



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2023 – 06:26 AM EDT

PDB ID : 4L1G  
Title : Crystal structure of the Bc1960 peptidoglycan N-acetylglucosamine deacetylase from *Bacillus cereus*  
Authors : Tsalafouta, A.; Fadouloglou, V.E.; Kokkinidis, M.  
Deposited on : 2013-06-03  
Resolution : 2.34 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.35.1  
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) : 2.35.1

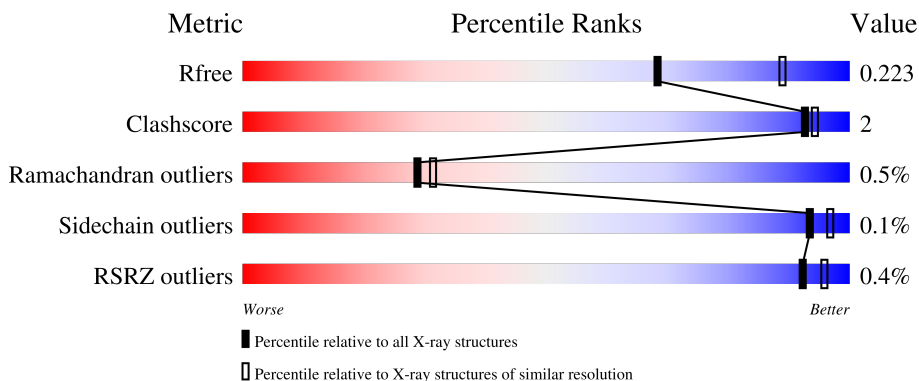
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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  $\geq 3$ , 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	273	 75% 22%
1	B	273	 74% 22%
1	C	273	 76% 22%
1	D	273	 74% 22%

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 7688 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 Peptidoglycan N-acetylglucosamine deacetylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	214	Total 1721	C 1109	N 290	O 320	S 2	0	1	0
1	B	214	Total 1723	C 1110	N 292	O 319	S 2	0	1	0
1	C	214	Total 1730	C 1114	N 292	O 322	S 2	0	2	0
1	D	213	Total 1699	C 1093	N 286	O 318	S 2	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

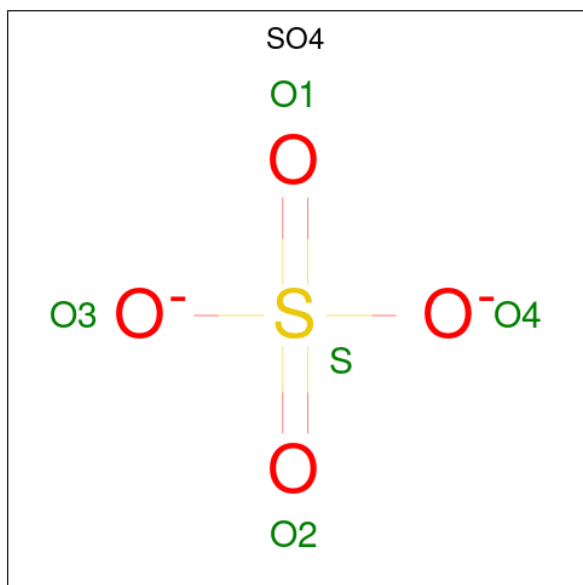
Chain	Residue	Modelled	Actual	Comment	Reference
A	268	HIS	-	expression tag	UNP Q81EK9
A	269	HIS	-	expression tag	UNP Q81EK9
A	270	HIS	-	expression tag	UNP Q81EK9
A	271	HIS	-	expression tag	UNP Q81EK9
A	272	HIS	-	expression tag	UNP Q81EK9
A	273	HIS	-	expression tag	UNP Q81EK9
B	268	HIS	-	expression tag	UNP Q81EK9
B	269	HIS	-	expression tag	UNP Q81EK9
B	270	HIS	-	expression tag	UNP Q81EK9
B	271	HIS	-	expression tag	UNP Q81EK9
B	272	HIS	-	expression tag	UNP Q81EK9
B	273	HIS	-	expression tag	UNP Q81EK9
C	268	HIS	-	expression tag	UNP Q81EK9
C	269	HIS	-	expression tag	UNP Q81EK9
C	270	HIS	-	expression tag	UNP Q81EK9
C	271	HIS	-	expression tag	UNP Q81EK9
C	272	HIS	-	expression tag	UNP Q81EK9
C	273	HIS	-	expression tag	UNP Q81EK9
D	268	HIS	-	expression tag	UNP Q81EK9
D	269	HIS	-	expression tag	UNP Q81EK9
D	270	HIS	-	expression tag	UNP Q81EK9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	271	HIS	-	expression tag	UNP Q81EK9
D	272	HIS	-	expression tag	UNP Q81EK9
D	273	HIS	-	expression tag	UNP Q81EK9

- 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		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	224	Total O 224 224	0	0
4	B	199	Total O 199 199	0	0
4	C	189	Total O 189 189	0	0
4	D	157	Total O 157 157	0	0



MET	TYR	R266	T54
PHE	ALA	LYS	D93
ALA	TYR	HIS	K94
PRO	TYR	HIS	R120
TYR	MET	HIS	
GLN	PRO	HIS	
TRP	TYR	HIS	
GLY	ASN		
LEU	PHE		
GLU	TYR		
ARG	TYR		
ASP	GLY		
VAL	ASP		
SER	GLN		
TYR	TYR		
ALA	ILE		
TYR	ASN		
MET	SER		
PRO	LEU		
TYR	PRO		
ASN	TYR		
SER	ALA		
PHE	TYR		
TYR	TYR		
TYR	ILE		
GLY	ASN		
ASP	SER		
TYR	LEU		
ILE	PRO		
ASN	TYR		
SER	ALA		
LEU	TYR		
PRO	TYR		
GLN	ALA		
ASN	TYR		
TYR	GLU		
GLU	VAL		
VAL	GLN		
MET	MET		
LYS	LYS		
ALA	ALA		
ASP	ASP		
ARG	ARG		
GLY	GLY		
SER	SER		
TRP	TRP		
T54			
D93			
K94			
R120			
P01171			
Y172			
Q192			
D199			
S235			
V236			
I243			
P244			
R266			

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.66Å 92.66Å 242.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.64 – 2.34 86.57 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.9 (30.64-2.34) 98.9 (86.57-2.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.36 (at 2.34Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.179 , 0.223 0.181 , 0.223	Depositor DCC
$R_{free}$ test set	2282 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.8	Xtrriage
Anisotropy	0.470	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7688	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.39 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1159e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, PXU, 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	0.24	0/1761	0.40	0/2390
1	B	0.24	0/1763	0.40	0/2393
1	C	0.23	0/1770	0.40	0/2403
1	D	0.23	0/1734	0.40	0/2354
All	All	0.23	0/7028	0.40	0/9540

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	171	PXU	Mainchain
1	D	171	PXU	Mainchain

## 5.2 Too-close contacts

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	1721	0	1694	5	0
1	B	1723	0	1696	7	0
1	C	1730	0	1694	3	0
1	D	1699	0	1666	6	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	10	0	0	0	0
2	D	10	0	0	0	0
3	A	4	0	3	0	0
3	B	4	0	3	1	0
3	C	4	0	3	0	0
3	D	4	0	3	1	0
4	A	224	0	0	0	0
4	B	199	0	0	2	0
4	C	189	0	0	0	0
4	D	157	0	0	1	0
All	All	7688	0	6762	21	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 2.

All (21) 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:D:54:THR:N	4:D:528:HOH:O	2.31	0.63
1:C:186:GLN:O	1:C:266:ARG:HD2	2.08	0.53
1:B:199:ASP:HB2	1:B:235:SER:HB2	1.95	0.48
1:B:172:TYR:H	3:B:302:ACT:H3	1.79	0.48
1:D:199:ASP:HB2	1:D:235:SER:HB2	1.97	0.47
1:A:168:ILE:HB	1:A:190:ILE:HG12	1.96	0.47
1:D:172:TYR:H	3:D:303:ACT:H3	1.80	0.47
1:B:72:LYS:NZ	4:B:581:HOH:O	2.35	0.46
1:B:56:PHE:O	1:B:59:VAL:HG22	2.16	0.44
1:B:116:ASN:HB2	4:B:556:HOH:O	2.16	0.44
1:C:85:LEU:HD23	1:C:117:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:93:ASP:OD2	1:D:120:ARG:NH2	2.41	0.43
1:C:170:PRO:HA	1:C:171:PXU:H8	1.85	0.43
1:B:263:SER:OG	1:B:265:GLU:OE1	2.37	0.42
1:A:199:ASP:HB2	1:A:235:SER:HB2	2.00	0.42
1:A:170:PRO:HA	1:A:171:PXU:H8	1.62	0.42
1:B:170:PRO:HA	1:B:171:PXU:H8	1.78	0.42
1:A:56:PHE:O	1:A:59:VAL:HG22	2.21	0.40
1:A:85:LEU:HD12	1:A:85:LEU:HA	1.83	0.40
1:D:94:LYS:HE2	1:D:236:VAL:HG12	2.03	0.40
1:D:243:ILE:HB	1:D:244:PRO:HD3	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	212/273 (78%)	206 (97%)	5 (2%)	1 (0%)	29	31
1	B	212/273 (78%)	206 (97%)	5 (2%)	1 (0%)	29	31
1	C	213/273 (78%)	209 (98%)	3 (1%)	1 (0%)	29	31
1	D	210/273 (77%)	204 (97%)	5 (2%)	1 (0%)	29	31
All	All	847/1092 (78%)	825 (97%)	18 (2%)	4 (0%)	29	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	192	GLN
1	C	192	GLN
1	D	192	GLN
1	B	192	GLN

### 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	186/237 (78%)	185 (100%)	1 (0%)	88	93
1	B	185/237 (78%)	185 (100%)	0	100	100
1	C	185/237 (78%)	185 (100%)	0	100	100
1	D	182/237 (77%)	182 (100%)	0	100	100
All	All	738/948 (78%)	737 (100%)	1 (0%)	93	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LEU

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](#)

4 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	PXU	B	171	1	6,8,9	2.73	2 (33%)	4,11,13	1.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	PXU	D	171	1	6,8,9	2.74	2 (33%)	4,11,13	1.12	0
1	PXU	A	171	1	6,8,9	2.75	2 (33%)	4,11,13	1.00	0
1	PXU	C	171	1	6,8,9	2.75	2 (33%)	4,11,13	0.87	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	PXU	B	171	1	-	0/0/12/15	0/1/1/1
1	PXU	D	171	1	-	0/0/12/15	0/1/1/1
1	PXU	A	171	1	-	0/0/12/15	0/1/1/1
1	PXU	C	171	1	-	0/0/12/15	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	171	PXU	O-C	5.68	1.38	1.19
1	C	171	PXU	O-C	5.67	1.38	1.19
1	A	171	PXU	O-C	5.65	1.38	1.19
1	B	171	PXU	O-C	5.64	1.38	1.19
1	A	171	PXU	CD-N	-3.40	1.33	1.47
1	B	171	PXU	CD-N	-3.37	1.33	1.47
1	C	171	PXU	CD-N	-3.34	1.33	1.47
1	D	171	PXU	CD-N	-3.29	1.34	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	171	PXU	1	0
1	A	171	PXU	1	0
1	C	171	PXU	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 ligands 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ACT	A	302	-	3,3,3	0.78	0	3,3,3	1.38	0
2	SO4	A	301	-	4,4,4	0.14	0	6,6,6	0.05	0
3	ACT	C	303	-	3,3,3	0.77	0	3,3,3	1.39	0
3	ACT	D	303	-	3,3,3	0.78	0	3,3,3	1.35	0
2	SO4	D	302	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	B	301	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	C	301	-	4,4,4	0.15	0	6,6,6	0.08	0
3	ACT	B	302	-	3,3,3	0.76	0	3,3,3	1.33	0
2	SO4	C	302	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	D	301	-	4,4,4	0.15	0	6,6,6	0.15	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	303	ACT	1	0
3	B	302	ACT	1	0

## 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	213/273 (78%)	-0.34	1 (0%) 91   95	8, 16, 29, 42	0
1	B	213/273 (78%)	-0.34	1 (0%) 91   95	6, 15, 27, 46	0
1	C	213/273 (78%)	-0.35	1 (0%) 91   95	6, 16, 31, 82	0
1	D	212/273 (77%)	-0.24	0 100   100	10, 21, 39, 54	0
All	All	851/1092 (77%)	-0.32	3 (0%) 92   96	6, 17, 34, 82	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	53	TRP	3.0
1	C	53	TRP	2.9
1	A	53	TRP	2.3

### 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<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(Å <sup>2</sup> )	Q<0.9
1	PXU	D	171	8/9	0.94	0.11	16,16,17,18	0
1	PXU	C	171	8/9	0.95	0.12	14,15,16,16	0
1	PXU	A	171	8/9	0.95	0.12	14,15,15,15	0
1	PXU	B	171	8/9	0.98	0.10	13,14,16,17	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<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(Å <sup>2</sup> )	Q<0.9
3	ACT	C	303	4/4	0.87	0.19	30,35,40,43	0
3	ACT	A	302	4/4	0.88	0.18	28,31,32,45	0
3	ACT	B	302	4/4	0.90	0.13	31,32,36,42	0
3	ACT	D	303	4/4	0.90	0.15	32,33,34,39	0
2	SO4	D	302	5/5	0.93	0.20	61,63,63,64	0
2	SO4	C	302	5/5	0.94	0.13	67,69,69,70	0
2	SO4	B	301	5/5	0.95	0.10	58,60,60,61	0
2	SO4	A	301	5/5	0.97	0.12	49,50,51,51	0
2	SO4	D	301	5/5	0.99	0.14	18,18,18,18	0
2	SO4	C	301	5/5	0.99	0.13	12,14,14,15	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.