

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

Jan 6, 2024 – 09:37 pm GMT

PDB ID : 5MC5

Title : Crystal Structure of delGlu452 mutant of Human Prolidase with Mn ions and

GlyPro ligand

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Deposited on : 2016-11-09

Resolution : 1.90 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 (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

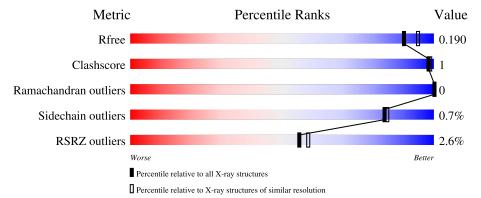
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	A	478	97%	<del>-</del>	
1	В	478	98%		

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
3	OH	В	501	-	-	X	-



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8566 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 Xaa-Pro dipeptidase.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace	
1	A	477	Total 3788	C 2394	N 661	O 704	S 29	0	13	0
1	В	478	Total 3768	C 2377	N 653	O 709	S 29	0	8	0

There are 2 discrepancies between the modelled and reference sequences:

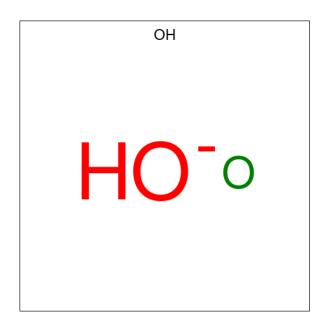
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP P12955
В	?	-	GLU	deletion	UNP P12955

• Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	В	2	Total Mn 2 2	0	0

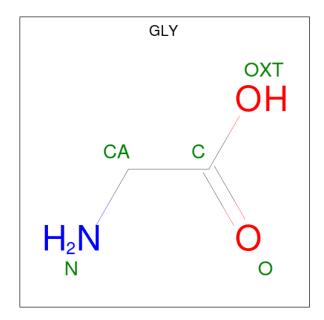
• Molecule 3 is HYDROXIDE ION (three-letter code: OH) (formula: HO).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 1 1	0	0
3	В	1	Total O 1 1	0	0

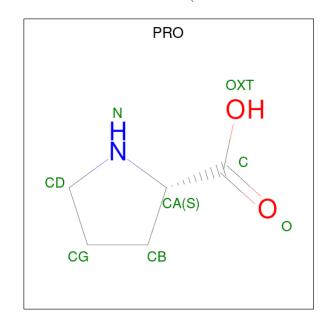
 $\bullet$  Molecule 4 is GLYCINE (three-letter code: GLY) (formula:  $\mathrm{C_2H_5NO_2}).$ 



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 4 2 1 1	0	0
4	В	1	Total C N O 4 2 1 1	0	0

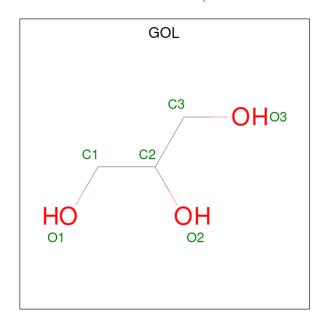


• Molecule 5 is PROLINE (three-letter code: PRO) (formula:  $C_5H_9NO_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf		
5	A	1	Total 8		N 1		0	0
5	В	1	Total 8		N 1		0	0

• Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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

#### • Molecule 7 is water.

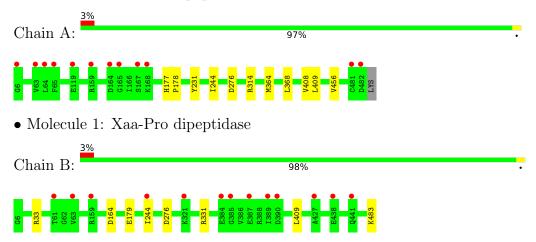
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
7	A	481	Total O 482 482	0	2
7	В	480	Total O 486 486	0	7



# 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: Xaa-Pro dipeptidase





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	103.78Å 108.04Å 211.34Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	46.58 - 1.90	Depositor
Resolution (A)	46.58 - 1.90	EDS
% Data completeness	99.8 (46.58-1.90)	Depositor
(in resolution range)	99.8 (46.58-1.90)	EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.30 (at 1.90Å)	Xtriage
Refinement program	PHENIX	Depositor
D.D.	0.148 , 0.181	Depositor
$R, R_{free}$	0.159 , $0.190$	DCC
$R_{free}$ test set	2101 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.2	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 53.0	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.033 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8566	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: OH, GOL, MN

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.30	0/3916	0.47	0/5296	
1	В	0.31	0/3873	0.47	0/5241	
All	All	0.31	0/7789	0.47	0/10537	

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	3788	0	3720	4	0
1	В	3768	0	3680	4	0
2	A	2	0	0	0	0
2	В	2	0	0	1	0
3	A	1	0	0	0	0
3	В	1	0	0	2	0
4	A	4	0	2	0	0
4	В	4	0	2	0	0
5	A	8	0	7	0	0
5	В	8	0	7	0	0
6	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	В	6	0	8	0	0
7	A	482	0	0	0	0
7	В	486	0	0	1	1
All	All	8566	0	7434	9	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 1.

The worst 5 of 9 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
2:B:500:MN:MN	3:B:501:OH:O	1.41	0.76
1:A:244:ILE:HB	1:A:276:ASP:HB3	1.80	0.63
1:A:408:VAL:HG22	1:A:456:VAL:HG22	1.83	0.61
1:B:244:ILE:HB	1:B:276:ASP:HB3	1.88	0.56
1:B:33:ARG:NE	1:B:179:GLU:OE1	2.44	0.47

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
7:B:966:HOH:O	7:B:1031:HOH:O[5_455]	2.17	0.03

### 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	488/478 (102%)	480 (98%)	8 (2%)	0	100	100
1	В	484/478 (101%)	476 (98%)	8 (2%)	0	100	100
All	All	972/956 (102%)	956 (98%)	16 (2%)	0	100	100



There are no Ramachandran outliers to report.

#### 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	412/400 (103%)	409 (99%)	3 (1%)	84	84	
1	В	408/400 (102%)	405 (99%)	3 (1%)	84	84	
All	All	820/800 (102%)	814 (99%)	6 (1%)	84	84	

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	164	ASP
1	В	409	LEU
1	В	483	LYS
1	A	314	ARG
1	A	231	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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 monosaccharides in this entry.



### 5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 4 are monoatomic and 2 are modelled with single atom - leaving 6 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	Trmo	Chain	Res	Link	В	ond leng	$_{ m gths}$	В	ond ang	cles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GLY	A	503	2	3,3,4	0.69	0	0,2,4	-	-
5	PRO	A	504	-	8,8,8	0.89	1 (12%)	10,10,10	1.34	2 (20%)
4	GLY	В	503	2	3,3,4	0.68	0	0,2,4	-	-
5	PRO	В	504	-	8,8,8	0.92	1 (12%)	10,10,10	1.34	2 (20%)
6	GOL	В	506	-	5,5,5	0.36	0	5,5,5	0.28	0
6	GOL	A	506	-	5,5,5	0.37	0	5,5,5	0.29	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	GLY	A	503	2	-	0/0/1/2	-
5	PRO	A	504	-	-	0/4/11/11	0/1/1/1
4	GLY	В	503	2	-	0/0/1/2	-
5	PRO	В	504	_	-	0/4/11/11	0/1/1/1
6	GOL	В	506	_	-	4/4/4/4	-
6	GOL	A	506	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
5	В	504	PRO	OXT-C	-2.30	1.23	1.30
5	A	504	PRO	OXT-C	-2.24	1.23	1.30

All (4) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
5	A	504	PRO	OXT-C-O	-2.46	118.51	124.09
5	В	504	PRO	OXT-C-O	-2.43	118.56	124.09
5	A	504	PRO	OXT-C-CA	2.19	120.67	113.40
5	В	504	PRO	OXT-C-CA	2.14	120.51	113.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	В	506	GOL	O1-C1-C2-O2
6	В	506	GOL	O1-C1-C2-C3
6	В	506	GOL	C1-C2-C3-O3
6	В	506	GOL	O2-C2-C3-O3

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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	477/478 (99%)	-0.03	12 (2%) 57 60	22, 29, 43, 76	0
1	В	478/478 (100%)	-0.11	13 (2%) 54 57	21, 30, 47, 72	0
All	All	955/956 (99%)	-0.07	25 (2%) 56 58	21, 30, 45, 76	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164[A]	ASP	3.6
1	A	482	ASP	3.6
1	A	6	GLY	3.6
1	A	119	GLU	3.4
1	A	64	LEU	3.2

### 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 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
6	GOL	В	506	6/6	0.65	0.28	67,68,74,77	0
3	ОН	A	501	1/1	0.79	0.19	46,46,46,46	0
6	GOL	A	506	6/6	0.85	0.17	56,56,63,65	0
4	GLY	В	503	4/5	0.90	0.24	44,44,44,44	0
4	GLY	A	503	4/5	0.91	0.15	43,43,43,43	0
2	MN	A	500	1/1	0.91	0.26	81,81,81,81	1
3	ОН	В	501	1/1	0.93	0.08	41,41,41,41	0
2	MN	В	500	1/1	0.95	0.08	105,105,105,105	1
5	PRO	В	504	8/8	0.95	0.16	44,44,44,44	0
5	PRO	A	504	8/8	0.97	0.13	43,43,44,46	0
2	MN	A	499	1/1	0.98	0.07	52,52,52,52	0
2	MN	В	499	1/1	0.99	0.04	50,50,50,50	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

