



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:13 AM GMT

PDB ID : 2PVA  
Title : OXIDIZED PENICILLIN V ACYLASE FROM B. SPHAERICUS  
Authors : Suresh, C.G.; Pundle, A.V.; Rao, K.N.; SivaRaman, H.; Brannigan, J.A.;  
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Deposited on : 1998-11-13  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

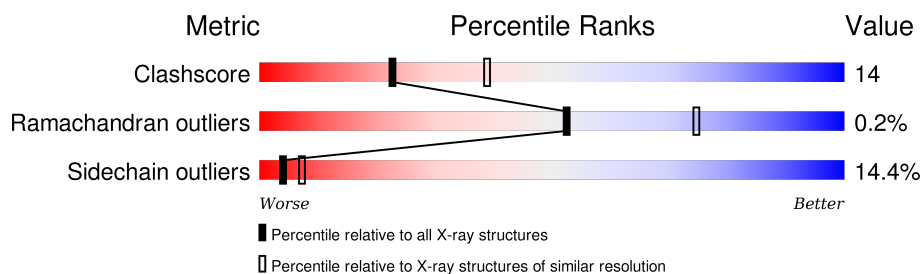
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	345	
1	B	345	
1	C	345	
1	D	345	

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
2	DTD	A	1001	X	-	-	-
2	DTD	B	1002	X	-	-	-
2	DTD	C	1003	X	-	-	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11209 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 PENICILLIN V ACYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	0	0
			2593	1648	423	509	13			
1	B	332	Total	C	N	O	S	0	0	0
			2593	1648	423	509	13			
1	C	332	Total	C	N	O	S	0	0	0
			2593	1648	423	509	13			
1	D	332	Total	C	N	O	S	0	0	0
			2593	1648	423	509	13			

There are 44 discrepancies between the modelled and reference sequences:

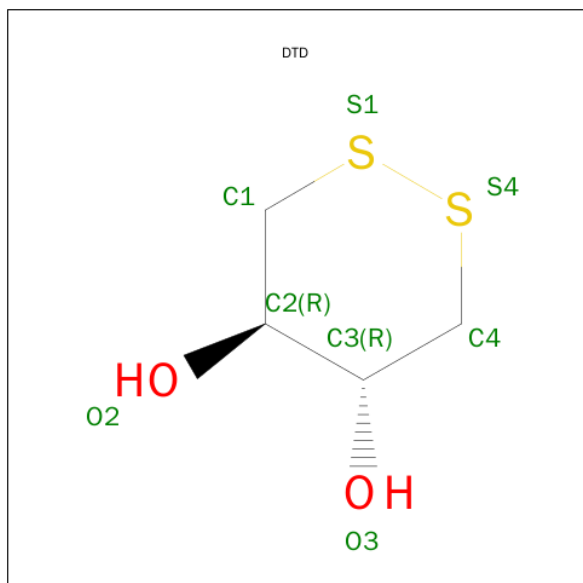
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	OCS	CYS	MODIFIED RESIDUE	UNP P12256
A	74A	THR	-	INSERTION	UNP P12256
A	74B	TYR	-	INSERTION	UNP P12256
A	74C	ALA	-	INSERTION	UNP P12256
A	74D	ASP	-	INSERTION	UNP P12256
A	74E	GLU	-	INSERTION	UNP P12256
A	74F	PRO	-	INSERTION	UNP P12256
A	74G	LYS	-	INSERTION	UNP P12256
A	74H	LYS	-	INSERTION	UNP P12256
A	74I	GLY	-	INSERTION	UNP P12256
A	74J	THR	-	INSERTION	UNP P12256
B	1	OCS	CYS	MODIFIED RESIDUE	UNP P12256
B	74A	THR	-	INSERTION	UNP P12256
B	74B	TYR	-	INSERTION	UNP P12256
B	74C	ALA	-	INSERTION	UNP P12256
B	74D	ASP	-	INSERTION	UNP P12256
B	74E	GLU	-	INSERTION	UNP P12256
B	74F	PRO	-	INSERTION	UNP P12256
B	74G	LYS	-	INSERTION	UNP P12256
B	74H	LYS	-	INSERTION	UNP P12256
B	74I	GLY	-	INSERTION	UNP P12256

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Chain	Residue	Modelled	Actual	Comment	Reference
B	74J	THR	-	INSERTION	UNP P12256
C	1	OCS	CYS	MODIFIED RESIDUE	UNP P12256
C	74A	THR	-	INSERTION	UNP P12256
C	74B	TYR	-	INSERTION	UNP P12256
C	74C	ALA	-	INSERTION	UNP P12256
C	74D	ASP	-	INSERTION	UNP P12256
C	74E	GLU	-	INSERTION	UNP P12256
C	74F	PRO	-	INSERTION	UNP P12256
C	74G	LYS	-	INSERTION	UNP P12256
C	74H	LYS	-	INSERTION	UNP P12256
C	74I	GLY	-	INSERTION	UNP P12256
C	74J	THR	-	INSERTION	UNP P12256
D	1	OCS	CYS	MODIFIED RESIDUE	UNP P12256
D	74A	THR	-	INSERTION	UNP P12256
D	74B	TYR	-	INSERTION	UNP P12256
D	74C	ALA	-	INSERTION	UNP P12256
D	74D	ASP	-	INSERTION	UNP P12256
D	74E	GLU	-	INSERTION	UNP P12256
D	74F	PRO	-	INSERTION	UNP P12256
D	74G	LYS	-	INSERTION	UNP P12256
D	74H	LYS	-	INSERTION	UNP P12256
D	74I	GLY	-	INSERTION	UNP P12256
D	74J	THR	-	INSERTION	UNP P12256

- Molecule 2 is DITHIANE DIOL (three-letter code: DTD) (formula:  $C_4H_8O_2S_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O S 8 4 2 2	0	0
2	B	1	Total C O S 8 4 2 2	0	0
2	C	1	Total C O S 8 4 2 2	0	0
2	D	1	Total C O S 8 4 2 2	0	0

- Molecule 3 is water.

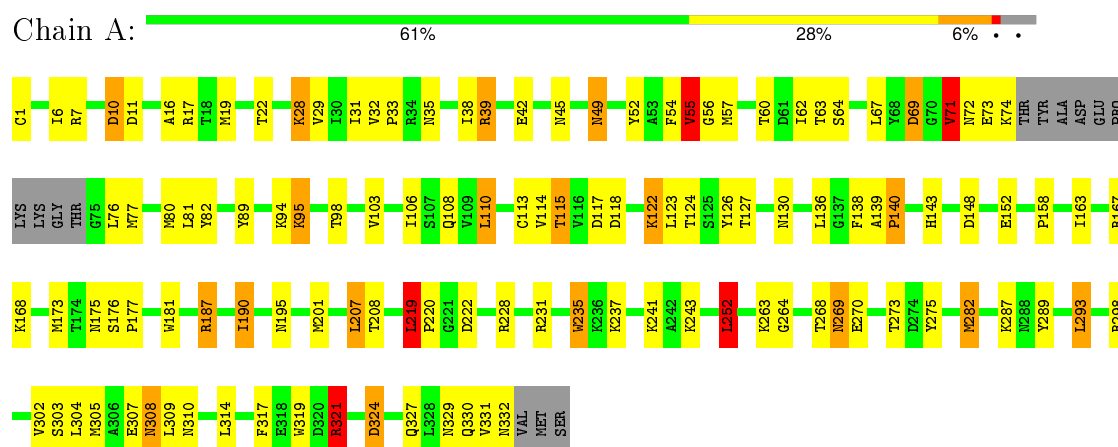
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	203	Total O 203 203	0	0
3	B	212	Total O 212 212	0	0
3	C	217	Total O 217 217	0	0
3	D	173	Total O 173 173	0	0

### 3 Residue-property plots

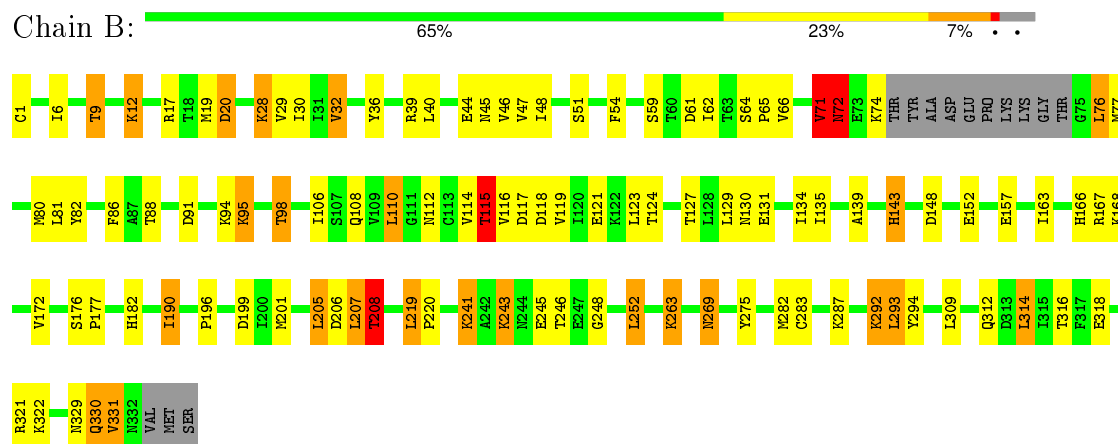
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

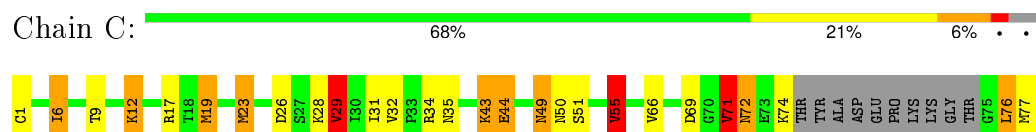
#### • Molecule 1: PENICILLIN V ACYLASE

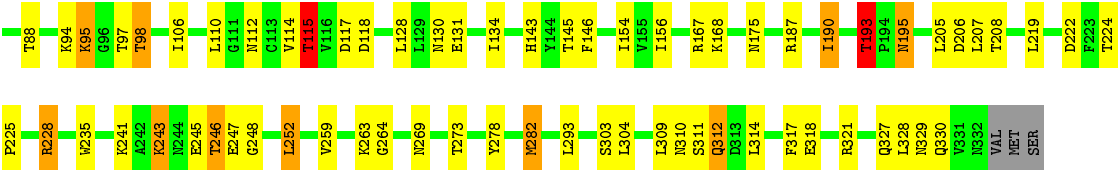


#### • Molecule 1: PENICILLIN V ACYLASE

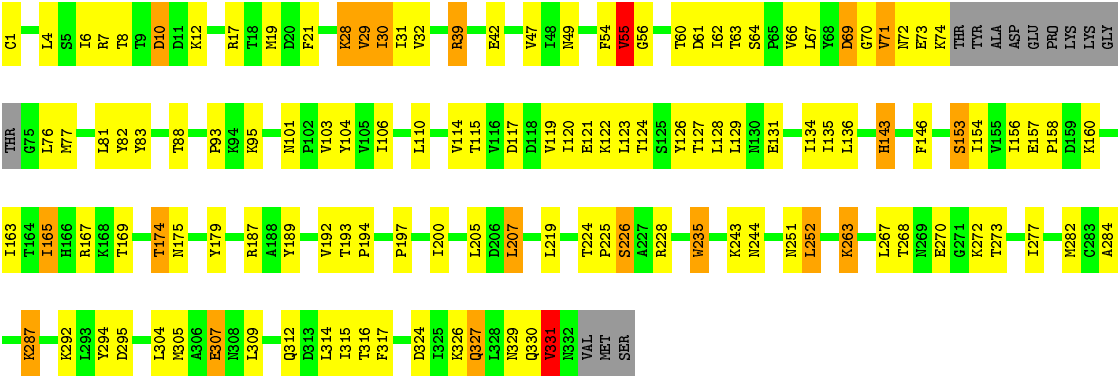


#### • Molecule 1: PENICILLIN V ACYLASE





● Molecule 1: PENICILLIN V ACYLASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.40 Å   208.40 Å   96.20 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	97.0 (20.00-2.50)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.196 , 0.245	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11209	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OCS, DTD

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	0.46	0/2639	1.23	16/3589 (0.4%)
1	B	0.46	0/2639	1.23	13/3589 (0.4%)
1	C	0.49	0/2639	1.28	13/3589 (0.4%)
1	D	0.40	0/2639	1.09	14/3589 (0.4%)
All	All	0.46	0/10556	1.21	56/14356 (0.4%)

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
1	B	0	1
1	C	0	2
1	D	0	2
All	All	0	7

There are no bond length outliers.

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	228	ARG	CD-NE-CZ	10.66	138.53	123.60
1	D	7	ARG	NE-CZ-NH1	10.12	125.36	120.30
1	D	7	ARG	CD-NE-CZ	9.95	137.53	123.60
1	C	55	VAL	CB-CA-C	-8.60	95.06	111.40
1	C	34	ARG	NE-CZ-NH2	8.60	124.60	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	140	PRO	Mainchain
1	A	55	VAL	Mainchain
1	B	72	ASN	Mainchain
1	C	29	VAL	Mainchain
1	C	329	ASN	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	2593	0	2563	90	0
1	B	2593	0	2563	66	0
1	C	2593	0	2563	58	0
1	D	2593	0	2563	80	0
2	A	8	0	8	0	0
2	B	8	0	8	1	0
2	C	8	0	8	0	0
2	D	8	0	8	0	0
3	A	203	0	0	16	0
3	B	212	0	0	14	0
3	C	217	0	0	15	0
3	D	173	0	0	9	0
All	All	11209	0	10284	282	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 14.

The worst 5 of 282 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:138:PHE:HB2	3:A:1177:HOH:O	1.46	1.12
1:C:312:GLN:HG3	3:C:1140:HOH:O	1.52	1.07
1:B:115:THR:HG22	1:B:118:ASP:H	1.26	0.96
1:B:116:VAL:HG21	1:B:152:GLU:HG2	1.50	0.94
1:B:241:LYS:HD2	3:B:1119:HOH:O	1.67	0.94

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	330/345 (96%)	315 (96%)	15 (4%)	0	100	100
1	B	330/345 (96%)	316 (96%)	13 (4%)	1 (0%)	46	68
1	C	330/345 (96%)	317 (96%)	13 (4%)	0	100	100
1	D	330/345 (96%)	305 (92%)	24 (7%)	1 (0%)	46	68
All	All	1320/1380 (96%)	1253 (95%)	65 (5%)	2 (0%)	52	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	330	GLN
1	D	331	VAL

### 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	288/299 (96%)	255 (88%)	33 (12%)	7	13
1	B	288/299 (96%)	244 (85%)	44 (15%)	3	6
1	C	288/299 (96%)	238 (83%)	50 (17%)	2	4
1	D	288/299 (96%)	249 (86%)	39 (14%)	5	9
All	All	1152/1196 (96%)	986 (86%)	166 (14%)	4	7

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	322	LYS
1	C	72	ASN
1	D	235	TRP
1	C	6	ILE
1	C	32	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	195	ASN
1	B	308	ASN
1	D	251	ASN
1	B	260	ASN
1	A	251	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	OCS	A	1	1	7,8,9	1.23	1 (14%)	7,11,13	2.60	4 (57%)
1	OCS	B	1	1	7,8,9	1.03	0	7,11,13	3.22	5 (71%)
1	OCS	C	1	1	7,8,9	0.96	0	7,11,13	2.16	3 (42%)
1	OCS	D	1	1	7,8,9	1.28	0	7,11,13	3.66	4 (57%)

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	OCS	A	1	1	-	0/4/7/9	0/0/0/0
1	OCS	B	1	1	-	0/4/7/9	0/0/0/0
1	OCS	C	1	1	-	0/4/7/9	0/0/0/0
1	OCS	D	1	1	-	0/4/7/9	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	OCS	CB-SG	2.23	1.81	1.77

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	OCS	CB-CA-C	-3.11	102.94	111.46
1	D	1	OCS	O-C-CA	-3.05	117.54	125.49
1	C	1	OCS	CB-CA-C	-2.85	103.65	111.46
1	A	1	OCS	OD2-SG-OD3	-2.81	105.06	111.61
1	A	1	OCS	O-C-CA	-2.54	118.87	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	OCS	1	0
1	B	1	OCS	1	0
1	C	1	OCS	1	0
1	D	1	OCS	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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$
2	DTD	A	1001	-	6,8,8	0.62	0	6,10,10	0.91	0
2	DTD	B	1002	-	6,8,8	0.51	0	6,10,10	1.28	1 (16%)
2	DTD	C	1003	-	6,8,8	0.71	0	6,10,10	1.19	1 (16%)
2	DTD	D	1004	-	6,8,8	0.57	0	6,10,10	1.15	1 (16%)

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
2	DTD	A	1001	-	1/1/2/2	0/0/11/11	0/0/1/1
2	DTD	B	1002	-	1/1/2/2	0/0/11/11	0/0/1/1
2	DTD	C	1003	-	1/1/2/2	0/0/11/11	0/0/1/1
2	DTD	D	1004	-	-	0/0/11/11	0/0/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1004	DTD	O3-C3-C2	-2.48	104.70	110.27
2	C	1003	DTD	O3-C3-C2	-2.31	105.10	110.27
2	B	1002	DTD	O2-C2-C1	-2.16	106.30	110.05

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1003	DTD	C2
2	A	1001	DTD	C2
2	B	1002	DTD	C2

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1002	DTD	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.