



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 7, 2017 – 04:37 PM EDT

PDB ID : 1E4E  
Title : D-alanyl-D-lactate ligase  
Authors : Roper, D.I.  
Deposited on : unknown  
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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

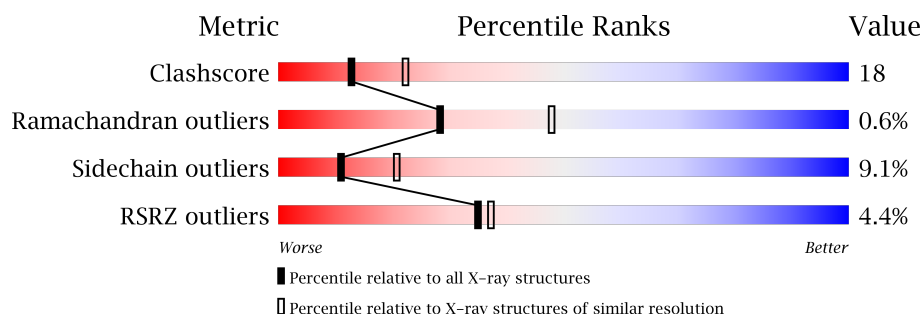
# 1 Overall quality at a glance

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	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (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.

Mol	Chain	Length	Quality of chain
1	A	343	
2	B	343	

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
6	SO4	A	1343	-	-	-	X
6	SO4	A	1344	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SO4	B	1342	-	-	-	X
7	GOL	A	1346	-	-	X	-
7	GOL	A	1347	-	-	-	X
7	GOL	A	1348	-	-	X	-
7	GOL	A	1350	-	-	-	X
7	GOL	A	990	-	-	X	-
7	GOL	B	1345	-	-	-	X
7	GOL	B	1346	-	-	X	X
7	GOL	B	1347	-	-	X	X
7	GOL	B	1348	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5750 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 VANCOMYCIN/TEICOPLANIN A-TYPE RESISTANCE PROTEIN VANA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	5	0	0
			2607	1653	443	496	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	GLU	ASP	conflict	UNP P25051
A	276	VAL	ALA	conflict	UNP P25051
A	282	THR	ALA	conflict	UNP P25051
A	328	SER	ALA	conflict	UNP P25051

- Molecule 2 is a protein called VANCOMYCIN/TEICOPLANIN A-TYPE RESISTANCE PROTEIN VANA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	340	Total	C	N	O	S	33	0	0
			2603	1650	446	492	15			

There are 5 discrepancies between the modelled and reference sequences:

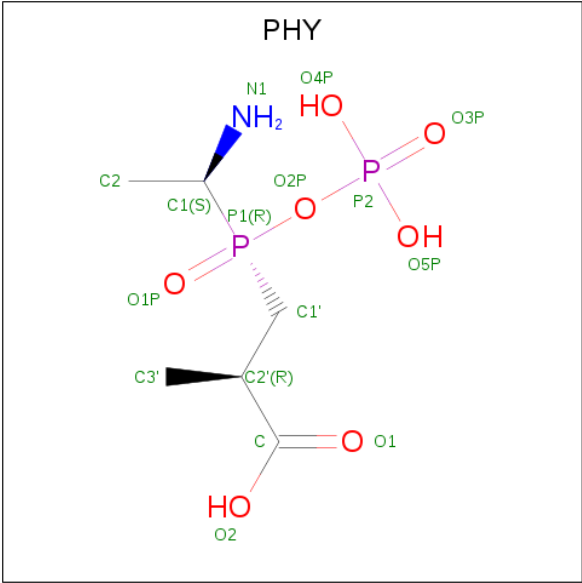
Chain	Residue	Modelled	Actual	Comment	Reference
B	62	GLU	ASP	conflict	UNP P25051
B	276	VAL	ALA	conflict	UNP P25051
B	282	THR	ALA	conflict	UNP P25051
B	298	ARG	ASN	conflict	UNP P25051
B	328	SER	ALA	conflict	UNP P25051

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is 1(S)-AMINOETHYL-(2-CARBOXYPROPYL)PHOSPHORYL-PHOSPHINI C ACID (three-letter code: PHY) (formula: C<sub>6</sub>H<sub>15</sub>NO<sub>7</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			14	5	1	6	2		

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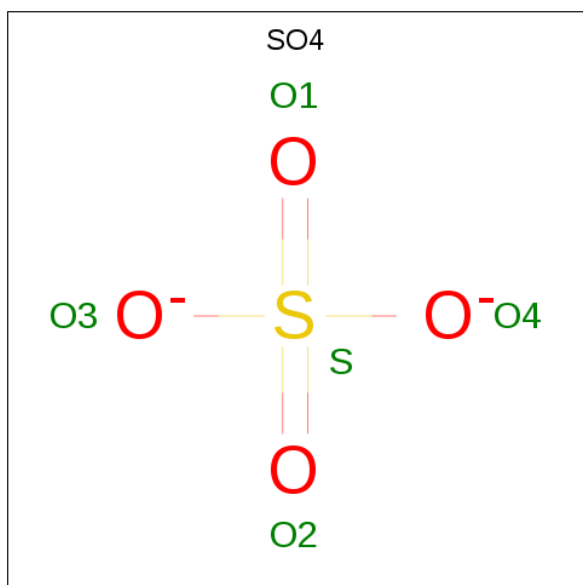
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			14	5	1	6	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Mg	0	0
			2	2		
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is water.

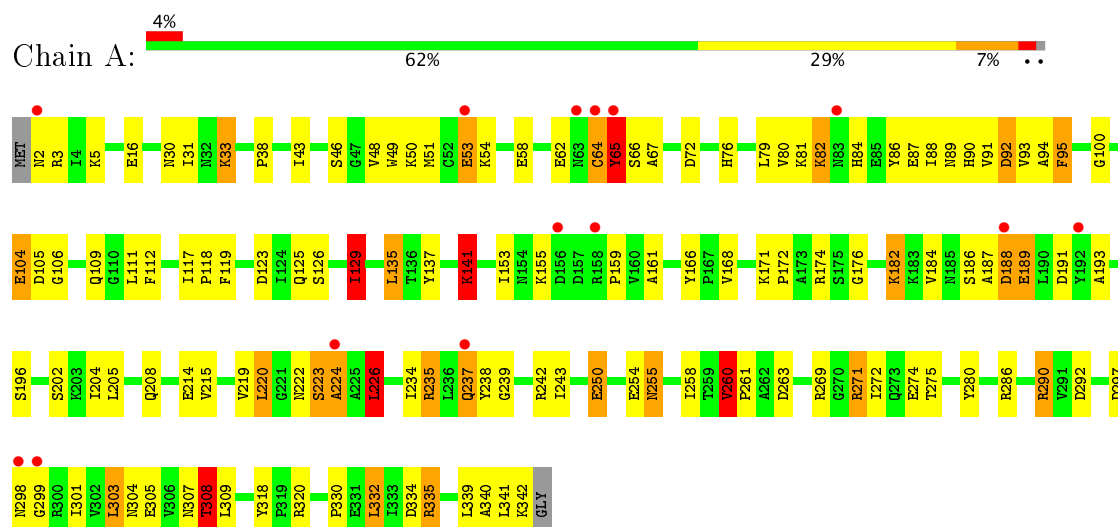
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	169	Total 169	O 169	0	0
8	A	1	Total 1	O 1	0	0
8	A	2	Total 2	O 2	0	0
8	A	3	Total 3	O 3	0	0
8	B	173	Total 173	O 173	0	0
8	B	1	Total 1	O 1	0	0
8	B	1	Total 1	O 1	0	0
8	B	5	Total 5	O 5	0	0



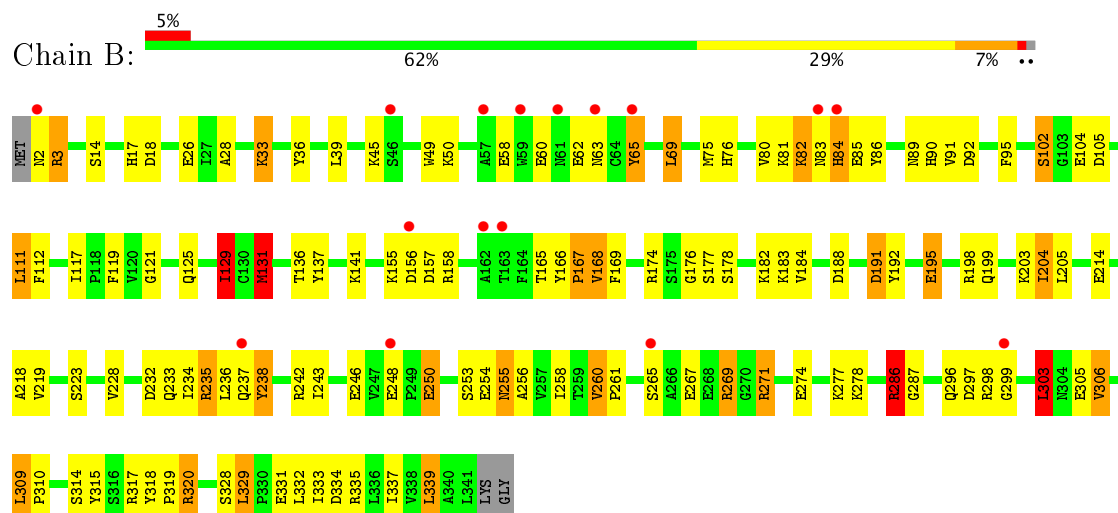
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: VANCOMYCIN/TEICOPLANIN A-TYPE RESISTANCE PROTEIN VANA



#### • Molecule 2: VANCOMYCIN/TEICOPLANIN A-TYPE RESISTANCE PROTEIN VANA



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.20Å 225.36Å 72.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 14.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.3 (15.00-2.50) 93.3 (14.86-2.50)	Depositor EDS
$R_{merge}$	0.58	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.88 (at 2.51Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.183 , 0.257 0.178 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	30.0	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 68.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.022 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5750	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, PHY, ADP, 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	1.41	15/2654 (0.6%)	1.52	49/3589 (1.4%)
2	B	1.51	20/2650 (0.8%)	1.61	46/3583 (1.3%)
All	All	1.46	35/5304 (0.7%)	1.57	95/7172 (1.3%)

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	208	GLN	CA-CB	-17.09	1.16	1.53
2	B	84	HIS	CA-CB	16.40	1.90	1.53
2	B	155	LYS	CB-CG	-15.31	1.11	1.52
2	B	62	GLU	CA-CB	-13.57	1.24	1.53
1	A	250	GLU	CD-OE1	10.83	1.37	1.25

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	269	ARG	NE-CZ-NH2	-16.84	111.88	120.30
2	B	269	ARG	NE-CZ-NH1	16.51	128.55	120.30
2	B	335	ARG	NE-CZ-NH2	-16.06	112.27	120.30
2	B	84	HIS	N-CA-CB	15.70	138.87	110.60
1	A	320	ARG	NE-CZ-NH2	-13.51	113.54	120.30

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	2607	0	2602	100	4
2	B	2603	0	2607	85	0
3	A	27	0	12	3	0
3	B	27	0	12	2	0
4	A	14	0	5	4	0
4	B	14	0	6	4	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	10	0	0	4	0
6	B	5	0	0	1	0
7	A	48	0	61	12	4
7	B	36	0	48	12	0
8	A	175	0	0	6	0
8	B	180	0	0	17	0
All	All	5750	0	5353	197	4

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 18.

The worst 5 of 197 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:51:MET:O	1:A:65:TYR:N	1.77	1.17
2:B:314:SER:HA	7:B:1347:GOL:H31	1.36	1.06
4:B:355:PHY:C2	4:B:355:PHY:P1	2.45	1.04
2:B:286:ARG:HD2	8:B:2149:HOH:O	1.59	1.01
4:A:355:PHY:C2	4:A:355:PHY:N1	2.25	1.00

All (4) 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)
1:A:64:CYS:O	7:A:990:GOL:O2[6_555]	1.83	0.37
1:A:65:TYR:CA	7:A:990:GOL:C1[6_555]	1.92	0.28
1:A:64:CYS:C	7:A:990:GOL:O2[6_555]	1.96	0.24
1:A:64:CYS:O	7:A:990:GOL:C2[6_555]	2.09	0.11

## 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	339/343 (99%)	319 (94%)	17 (5%)	3 (1%)	20	36
2	B	338/343 (98%)	322 (95%)	15 (4%)	1 (0%)	44	66
All	All	677/686 (99%)	641 (95%)	32 (5%)	4 (1%)	28	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	SER
1	A	224	ALA
2	B	102	SER
1	A	226	LEU

### 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	279/285 (98%)	254 (91%)	25 (9%)	11	21
2	B	279/285 (98%)	253 (91%)	26 (9%)	10	20
All	All	558/570 (98%)	507 (91%)	51 (9%)	11	21

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	308	THR
2	B	82	LYS

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Mol	Chain	Res	Type
2	B	329	LEU
2	B	63	ASN
2	B	95	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	ASN
2	B	30	ASN
2	B	154	ASN
1	A	90	HIS
2	B	125	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 4 are monoatomic - leaving 21 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
6	SO4	A	1343	-	4,4,4	0.09	0	6,6,6	1.28	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	A	1344	-	4,4,4	0.33	0	6,6,6	0.40	0
7	GOL	A	1345	-	5,5,5	1.65	1 (20%)	5,5,5	2.74	3 (60%)
7	GOL	A	1346	-	5,5,5	1.09	0	5,5,5	1.99	2 (40%)
7	GOL	A	1347	-	5,5,5	0.62	0	5,5,5	0.80	0
7	GOL	A	1348	-	5,5,5	0.50	0	5,5,5	2.07	3 (60%)
7	GOL	A	1349	-	5,5,5	0.46	0	5,5,5	0.32	0
7	GOL	A	1350	-	5,5,5	0.42	0	5,5,5	0.38	0
3	ADP	A	350	5	25,29,29	1.47	4 (16%)	24,45,45	1.87	2 (8%)
4	PHY	A	355	5	2,11,15	1.02	0	1,14,23	0.60	0
7	GOL	A	990	-	5,5,5	0.48	0	5,5,5	1.71	2 (40%)
7	GOL	A	996	-	5,5,5	0.52	0	5,5,5	0.48	0
6	SO4	B	1342	-	4,4,4	0.41	0	6,6,6	0.84	0
7	GOL	B	1343	-	5,5,5	0.27	0	5,5,5	1.37	1 (20%)
7	GOL	B	1344	-	5,5,5	0.32	0	5,5,5	0.30	0
7	GOL	B	1345	-	5,5,5	0.31	0	5,5,5	1.84	2 (40%)
7	GOL	B	1346	-	5,5,5	0.40	0	5,5,5	0.44	0
7	GOL	B	1347	-	5,5,5	0.60	0	5,5,5	1.01	1 (20%)
7	GOL	B	1348	-	5,5,5	0.39	0	5,5,5	0.56	0
3	ADP	B	350	5	25,29,29	1.41	3 (12%)	24,45,45	2.01	5 (20%)
4	PHY	B	355	5	2,11,15	0.54	0	1,14,23	0.51	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
6	SO4	A	1343	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1344	-	-	0/0/0/0	0/0/0/0
7	GOL	A	1345	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1346	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1347	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1348	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1349	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1350	-	-	0/4/4/4	0/0/0/0
3	ADP	A	350	5	-	0/12/32/32	0/3/3/3
4	PHY	A	355	5	-	0/1/12/21	0/0/0/0
7	GOL	A	990	-	-	0/4/4/4	0/0/0/0
7	GOL	A	996	-	-	0/4/4/4	0/0/0/0
6	SO4	B	1342	-	-	0/0/0/0	0/0/0/0
7	GOL	B	1343	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	B	1344	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1345	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1346	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1347	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1348	-	-	0/4/4/4	0/0/0/0
3	ADP	B	350	5	-	0/12/32/32	0/3/3/3
4	PHY	B	355	5	-	0/1/12/21	0/0/0/0

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1345	GOL	O2-C2	-2.80	1.35	1.43
3	B	350	ADP	C3'-C4'	-2.53	1.46	1.53
3	A	350	ADP	O3'-C3'	-2.43	1.37	1.43
3	A	350	ADP	PB-O3B	-2.41	1.44	1.54
3	B	350	ADP	C2-N1	2.70	1.39	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	350	ADP	N3-C2-N1	-7.65	122.20	128.86
3	B	350	ADP	N3-C2-N1	-7.36	122.45	128.86
7	A	1345	GOL	O2-C2-C3	-4.15	89.25	108.84
7	A	1345	GOL	C3-C2-C1	-3.91	95.98	111.52
7	A	1346	GOL	O3-C3-C2	-2.91	95.40	110.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1344	SO4	4	0
7	A	1346	GOL	5	0
7	A	1347	GOL	2	0
7	A	1348	GOL	4	0
7	A	1350	GOL	1	0
3	A	350	ADP	3	0
4	A	355	PHY	4	0
7	A	990	GOL	0	4
6	B	1342	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1346	GOL	5	0
7	B	1347	GOL	5	0
7	B	1348	GOL	2	0
3	B	350	ADP	2	0
4	B	355	PHY	4	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	341/343 (99%)	-0.01	14 (4%)	38 40	41, 52, 72, 88	1 (0%)
2	B	340/343 (99%)	0.07	16 (4%)	32 34	39, 50, 72, 86	8 (2%)
All	All	681/686 (99%)	0.03	30 (4%)	35 37	39, 51, 72, 88	9 (1%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	TYR	6.7
2	B	83	ASN	4.6
1	A	63	ASN	4.4
2	B	84	HIS	4.0
2	B	63	ASN	3.6

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	GOL	A	1350	6/6	0.57	0.49	11.60	125,126,126,127	0
7	GOL	B	1347	6/6	0.86	0.40	10.18	82,84,87,88	0
7	GOL	A	1347	6/6	0.70	0.45	8.19	61,67,74,80	0
6	SO4	A	1343	5/5	0.97	0.26	5.01	56,59,62,65	0
7	GOL	B	1346	6/6	0.65	0.38	4.94	95,100,101,103	0
7	GOL	B	1345	6/6	0.73	0.29	4.52	68,72,73,74	0
7	GOL	B	1348	6/6	0.46	0.59	4.39	92,94,94,94	0
6	SO4	A	1344	5/5	0.96	0.27	4.22	93,96,98,98	0
6	SO4	B	1342	5/5	0.97	0.20	3.64	50,54,56,57	0
4	PHY	A	355	14/16	0.94	0.15	0.45	34,40,42,44	0
4	PHY	B	355	14/16	0.96	0.14	0.27	33,35,39,39	0
7	GOL	A	1345	6/6	0.94	0.20	-0.02	47,57,62,66	0
7	GOL	A	990	6/6	0.79	0.24	-0.16	73,80,85,92	0
7	GOL	A	1346	6/6	0.95	0.18	-0.35	71,72,73,73	0
5	MG	A	360	1/1	0.91	0.12	-0.81	46,46,46,46	0
3	ADP	A	350	27/27	0.97	0.11	-1.14	41,47,51,52	0
3	ADP	B	350	27/27	0.96	0.12	-1.23	33,45,50,51	0
5	MG	B	360	1/1	0.92	0.11	-2.18	42,42,42,42	0
7	GOL	A	1349	6/6	0.47	0.60	-	106,108,109,109	0
7	GOL	A	1348	6/6	0.87	0.31	-	83,84,85,87	0
5	MG	A	365	1/1	0.97	0.06	-	42,42,42,42	0
7	GOL	B	1343	6/6	0.73	0.31	-	99,101,102,103	0
5	MG	B	365	1/1	0.98	0.08	-	38,38,38,38	0
7	GOL	A	996	6/6	0.56	0.46	-	116,117,118,119	0
7	GOL	B	1344	6/6	0.86	0.40	-	104,107,108,112	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.