wwPDB X-ray Structure Validation Summary Report (i)

Mar 1, 2026 – 09:46 AM UTC

PDB ID	:	1MU9 / pdb_00001mu9
Title	:	Crystal Structure of a Human Tyrosyl-DNA Phosphodiesterase (Tdp1)-Vanadate Complex
Authors	:	Davies, D.R.; Interthal, H.; Champoux, J.J.; Hol, W.G.J.
Deposited on	:	2002-09-23
Resolution	:	2.05 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*
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:

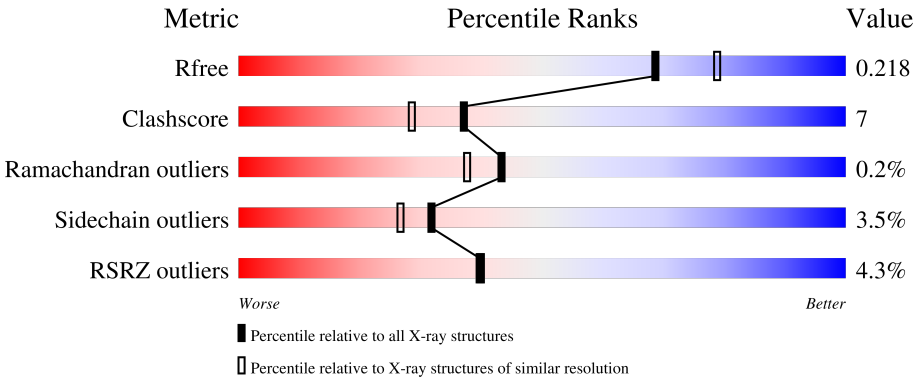
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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}	180053	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	485	4% 75% 11% • 12%
1	B	485	3% 73% 14% • 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7146 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 Tyrosyl-DNA Phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	425	Total	C	N	O	S	0	0	0
			3393	2208	573	601	11			
1	B	434	Total	C	N	O	S	0	0	0
			3452	2242	584	615	11			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	124	MET	-	cloning artifact	GB 20127586
A	125	GLY	-	cloning artifact	GB 20127586
A	126	SER	-	cloning artifact	GB 20127586
A	127	SER	-	cloning artifact	GB 20127586
A	128	HIS	-	cloning artifact	GB 20127586
A	129	HIS	-	cloning artifact	GB 20127586
A	130	HIS	-	cloning artifact	GB 20127586
A	131	HIS	-	cloning artifact	GB 20127586
A	132	HIS	-	cloning artifact	GB 20127586
A	133	HIS	-	cloning artifact	GB 20127586
A	134	SER	-	cloning artifact	GB 20127586
A	135	SER	-	cloning artifact	GB 20127586
A	136	GLY	-	cloning artifact	GB 20127586
A	137	LEU	-	cloning artifact	GB 20127586
A	138	VAL	-	cloning artifact	GB 20127586
A	139	PRO	-	cloning artifact	GB 20127586
A	140	ARG	-	cloning artifact	GB 20127586
A	141	GLY	-	cloning artifact	GB 20127586
A	142	SER	-	cloning artifact	GB 20127586
A	143	HIS	-	cloning artifact	GB 20127586
A	144	MET	-	cloning artifact	GB 20127586
A	145	LEU	-	cloning artifact	GB 20127586
A	146	GLU	-	cloning artifact	GB 20127586
A	147	ASP	-	cloning artifact	GB 20127586
A	148	PRO	-	cloning artifact	GB 20127586

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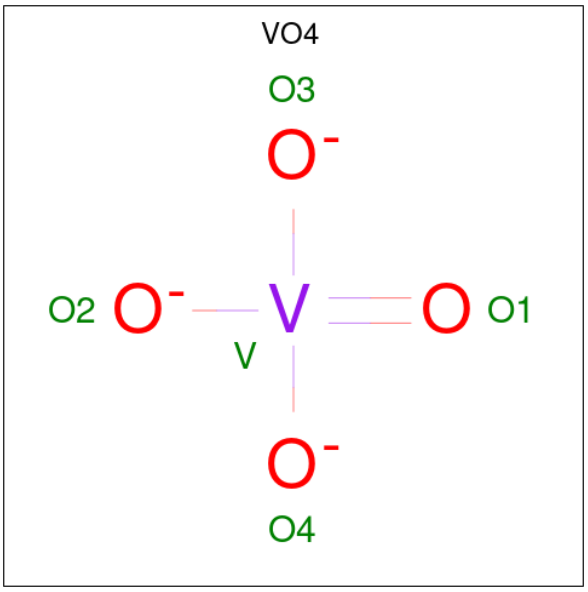
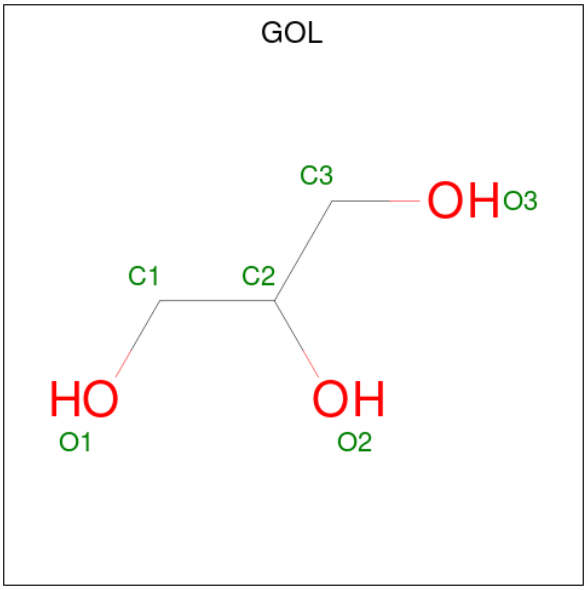
Chain	Residue	Modelled	Actual	Comment	Reference
A	322	ASN	ASP	engineered mutation	GB 20127586
A	328	THR	MET	engineered mutation	GB 20127586
A	548	LEU	PHE	engineered mutation	GB 20127586
B	124	MET	-	cloning artifact	GB 20127586
B	125	GLY	-	cloning artifact	GB 20127586
B	126	SER	-	cloning artifact	GB 20127586
B	127	SER	-	cloning artifact	GB 20127586
B	128	HIS	-	cloning artifact	GB 20127586
B	129	HIS	-	cloning artifact	GB 20127586
B	130	HIS	-	cloning artifact	GB 20127586
B	131	HIS	-	cloning artifact	GB 20127586
B	132	HIS	-	cloning artifact	GB 20127586
B	133	HIS	-	cloning artifact	GB 20127586
B	134	SER	-	cloning artifact	GB 20127586
B	135	SER	-	cloning artifact	GB 20127586
B	136	GLY	-	cloning artifact	GB 20127586
B	137	LEU	-	cloning artifact	GB 20127586
B	138	VAL	-	cloning artifact	GB 20127586
B	139	PRO	-	cloning artifact	GB 20127586
B	140	ARG	-	cloning artifact	GB 20127586
B	141	GLY	-	cloning artifact	GB 20127586
B	142	SER	-	cloning artifact	GB 20127586
B	143	HIS	-	cloning artifact	GB 20127586
B	144	MET	-	cloning artifact	GB 20127586
B	145	LEU	-	cloning artifact	GB 20127586
B	146	GLU	-	cloning artifact	GB 20127586
B	147	ASP	-	cloning artifact	GB 20127586
B	148	PRO	-	cloning artifact	GB 20127586
B	322	ASN	ASP	engineered mutation	GB 20127586
B	328	THR	MET	engineered mutation	GB 20127586
B	548	LEU	PHE	engineered mutation	GB 20127586

- Molecule 2 is VANADATE ION (CCD ID: VO4) (formula: O_4V).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O V 3 2 1	0	0
2	B	1	Total O V 3 2 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

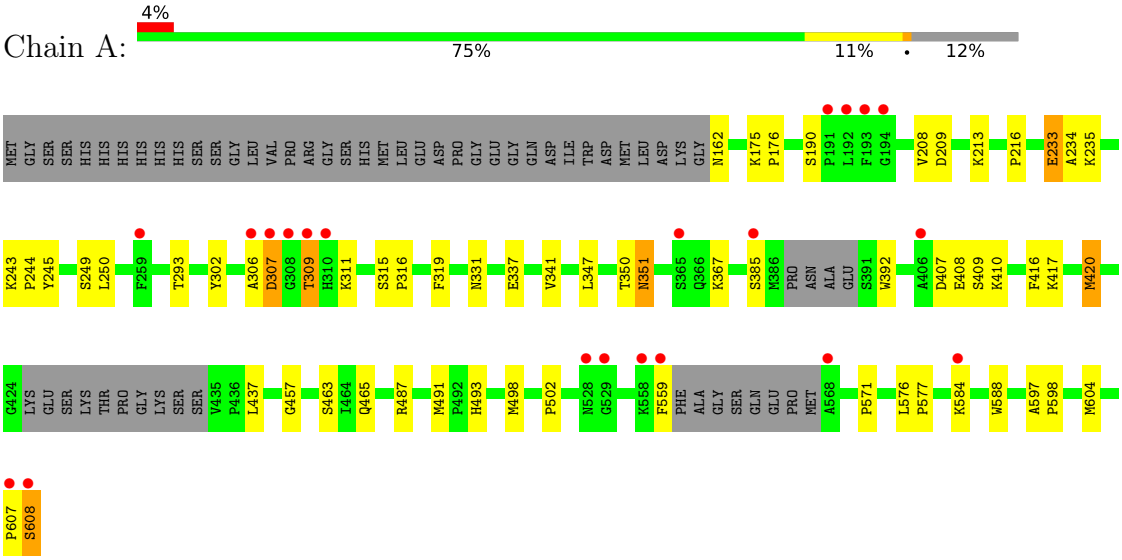
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	136	Total O 136 136	0	0
4	B	147	Total O 147 147	0	0

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.

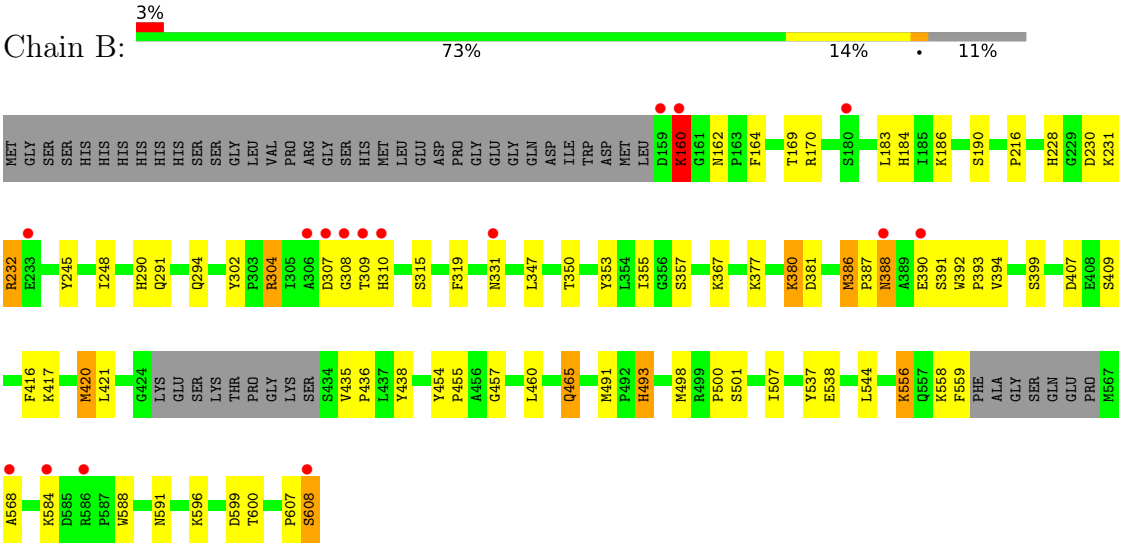
• Molecule 1: Tyrosyl-DNA Phosphodiesterase

Chain A:



• Molecule 1: Tyrosyl-DNA Phosphodiesterase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.03Å 104.98Å 194.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.97 – 2.05 19.97 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.97-2.05) 99.6 (19.97-2.05)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.46 (at 2.06Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.199 , 0.214 0.203 , 0.218	Depositor DCC
R_{free} test set	3291 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	25.8	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7146	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: VO4, GOL

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	0.71	2/3504 (0.1%)	1.04	8/4765 (0.2%)
1	B	0.75	1/3565 (0.0%)	1.03	6/4849 (0.1%)
All	All	0.73	3/7069 (0.0%)	1.03	14/9614 (0.1%)

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	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	604	MET	SD-CE	7.42	1.98	1.79
1	A	498	MET	SD-CE	-6.77	1.62	1.79
1	B	420	MET	SD-CE	5.24	1.92	1.79

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	306	ALA	CA-C-N	6.91	134.74	121.54
1	A	306	ALA	C-N-CA	6.91	134.74	121.54
1	A	493	HIS	N-CA-C	-6.20	104.09	113.89
1	B	309	THR	N-CA-C	-5.86	101.33	110.42
1	A	216	PRO	O-C-N	5.85	123.90	121.15

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	307	ASP	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	3393	0	3330	35	0
1	B	3452	0	3377	62	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	6	0	6	0	0
3	B	6	0	6	0	0
4	A	136	0	0	2	0
4	B	147	0	0	2	0
All	All	7146	0	6719	97	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.

The worst 5 of 97 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:498:MET:CE	1:B:507:ILE:HG21	1.64	1.26
1:A:607:PRO:O	1:A:608:SER:HB2	1.40	1.13
1:B:498:MET:HE1	1:B:507:ILE:HG21	1.15	1.08
1:B:607:PRO:O	1:B:608:SER:HB2	1.50	1.06
1:B:160:LYS:HG3	1:B:160:LYS:O	1.53	1.04

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	417/485 (86%)	401 (96%)	15 (4%)	1 (0%)	43	37
1	B	428/485 (88%)	408 (95%)	19 (4%)	1 (0%)	43	37
All	All	845/970 (87%)	809 (96%)	34 (4%)	2 (0%)	43	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	307	ASP
1	B	160	LYS

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	366/421 (87%)	356 (97%)	10 (3%)	39	36
1	B	371/421 (88%)	355 (96%)	16 (4%)	26	20
All	All	737/842 (88%)	711 (96%)	26 (4%)	32	27

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	315	SER
1	B	367	LYS
1	B	600	THR
1	B	355	ILE
1	B	380	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	331	ASN

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Mol	Chain	Res	Type
1	B	489	ASN
1	B	528	ASN
1	B	465	GLN
1	A	489	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)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides 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	VO4	B	609	1,3	0,2,4	-	-	-		
2	VO4	A	609	1,3	0,2,4	-	-	-		
3	GOL	B	610	2	5,5,5	0.75	0	5,5,5	1.24	0
3	GOL	A	610	2	5,5,5	0.62	0	5,5,5	2.37	2 (40%)

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
3	GOL	B	610	2	-	0/4/4/4	-
3	GOL	A	610	2	-	0/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	610	GOL	C3-C2-C1	4.72	129.10	111.80
3	A	610	GOL	O3-C3-C2	2.05	119.59	110.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	425/485 (87%)	0.20	21 (4%)	35	35	17, 31, 52, 69	0
1	B	434/485 (89%)	-0.21	16 (3%)	45	45	12, 24, 42, 66	0
All	All	859/970 (88%)	-0.01	37 (4%)	40	40	12, 27, 48, 69	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	608	SER	4.2
1	A	608	SER	3.9
1	A	193	PHE	3.9
1	A	194	GLY	3.7
1	A	308	GLY	3.5

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

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	B-factors(Å^2)	Q<0.9
3	GOL	B	610	6/6	0.88	0.12	20,24,30,34	0
3	GOL	A	610	6/6	0.90	0.11	27,31,34,38	0
2	VO4	A	609	3/5	0.99	0.05	27,27,28,29	0
2	VO4	B	609	3/5	1.00	0.04	21,21,23,23	0

6.5 Other polymers (i)

There are no such residues in this entry.