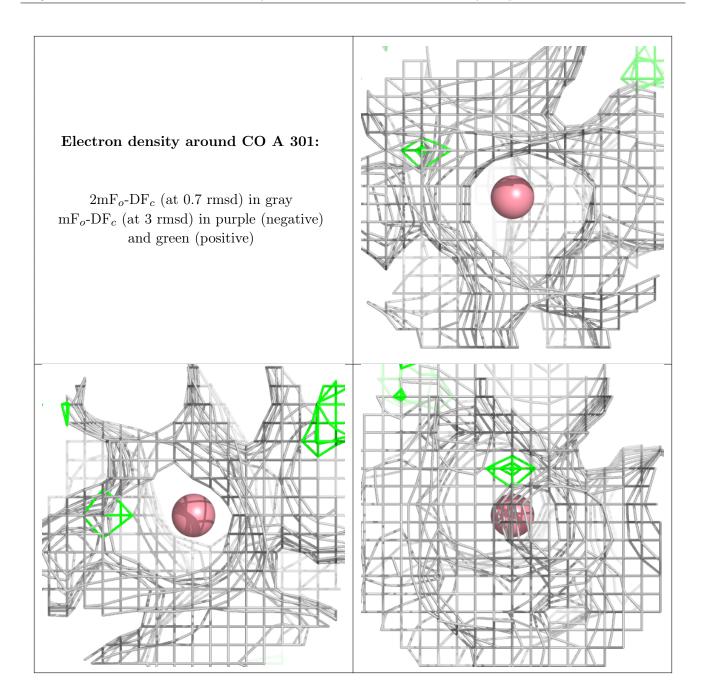












## 6.5 Other polymers (i)

There are no such residues in this entry.

