



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2020 – 04:06 PM EST

PDB ID : 6XK1  
Title : Biuret Hydrolase (BiuH) from Rhodococcus sp. Mel C169S Apo form  
Authors : Tassoulas, L.T.; Elias, M.H.; Wackett, L.P.  
Deposited on : 2020-06-25  
Resolution : 1.70 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
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
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)	:	2.14.6

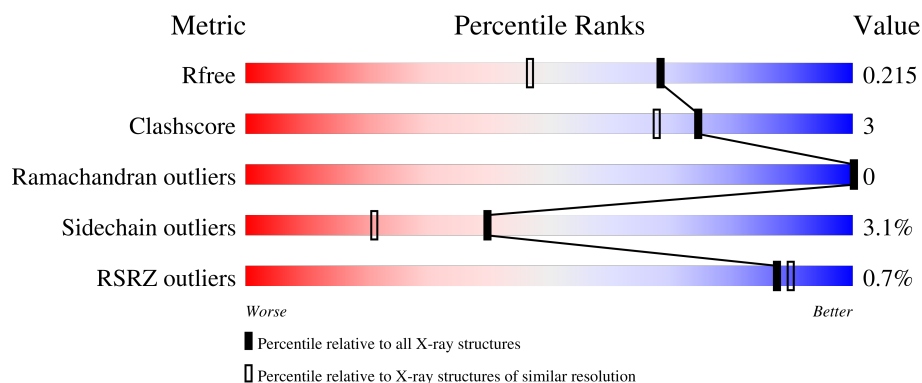
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	244	<div> <div>87%</div> <div>5% 7%</div> </div>
1	B	244	<div> <div>85%</div> <div>7% • 7%</div> </div>
1	C	244	<div> <div>84%</div> <div>9% • 7%</div> </div>
1	D	244	<div> <div>2%</div> <div>88%</div> <div>6% 6%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7365 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 Biuret hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1701	1063	301	328	9			
1	B	227	Total	C	N	O	S	0	0	0
			1709	1068	302	329	10			
1	C	228	Total	C	N	O	S	0	0	0
			1716	1072	303	331	10			
1	D	230	Total	C	N	O	S	0	0	0
			1730	1081	305	334	10			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP H8ZKV9
A	-1	SER	-	expression tag	UNP H8ZKV9
A	0	HIS	-	expression tag	UNP H8ZKV9
A	169	SER	CYS	engineered mutation	UNP H8ZKV9
B	-2	GLY	-	expression tag	UNP H8ZKV9
B	-1	SER	-	expression tag	UNP H8ZKV9
B	0	HIS	-	expression tag	UNP H8ZKV9
B	169	SER	CYS	engineered mutation	UNP H8ZKV9
C	-2	GLY	-	expression tag	UNP H8ZKV9
C	-1	SER	-	expression tag	UNP H8ZKV9
C	0	HIS	-	expression tag	UNP H8ZKV9
C	169	SER	CYS	engineered mutation	UNP H8ZKV9
D	-2	GLY	-	expression tag	UNP H8ZKV9
D	-1	SER	-	expression tag	UNP H8ZKV9
D	0	HIS	-	expression tag	UNP H8ZKV9
D	169	SER	CYS	engineered mutation	UNP H8ZKV9


- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	136	Total 136	O 136	0	0
2	B	154	Total 154	O 154	0	0
2	C	116	Total 116	O 116	0	0
2	D	103	Total 103	O 103	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: Biuret hydrolase

Chain A: 




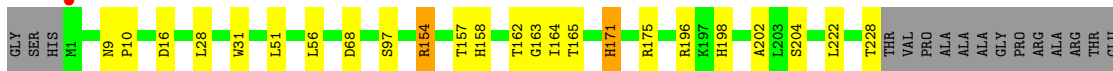
- Molecule 1: Biuret hydrolase

Chain B: 




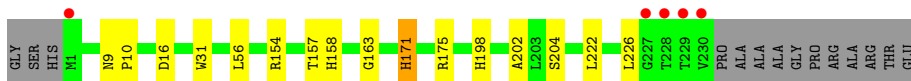
- Molecule 1: Biuret hydrolase

Chain C: 



- Molecule 1: Biuret hydrolase

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.10Å 104.40Å 135.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.84 – 1.70 56.77 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (56.84-1.70) 99.9 (56.77-1.70)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.184 , 0.208 0.196 , 0.215	Depositor DCC
$R_{free}$ test set	4864 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 35.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7365	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 9.33% 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](#)

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	0.77	0/1740	0.83	1/2373 (0.0%)
1	B	0.78	0/1748	0.87	2/2383 (0.1%)
1	C	0.78	0/1755	0.85	1/2393 (0.0%)
1	D	0.75	0/1769	0.83	0/2413
All	All	0.77	0/7012	0.84	4/9562 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	152	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	C	154	ARG	NE-CZ-NH2	5.91	123.25	120.30
1	A	180	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	196	ARG	CG-CD-NE	5.01	122.32	111.80

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	1701	0	1660	10	0
1	B	1709	0	1672	12	0
1	C	1716	0	1679	14	0
1	D	1730	0	1695	10	0
2	A	136	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	154	0	0	2	0
2	C	116	0	0	1	0
2	D	103	0	0	0	0
All	All	7365	0	6706	43	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 3.

All (43) 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:B:171:HIS:HD2	1:B:175:ARG:HE	1.29	0.80
1:D:171:HIS:HD2	1:D:175:ARG:HE	1.28	0.79
1:C:171:HIS:HD2	1:C:175:ARG:HE	1.31	0.78
1:B:61:ARG:HD2	2:B:416:HOH:O	1.81	0.78
1:A:171:HIS:HD2	1:A:175:ARG:HE	1.31	0.74
1:A:61:ARG:NH2	2:A:301:HOH:O	2.28	0.64
1:D:157:THR:OG1	1:D:158:HIS:HD2	1.82	0.63
1:A:198:HIS:HE1	1:D:204:SER:OG	1.83	0.61
1:A:157:THR:OG1	1:A:158:HIS:HD2	1.84	0.61
1:B:157:THR:OG1	1:B:158:HIS:HD2	1.84	0.60
1:C:28:LEU:HD22	1:C:162:THR:OG1	2.01	0.60
1:C:157:THR:OG1	1:C:158:HIS:HD2	1.84	0.60
1:D:171:HIS:CD2	1:D:175:ARG:HE	2.17	0.58
1:A:204:SER:OG	1:D:198:HIS:HE1	1.87	0.58
1:A:171:HIS:CD2	1:A:175:ARG:HE	2.20	0.55
1:B:171:HIS:CD2	1:B:175:ARG:HE	2.18	0.52
1:C:171:HIS:CD2	1:C:175:ARG:HE	2.20	0.51
1:B:171:HIS:HD2	1:B:175:ARG:NE	2.04	0.50
1:A:171:HIS:HD2	1:A:175:ARG:NE	2.06	0.50
1:C:171:HIS:HD2	1:C:175:ARG:NE	2.05	0.47
1:C:51:LEU:HD21	1:C:196:ARG:CZ	2.44	0.47
1:C:51:LEU:CD2	1:C:196:ARG:CZ	2.93	0.47
1:C:198:HIS:HD2	2:C:348:HOH:O	1.97	0.46
1:A:198:HIS:HD2	2:A:363:HOH:O	1.98	0.46
1:B:198:HIS:HE1	1:C:204:SER:HB3	1.81	0.46
1:D:171:HIS:HD2	1:D:175:ARG:NE	2.04	0.45
1:B:189:ASP:OD2	1:B:219:SER:HB2	2.18	0.44
1:B:1:MET:N	2:B:302:HOH:O	2.50	0.43
1:B:171:HIS:HE1	1:B:202:ALA:O	2.01	0.43
1:C:9:ASN:HA	1:C:10:PRO:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:TRP:CE2	1:C:163:GLY:HA2	2.54	0.42
1:C:171:HIS:HE1	1:C:202:ALA:O	2.02	0.42
1:B:31:TRP:CE2	1:B:163:GLY:HA2	2.55	0.42
1:C:164:ILE:HA	1:C:165:THR:HA	1.85	0.41
1:A:31:TRP:CE2	1:A:163:GLY:HA2	2.55	0.41
1:B:9:ASN:HA	1:B:10:PRO:HA	1.91	0.41
1:D:16:ASP:OD1	1:D:158:HIS:HE1	2.04	0.41
1:D:9:ASN:HA	1:D:10:PRO:HA	1.89	0.41
1:D:171:HIS:HE1	1:D:202:ALA:O	2.03	0.41
1:D:31:TRP:CE2	1:D:163:GLY:HA2	2.56	0.41
1:C:16:ASP:OD1	1:C:158:HIS:HE1	2.03	0.40
1:A:171:HIS:HE1	1:A:202:ALA:O	2.05	0.40
1:B:16:ASP:OD1	1:B:158:HIS:HE1	2.04	0.40

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	A	224/244 (92%)	219 (98%)	5 (2%)	0	100	100
1	B	225/244 (92%)	219 (97%)	6 (3%)	0	100	100
1	C	226/244 (93%)	220 (97%)	6 (3%)	0	100	100
1	D	228/244 (93%)	221 (97%)	7 (3%)	0	100	100
All	All	903/976 (92%)	879 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	178/190 (94%)	175 (98%)	3 (2%)	60	46
1	B	179/190 (94%)	172 (96%)	7 (4%)	32	13
1	C	180/190 (95%)	173 (96%)	7 (4%)	32	13
1	D	182/190 (96%)	177 (97%)	5 (3%)	44	26
All	All	719/760 (95%)	697 (97%)	22 (3%)	40	21

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LEU
1	A	171	HIS
1	A	226	LEU
1	B	1	MET
1	B	56	LEU
1	B	171	HIS
1	B	196	ARG
1	B	219	SER
1	B	222	LEU
1	B	226	LEU
1	C	56	LEU
1	C	68	ASP
1	C	97	SER
1	C	154	ARG
1	C	171	HIS
1	C	222	LEU
1	C	228	THR
1	D	56	LEU
1	D	154	ARG
1	D	171	HIS
1	D	222	LEU
1	D	226	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS
1	A	171	HIS
1	A	198	HIS
1	A	209	GLN
1	B	158	HIS
1	B	171	HIS
1	B	198	HIS
1	C	158	HIS
1	C	171	HIS
1	C	198	HIS
1	D	158	HIS
1	D	171	HIS
1	D	198	HIS

### 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](#)

There are no ligands in this entry.

## 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<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	226/244 (92%)	-0.14	0	100 100	12, 17, 27, 45	0
1	B	227/244 (93%)	-0.11	0	100 100	12, 17, 26, 46	0
1	C	228/244 (93%)	-0.02	1 (0%)	92 93	12, 20, 32, 50	0
1	D	230/244 (94%)	0.09	5 (2%)	62 66	14, 21, 34, 60	0
All	All	911/976 (93%)	-0.04	6 (0%)	87 90	12, 18, 31, 60	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	228	THR	3.9
1	D	227	GLY	3.3
1	D	230	VAL	2.8
1	D	1	MET	2.7
1	C	1	MET	2.3
1	D	229	THR	2.0

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.