

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

#### Dec 3, 2023 - 10:50 am GMT

PDB ID	:	2BU3
Title	:	Acyl-enzyme intermediate between Alr0975 and glutathione at pH 3.4
Authors	:	Vivares, D.; Arnoux, P.; Pignol, D.
Deposited on	:	2005-06-08
Resolution	:	1.40  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* 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:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
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 1.40 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		
	$(\# { m Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m A}))$		
$R_{free}$	130704	1714 (1.40-1.40)		
Clashscore	141614	1812 (1.40-1.40)		
Ramachandran outliers	138981	1763 (1.40-1.40)		
Sidechain outliers	138945	1762 (1.40-1.40)		
RSRZ outliers	127900	1674 (1.40-1.40)		



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3634 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 ALR0975 PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	А	200	Total 1591	C 1013	N 275	O 297	S 1	${ m Se} 5$	0	1	0
1	В	204	Total 1621	C 1032	N 278	O 305	S 1	${ m Se}{5}$	0	0	0

• Molecule 2 is GAMMA-GLUTAMYLCYSTEINE (three-letter code: 3GC) (formula:  $C_8H_{14}N_2O_5S$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	Δ	1	Total	С	Ν	0	S	0	0
2		1	15	8	2	4	1	0	0
9	P	1	Total	С	Ν	Ο	$\mathbf{S}$	0	0
	D		15	8	2	4	1		0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Cl 1 1	0	0
3	В	1	Total Cl 1 1	0	0

• Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Ca 1 1	0	0
4	В	1	Total Ca 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	183	Total O 183 183	0	0
5	В	205	Total         O           205         205	0	0

SEQUENCE-PLOTS INFOmissingINFO



## 3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	56.25Å 58.26Å 72.56Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $108.87^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{B}_{\mathrm{ascolution}}(\hat{\boldsymbol{\lambda}})$	29.59 - 1.40	Depositor
Resolution (A)	29.59 - 1.40	EDS
% Data completeness	99.6 (29.59-1.40)	Depositor
(in resolution range)	99.6 (29.59-1.40)	EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.42 (at 1.40 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
B B.	0.174 , $0.188$	Depositor
$\Lambda, \Lambda_{free}$	0.173 , $0.187$	DCC
$R_{free}$ test set	1744 reflections $(2.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	8.9	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.42 , $52.0$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3634	wwPDB-VP
Average B, all atoms $(Å^2)$	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.38% 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.

# 4 Model quality (i)

## 4.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, CA, 3GC

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).

Mal	Chain	Bond	lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.40	0/1618	0.57	0/2176	
1	В	0.38	0/1647	0.55	0/2218	
All	All	0.39	0/3265	0.56	0/4394	

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 4.2 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	А	1591	0	1587	20	0
1	В	1621	0	1609	15	0
2	А	15	0	12	0	0
2	В	15	0	12	0	0
3	А	1	0	0	0	0
3	В	1	0	0	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
5	А	183	0	0	2	1
5	В	205	0	0	2	1
All	All	3634	0	3220	34	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 5.

All (34) 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:173[B]:ARG:NH1	5:A:2138:HOH:O	1.96	0.98
1:B:80:ASN:HD21	1:B:98:PHE:H	1.24	0.85
1:A:132:ILE:HG22	1:A:137:VAL:CG2	2.11	0.81
1:A:80:ASN:HD21	1:A:98:PHE:H	1.28	0.80
1:A:120:ARG:HG3	1:A:121:GLN:HG3	1.73	0.70
1:B:33:LEU:HB3	1:B:210:VAL:HG11	1.75	0.68
1:A:132:ILE:CG2	1:A:137:VAL:CG2	2.72	0.67
1:A:139:VAL:CG2	1:A:235:VAL:CG1	2.74	0.65
1:B:116:GLU:OE2	5:B:2097:HOH:O	2.14	0.64
1:B:33:LEU:HB3	1:B:210:VAL:CG1	2.28	0.64
1:A:162:GLN:HE21	1:A:165:ASN:HD21	1.48	0.62
1:A:99:THR:HG22	1:A:102:ASN:H	1.64	0.60
1:A:102:ASN:HD22	1:A:102:ASN:C	2.04	0.60
1:B:99:THR:H	1:B:102:ASN:ND2	2.01	0.59
1:A:139:VAL:HG23	1:A:235:VAL:CG1	2.33	0.58
1:B:102:ASN:C	1:B:102:ASN:HD22	2.06	0.58
1:A:132:ILE:HG22	1:A:137:VAL:HG23	1.87	0.56
1:B:137:VAL:HG23	1:B:238:SER:O	2.07	0.55
1:B:99:THR:H	1:B:102:ASN:HD21	1.56	0.53
1:B:139:VAL:CG2	1:B:235:VAL:CG1	2.87	0.52
1:A:140:LYS:HE2	1:A:142:ASN:OD1	2.10	0.51
1:A:139:VAL:CG2	1:A:235:VAL:HG11	2.43	0.49
1:B:167:VAL:HG22	1:B:236:PHE:CD2	2.48	0.49
1:A:132:ILE:CG2	1:A:137:VAL:HG21	2.42	0.48
1:A:139:VAL:HG22	1:A:235:VAL:HG13	1.98	0.45
1:B:167:VAL:HG22	1:B:236:PHE:HD2	1.82	0.44
1:B:132:ILE:HG22	1:B:137:VAL:HG13	1.99	0.44
1:B:173:ARG:HH11	1:B:178:GLN:NE2	2.16	0.43
1:A:162:GLN:NE2	1:A:165:ASN:HD21	2.15	0.43
1:B:116:GLU:CD	5:B:2097:HOH:O	2.55	0.43
1:A:99:THR:HG23	5:A:2065:HOH:O	2.19	0.42
1:A:132:ILE:HG23	1:A:137:VAL:HG21	2.03	0.41
1:A:95:TYR:OH	1:B:206:LYS:HE3	2.21	0.41
1:A:99:THR:HG22	1:A:102:ASN:N	2.34	0.40

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)	
5:A:2018:HOH:O	5:B:2132:HOH:O[2_545]	2.16	0.04	

### 4.3 Torsion angles (i)

#### 4.3.1 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	Percer	ntiles
1	А	195/254~(77%)	188 (96%)	6 (3%)	1 (0%)	29	9
1	В	200/254~(79%)	194 (97%)	5(2%)	1 (0%)	29	9
All	All	395/508~(78%)	382 (97%)	11 (3%)	2(0%)	29	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	180	ARG
1	В	180	ARG

#### 4.3.2 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	176/219~(80%)	173~(98%)	3~(2%)	60 31		
1	В	179/219~(82%)	175~(98%)	4 (2%)	52 19		
All	All	355/438~(81%)	348~(98%)	7~(2%)	55 23		

All (7) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	61	PHE
1	А	99	THR
1	А	102	ASN
1	В	61	PHE
1	В	69	TYR
1	В	102	ASN
1	В	137	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	39	ASN
1	А	80	ASN
1	А	102	ASN
1	А	155	GLN
1	А	162	GLN
1	А	170	ASN
1	А	178	GLN
1	А	222	ASN
1	В	67	GLN
1	В	80	ASN
1	В	102	ASN
1	В	155	GLN
1	В	170	ASN
1	В	178	GLN
1	В	193	GLN
1	В	222	ASN

#### 4.3.3 RNA (i)

There are no RNA molecules in this entry.

#### 4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

### 4.5 Carbohydrates (i)

There are no monosaccharides in this entry.



### 4.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	Chain	Chain	Chain	Chain	Dag	Tinle	Bo	ond leng	$_{\rm ths}$	В	ond ang	les
INIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2			
2	3GC	А	1240	1	$12,\!14,\!15$	1.74	2 (16%)	$16,\!17,\!19$	2.49	4 (25%)			
2	3GC	В	1240	1	12,14,15	1.65	2 (16%)	16,17,19	2.48	5 (31%)			

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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
2	3GC	А	1240	1	-	0/16/17/19	-
2	$3 \mathrm{GC}$	В	1240	1	-	0/16/17/19	-

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	А	1240	3GC	OE1-CD1	4.63	1.32	1.23
2	В	1240	3GC	OE1-CD1	4.44	1.32	1.23
2	А	1240	3GC	CD1-N2	-3.00	1.27	1.34
2	В	1240	3GC	CD1-N2	-2.83	1.27	1.34

All (4) bond length outliers are listed below:

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	1240	3GC	CB2-CA2-N2	-5.78	103.04	111.28
2	В	1240	3GC	C2-CA2-N2	5.43	119.53	109.73
2	А	1240	3GC	C2-CA2-N2	5.33	119.35	109.73
2	В	1240	3GC	CB2-CA2-N2	-4.75	104.50	111.28
2	В	1240	3GC	CB1-CG1-CD1	-4.68	102.59	113.04
2	А	1240	3GC	CB1-CG1-CD1	-4.14	103.79	113.04
2	В	1240	3GC	OE1-CD1-CG1	-2.71	117.06	122.02

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	J	1	I J				
Mol	Chain	$\mathbf{Res}$	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	1240	3GC	CB2-CA2-C2	-2.68	104.77	111.31
2	В	1240	3GC	CB2-CA2-C2	-2.42	105.39	111.31

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There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 4.7 Other polymers (i)

There are no such residues in this entry.

### 4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 5 Fit of model and data (i)

## 5.1 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	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	195/254~(76%)	0.31	10 (5%) 28 27	3, 7, 16, 23	0
1	В	199/254~(78%)	0.35	14 (7%) 16 15	3, 7, 16, 19	0
All	All	394/508~(77%)	0.33	24 (6%) 21 19	3, 7, 16, 23	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	95	TYR	9.2	
1	В	180	ARG	4.7	
1	А	105	SER	3.4	
1	В	193	GLN	3.3	
1	А	179	GLU	3.1	
1	В	96	ARG	3.1	
1	В	93	SER	3.1	
1	В	85	ASN	3.0	
1	А	193	GLN	2.9	
1	В	179	GLU	2.9	
1	А	31	PRO	2.8	
1	В	32	ASN	2.8	
1	В	94	PRO	2.7	
1	В	107	GLU	2.6	
1	В	95	TYR	2.6	
1	В	106	ASN	2.5	
1	А	116	GLU	2.5	
1	В	108	LYS	2.3	
1	А	67	GLN	2.3	
1	В	67	GLN	2.2	
1	A	96	ARG	2.2	
1	А	138	LYS	2.1	
1	В	239	LYS	2.1	
1	А	85	ASN	2.0	



#### 5.2 Non-standard residues in protein, DNA, RNA chains (i)

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

#### 5.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.4 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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
2	3GC	А	1240	15/16	0.95	0.09	6,8,11,16	0
2	3GC	В	1240	15/16	0.96	0.07	6,7,9,13	0
4	CA	В	1242	1/1	0.97	0.24	22,22,22,22	0
3	CL	В	1241	1/1	0.99	0.04	9,9,9,9	0
3	CL	А	1241	1/1	0.99	0.03	10,10,10,10	0
4	CA	А	1242	1/1	1.00	0.10	11,11,11,11	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.







## 5.5 Other polymers (i)

There are no such residues in this entry.

