

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

#### Nov 6, 2023 – 07:47 PM EST

PDB ID : 2H5D

Title: 0.9A resolution crystal structure of alpha-lytic protease complexed with a tran-

sition state analogue, MeOSuc-Ala-Ala-Pro-Val boronic acid

Authors: Fuhrmann, C.N.; Agard, D.A.

Deposited on : 2006-05-25

Resolution : 0.90 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul: 1.8.5 (274361), 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)

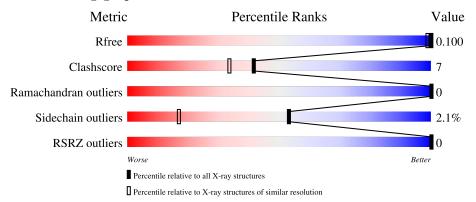
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 0.90 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1061 (1.04-0.76)
Clashscore	141614	1132 (1.04-0.76)
Ramachandran outliers	138981	1055 (1.04-0.76)
Sidechain outliers	138945	1056 (1.04-0.76)
RSRZ outliers	127900	1028 (1.04-0.76)

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	198	90%		9%	<del>-</del>
2	В	5	60%	40%		

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	SO4	A	248	-	-	X	-
3	SO4	A	251	-	-	X	-
4	GOL	В	204[C]	-	-	X	-



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3751 atoms, of which 1537 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.

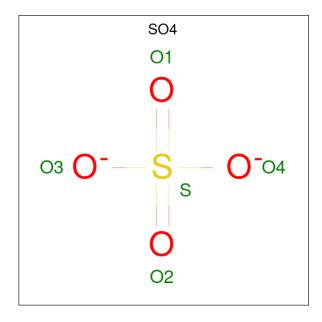
• Molecule 1 is a protein called ALPHA-LYTIC PROTEASE.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	A	198	Total 3042	C 939	H 1485	N 305	O 305	S 8	0	22	0

• Molecule 2 is a protein called MEOSUC-ALA-ALA-PRO-ALA BORONIC ACID IN-HIBITOR.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
9	D	5	Total	В	С	Н	N	О	0	9	0
	Б	9	88	1	31	37	6	13	U	) )	

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
3	A	1	Total O S	0	0	
			5 4 1			
3	A	1	Total O S	0	0	
	71	1	5 4 1	U		
3	٨	1	Total O S	0	0	
3	A	1	5   4   1	0	U	
3	Λ	1	Total O S	0	0	
3	A	1	5 4 1	U	U	
3	Λ	1	Total O S	0	0	
3	A	1	5 4 1	U	U	
3	D	1	Total O S	0	0	
3	D	1	5 4 1		U	

 $\bullet$  Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $\mathrm{C_3H_8O_3}).$ 



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	В	1	Total 30	C 9	H 15	O 6	0	1

• Molecule 5 is water.

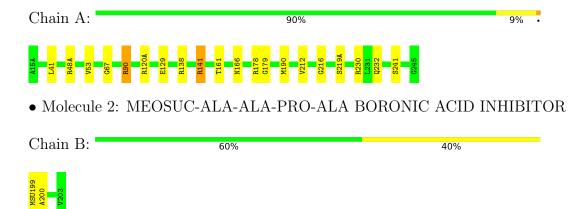
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	423	Total O 541 541	0	113
5	В	9	Total O 10 10	0	1



# 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: ALPHA-LYTIC PROTEASE





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	65.77Å 65.77Å 79.55Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	20.00 - 0.90	Depositor
rtesolution (A)	28.48 - 0.90	EDS
% Data completeness	99.9 (20.00-0.90)	Depositor
(in resolution range)	96.9 (28.48-0.90)	EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.44 (at 0.90Å)	Xtriage
Refinement program	SHELXL-97	Depositor
Ρ. Р.	0.081 , 0.091	Depositor
$R, R_{free}$	0.093 , $0.100$	DCC
$R_{free}$ test set	7357 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	5.5	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.40 , 143.5	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.99	EDS
Total number of atoms	3751	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.98% 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: MSU, GOL, B2V, 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	Bo	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.94	6/1586 (0.4%)	1.17	$13/2143 \ (0.6\%)$	
2	В	0.95	0/27	0.99	0/38	
All	All	0.94	6/1613 (0.4%)	1.16	13/2181 (0.6%)	

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	A	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	Ideal(A)
1	A	178	ARG	CZ-NH2	6.07	1.41	1.33
1	A	178	ARG	NE-CZ	-5.77	1.25	1.33
1	A	241	SER	C-N	-5.60	1.21	1.34
1	A	67	GLY	CA-C	-5.54	1.43	1.51
1	A	178	ARG	CZ-NH1	5.14	1.39	1.33
1	A	219(A)	SER	CA-CB	5.09	1.60	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	178	ARG	NE-CZ-NH1	-9.00	115.80	120.30
1	A	48(A)[A]	ARG	CD-NE-CZ	7.55	134.17	123.60
1	A	48(A)[B]	ARG	CD-NE-CZ	7.55	134.17	123.60
1	A	48(A)[C]	ARG	CD-NE-CZ	7.55	134.17	123.60
1	A	48(A)[D]	ARG	CD-NE-CZ	7.55	134.17	123.60



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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	90[A]	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	90[B]	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	230	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	A	48(A)[A]	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	48(A)[B]	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	48(A)[C]	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	48(A)[D]	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	230	ARG	NE-CZ-NH1	6.02	123.31	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	ARG	Sidechain
1	A	41[B]	LEU	Mainchain

#### 5.2 Too-close contacts (i)

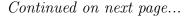
In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1557	1485	1484	7	0
2	В	51	37	48	4	0
3	A	35	0	0	9	0
3	В	5	0	0	0	0
4	В	15	15	18	4	0
5	A	541	0	0	15	0
5	В	10	0	0	4	0
All	All	2214	1537	1550	23	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 7.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1			Clash overlap (Å)
4:B:204[C]:GOL:C3	5:B:654:HOH:O	1.70	1.31





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Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ ({\rm \AA})$	overlap (Å)
1:A:141[A]:ARG:NH1	5:A:623:HOH:O	1.57	1.20
3:A:248:SO4:O3	5:A:357[B]:HOH:O	1.60	1.19
3:A:248:SO4:O4	5:A:705[B]:HOH:O	1.56	1.19
3:A:252:SO4:O4	5:A:609[A]:HOH:O	1.72	1.05
4:B:204[C]:GOL:H32	5:B:654:HOH:O	1.41	0.99
3:A:248:SO4:S	5:A:616:HOH:O	2.35	0.83
1:A:161[B]:THR:HG21	5:A:554:HOH:O	1.93	0.69
4:B:204[C]:GOL:H31	5:B:654:HOH:O	1.60	0.68
1:A:166:ASN:HD22	1:A:179:GLY:HA2	1.60	0.66
3:A:247:SO4:O3	5:A:480[A]:HOH:O	2.12	0.64
4:B:204[C]:GOL:C2	5:B:654:HOH:O	2.26	0.61
3:A:251:SO4:S	5:A:707:HOH:O	2.57	0.59
3:A:249:SO4:O2	5:A:616:HOH:O	2.17	0.57
5:A:688:HOH:O	2:B:199[A]:MSU:CT	2.52	0.56
3:A:251:SO4:O3	5:A:707:HOH:O	2.18	0.55
3:A:248:SO4:O2	5:A:616:HOH:O	2.19	0.51
5:A:688:HOH:O	2:B:199[A]:MSU:HT2	2.10	0.51
1:A:129[B]:GLU:HG3	1:A:232:GLN:NE2	2.28	0.48
5:A:688:HOH:O	2:B:199[A]:MSU:HT3	2.15	0.47
1:A:120(A)[A]:ARG:NH1	5:A:575[A]:HOH:O	2.38	0.45
1:A:216:GLY:C	2:B:200[B]:ALA:HA	2.40	0.42
1:A:53[B]:VAL:HG12	1:A:212:VAL:HG11	2.03	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	Perce	ntiles
1	A	217/198 (110%)	205 (94%)	12 (6%)	0	100	100
2	В	3/5 (60%)	3 (100%)	0	0	100	100
All	All	220/203 (108%)	208 (94%)	12 (6%)	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	163/142 (115%)	158 (97%)	5 (3%)	40 8
2	В	1/1 (100%)	1 (100%)	0	100 100
All	All	164/143 (115%)	159 (97%)	5 (3%)	53 9

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90[A]	ARG
1	A	90[B]	ARG
1	A	141[A]	ARG
1	A	141[B]	ARG
1	A	190	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	$\mathbf{Type}$
1	A	101	ASN
1	A	166	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)

1 non-standard protein/DNA/RNA residue is 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	Res Link	B	ond leng	${ m gths}$	Bond angles		
	IVIOI	туре			Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
Ī	2	B2V	В	203	1,2	2,7,7	0.13	0	4,9,9	0.50	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.

$\mathbf{Mol}$	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
2	B2V	В	203	1,2	-	0/4/8/8	-

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.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

11 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).



Mal	Trino	Chain	Res	Link	В	ond leng	$_{ m gths}$	В	ond ang	gles
Mol	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	A	247	-	4,4,4	0.38	0	6,6,6	0.54	0
3	SO4	A	251	-	4,4,4	0.28	0	6,6,6	0.62	0
4	GOL	В	204[A]	-	4,4,5	0.44	0	3,3,5	0.47	0
4	GOL	В	204[B]	-	4,4,5	0.34	0	3,3,5	0.65	0
3	SO4	A	249	-	4,4,4	0.25	0	6,6,6	1.93	1 (16%)
3	SO4	A	252	-	4,4,4	0.50	0	6,6,6	1.56	2 (33%)
3	SO4	A	246	-	4,4,4	0.38	0	6,6,6	0.33	0
3	SO4	В	208	-	4,4,4	0.50	0	6,6,6	0.85	0
3	SO4	A	250	_	4,4,4	0.38	0	6,6,6	0.73	0
3	SO4	A	248	-	4,4,4	0.64	0	6,6,6	1.26	0
4	GOL	В	204[C]	-	4,4,5	0.42	0	3,3,5	0.84	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	GOL	В	204[A]	-	-	0/2/2/4	-
4	GOL	В	204[B]	-	-	0/2/2/4	-
4	GOL	В	204[C]	-	-	0/2/2/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
3	A	249	SO4	O3-S-O1	-3.80	89.46	109.31
3	A	252	SO4	O3-S-O1	2.72	123.48	109.31
3	A	252	SO4	O4-S-O3	-2.35	99.04	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	247	SO4	1	0
3	A	251	SO4	2	0
3	A	249	SO4	1	0
3	A	252	SO4	1	0



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	Mol	Chain	Res	Type	Clashes	Symm-Clashes
	3	A	248	SO4	4	0
ſ	4	В	204[C]	GOL	4	0

# 5.7 Other polymers (i)

There are no such residues in this entry.

# 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	222(C):SER	C	223[B]:GLN	N	1.20



## 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	<RSRZ $>$	#	∤RSR	Z>2	$OWAB(A^2)$	Q < 0.9
1	A	198/198 (100%)	-1.13	0	100	100	3, 5, 11, 22	0
2	В	3/5~(60%)	-0.82	0	100	100	6, 6, 6, 10	0
All	All	201/203 (99%)	-1.13	0	100	100	3, 5, 11, 22	0

There are no RSRZ outliers to report.

#### 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	B2V	В	203	8/8	1.00	0.04	3,5,8,8	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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	SO4	A	252	5/5	0.92	0.12	15,21,38,39	5



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	SO4	A	248	5/5	0.94	0.15	12,13,14,14	5
3	SO4	A	251	5/5	0.97	0.09	12,13,15,18	5
3	SO4	A	250	5/5	0.97	0.08	21,21,24,24	5
3	SO4	A	249	5/5	0.98	0.10	6,8,13,25	5
3	SO4	A	247	5/5	0.98	0.09	10,14,17,19	5
3	SO4	В	208	5/5	0.98	0.09	9,10,18,20	5
4	GOL	В	204[A]	5/6	0.99	0.14	3,4,4,6	10
4	GOL	В	204[B]	5/6	0.99	0.14	2,3,4,4	10
4	GOL	В	204[C]	5/6	0.99	0.14	2,4,8,8	10
3	SO4	A	246	5/5	1.00	0.02	4,5,6,6	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

