



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 03:34 AM BST

PDB ID : 5WFI
Title : X-ray structure of MHV PLP2 (Cys1716Ser) catalytic mutant in complex with free ubiquitin
Authors : Mesecar, A.D.; Chen, Y.
Deposited on : 2017-07-12
Resolution : 1.85 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 ⓘ symbol.

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 : 2.13.1
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) : 2.13.1

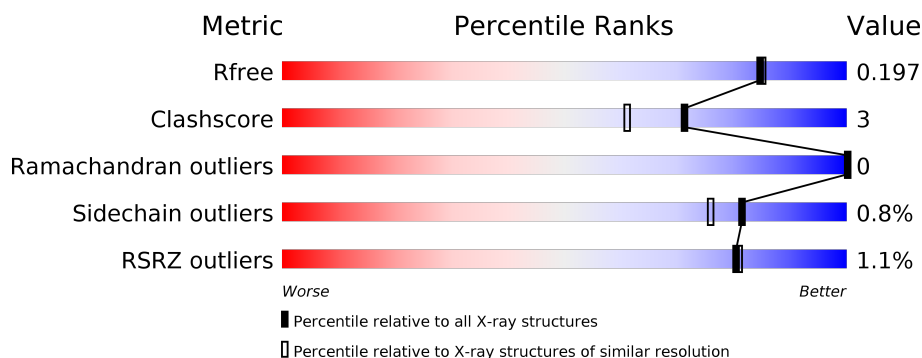
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 ≥ 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	303	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 11%, green 88%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 88% 11% • </div> </div>
1	B	303	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 6%, green 94%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 94% 6% </div> </div>
2	C	76	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 12%, green 88%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 88% 12% </div> </div>
2	D	76	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 4%, green 96%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 96% • </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6716 atoms, of which 20 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 papain-like protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	7	0
			2376	1520	397	432	27			
1	B	303	Total	C	N	O	S	0	10	0
			2410	1545	401	437	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1716	SER	CYS	engineered mutation	UNP P0C6X9
B	1716	SER	CYS	engineered mutation	UNP P0C6X9

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	76	Total	C	N	O	S	0	0	0
			602	378	105	118	1			
2	D	76	Total	C	N	O	S	0	0	0
			602	378	105	118	1			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 6	C 3	O 3	0	0	
3	A	1	Total 6	C 3	O 3	0	0	
3	A	1	Total 14	C 3	H 8	O 3	0	0
3	B	1	Total 6	C 3	O 3	0	0	
3	B	1	Total 6	C 3	O 3	0	0	
3	B	1	Total 6	C 3	O 3	0	0	
3	C	1	Total 6	C 3	O 3	0	0	
3	C	1	Total 14	C 3	H 8	O 3	0	0
3	D	1	Total 6	C 3	O 3	0	0	
3	D	1	Total 6	C 3	O 3	0	0	

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			5	1	2	2		
4	B	1	Total	C	H	O	0	0
			5	1	2	2		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		
5	A	1	Total	Zn	0	0
			1	1		

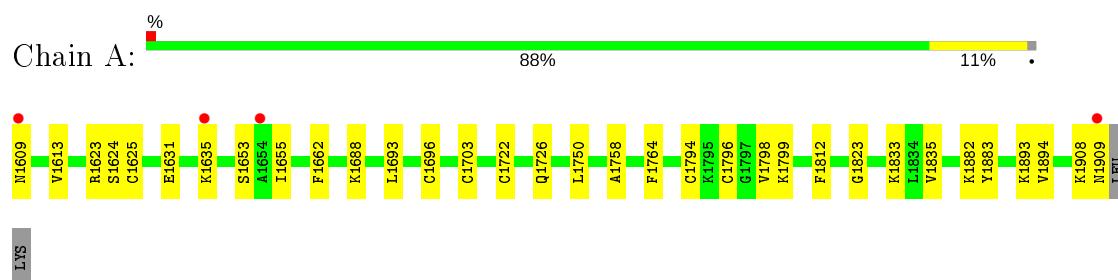
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	223	Total	O	0	0
			223	223		
6	B	272	Total	O	0	0
			272	272		
6	C	39	Total	O	0	0
			39	39		
6	D	104	Total	O	0	0
			104	104		

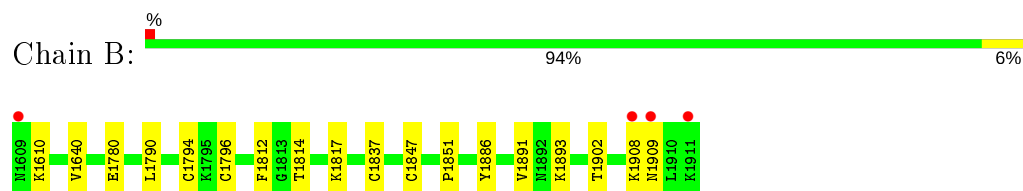
3 Residue-property plots

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.

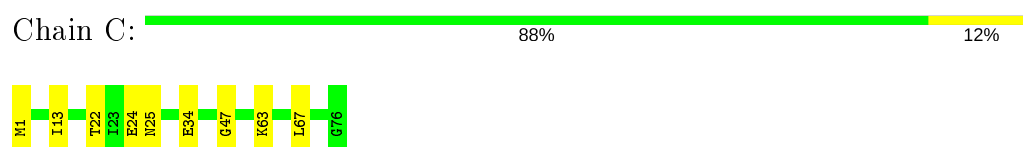
- Molecule 1: papain-like protease



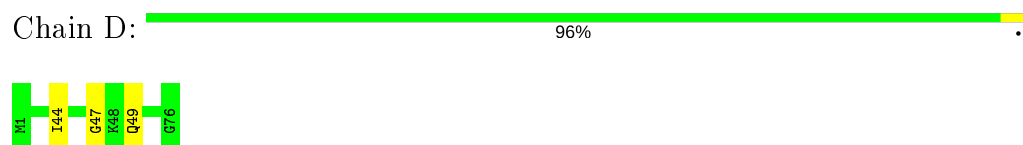
- Molecule 1: papain-like protease



- Molecule 2: Ubiquitin



- Molecule 2: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	199.51Å 43.39Å 110.16Å 90.00° 114.85° 90.00°	Depositor
Resolution (Å)	37.58 – 1.85 37.58 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (37.58-1.85) 95.2 (37.58-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 1.85Å)	Xtriage
Refinement program	PHENIX (1.10 _2155: ???)	Depositor
R, R_{free}	0.157 , 0.197 0.157 , 0.197	Depositor DCC
R_{free} test set	2000 reflections (2.72%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6716	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, ZN, FMT

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	0.33	0/2450	0.51	0/3308
1	B	0.36	0/2490	0.52	0/3363
2	C	0.30	0/608	0.50	0/816
2	D	0.35	0/608	0.54	0/816
All	All	0.34	0/6156	0.51	0/8303

There are no bond length outliers.

There are no bond angle outliers.

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	2376	0	2355	22	1
1	B	2410	0	2404	15	0
2	C	602	0	629	7	0
2	D	602	0	629	2	0
3	A	18	8	24	1	0
3	B	18	0	24	0	0
3	C	12	8	16	0	0
3	D	12	0	16	0	0
4	A	3	2	1	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	3	2	1	0	1
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	223	0	0	1	2
6	B	272	0	0	2	2
6	C	39	0	0	0	2
6	D	104	0	0	0	0
All	All	6696	20	6099	42	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 3.

All (42) 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:1623:ARG:NH1	1:A:1625[B]:CYS:SG	2.61	0.73
1:A:1662:PHE:CD1	3:A:2001:GOL:H32	2.34	0.62
1:B:1780:GLU:OE1	6:B:2101:HOH:O	2.16	0.60
2:C:22:THR:OG1	2:C:24:GLU:HG3	2.01	0.60
1:B:1851:PRO:HG3	1:B:1902[A]:THR:CG2	2.32	0.59
1:B:1851:PRO:HG3	1:B:1902[A]:THR:HG22	1.85	0.58
1:B:1817:LYS:HE2	6:B:2103:HOH:O	2.05	0.55
1:A:1653[B]:SER:OG	1:A:1655:ILE:HG12	2.07	0.54
1:A:1794:CYS:SG	1:A:1796:CYS:HB2	2.47	0.53
1:A:1613:VAL:HG23	1:A:1625[A]:CYS:SG	2.50	0.51
2:C:1:MET:HE2	2:C:63:LYS:CA	2.41	0.50
1:A:1696[B]:CYS:SG	1:A:1750:LEU:HD22	2.53	0.49
1:A:1794:CYS:HB3	1:A:1833:LYS:HA	1.95	0.48
1:A:1894:VAL:CG1	1:B:1893:LYS:HD3	2.43	0.48
1:A:1631:GLU:CD	1:A:1635:LYS:HD3	2.35	0.47
2:C:13:ILE:HD11	2:C:34:GLU:HG3	1.95	0.47
1:A:1908:LYS:O	1:A:1909:ASN:HB2	2.15	0.47
1:A:1624[A]:SER:OG	6:A:2101:HOH:O	2.20	0.47
1:A:1823:GLY:HA2	1:A:1835:VAL:O	2.14	0.47
1:B:1886:TYR:CD2	1:B:1891:VAL:HG22	2.50	0.47
1:B:1908:LYS:O	1:B:1909:ASN:HB2	2.15	0.47
2:C:1:MET:HE2	2:C:63:LYS:HA	1.96	0.46
1:A:1798:VAL:O	1:A:1799:LYS:HD3	2.16	0.46
1:A:1883:TYR:O	1:A:1893:LYS:HD2	2.15	0.46
1:A:1688:LYS:HD3	1:A:1758:ALA:HA	1.99	0.45
1:B:1790:LEU:HD23	1:B:1837:CYS:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:44:ILE:CD1	2:D:49:GLN:HG2	2.46	0.45
1:A:1908:LYS:HG2	1:A:1909:ASN:N	2.33	0.44
1:A:1696[A]:CYS:HG	1:A:1764:PHE:HE1	1.63	0.43
1:B:1851:PRO:CG	1:B:1902[A]:THR:HG22	2.49	0.43
1:B:1814:THR:O	1:B:1847:CYS:HB3	2.18	0.42
1:B:1794:CYS:SG	1:B:1796:CYS:HB2	2.60	0.42
1:A:1894:VAL:HG12	1:B:1893:LYS:HD3	2.02	0.42
2:C:22:THR:OG1	2:C:24:GLU:CG	2.68	0.42
1:B:1851:PRO:HG3	1:B:1902[A]:THR:HG21	2.01	0.41
1:B:1812:PHE:O	2:D:47:GLY:HA2	2.19	0.41
1:A:1882:LYS:HB3	1:A:1883:TYR:CE2	2.55	0.41
1:A:1882:LYS:HA	1:A:1883:TYR:HA	1.77	0.41
1:A:1812:PHE:O	2:C:47:GLY:HA2	2.20	0.41
1:B:1610:LYS:HE3	1:B:1610:LYS:HB3	1.92	0.41
1:A:1722:CYS:O	1:A:1726:GLN:HG3	2.21	0.40
2:C:24:GLU:HG3	2:C:25:ASN:N	2.37	0.40

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)
6:A:2125:HOH:O	6:B:2349:HOH:O[2_565]	1.91	0.29
6:B:2296:HOH:O	6:C:236:HOH:O[4_546]	1.94	0.26
1:A:1623:ARG:NH2	4:B:2004:FMT:O1[2_565]	2.14	0.06
6:A:2279:HOH:O	6:C:225:HOH:O[1_545]	2.18	0.02

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	306/303 (101%)	298 (97%)	8 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	311/303 (103%)	302 (97%)	9 (3%)	0	100	100
2	C	74/76 (97%)	74 (100%)	0	0	100	100
2	D	74/76 (97%)	74 (100%)	0	0	100	100
All	All	765/758 (101%)	748 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	268/263 (102%)	265 (99%)	3 (1%)	73	65
1	B	273/263 (104%)	272 (100%)	1 (0%)	91	89
2	C	68/68 (100%)	67 (98%)	1 (2%)	65	53
2	D	68/68 (100%)	68 (100%)	0	100	100
All	All	677/662 (102%)	672 (99%)	5 (1%)	81	79

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

Mol	Chain	Res	Type
1	A	1609	ASN
1	A	1693	LEU
1	A	1703	CYS
1	B	1640	VAL
2	C	67	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1909	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	$\# Z > 2$
3	GOL	A	2003	-	5,5,5	0.34	0	5,5,5	0.33	0
4	FMT	A	2004	-	0,2,2	0.00	-	0,1,1	0.00	-
3	GOL	B	2003	-	5,5,5	0.35	0	5,5,5	0.33	0
3	GOL	A	2001	-	5,5,5	0.40	0	5,5,5	0.30	0
3	GOL	D	102	-	5,5,5	0.31	0	5,5,5	0.53	0
3	GOL	A	2002	-	5,5,5	0.36	0	5,5,5	0.46	0
3	GOL	B	2002	-	5,5,5	0.36	0	5,5,5	0.34	0
3	GOL	D	101	-	5,5,5	0.22	0	5,5,5	0.54	0
3	GOL	C	101	-	5,5,5	0.35	0	5,5,5	0.58	0
3	GOL	C	102	-	5,5,5	0.33	0	5,5,5	0.34	0
3	GOL	B	2001	-	5,5,5	0.39	0	5,5,5	0.18	0
4	FMT	B	2004	-	0,2,2	0.00	-	0,1,1	0.00	-

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	2003	-	-	2/4/4/4	-
3	GOL	A	2001	-	-	1/4/4/4	-
3	GOL	D	102	-	-	1/4/4/4	-
3	GOL	A	2002	-	-	2/4/4/4	-
3	GOL	B	2002	-	-	2/4/4/4	-
3	GOL	D	101	-	-	0/4/4/4	-
3	GOL	C	101	-	-	2/4/4/4	-
3	GOL	C	102	-	-	0/4/4/4	-
3	GOL	B	2001	-	-	2/4/4/4	-
3	GOL	A	2003	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	2003	GOL	O1-C1-C2-O2
3	B	2003	GOL	O1-C1-C2-C3
3	A	2002	GOL	O1-C1-C2-O2
3	A	2002	GOL	O1-C1-C2-C3
3	C	101	GOL	O1-C1-C2-C3
3	B	2001	GOL	O1-C1-C2-C3
3	C	101	GOL	O1-C1-C2-O2
3	B	2002	GOL	O1-C1-C2-C3
3	B	2001	GOL	O1-C1-C2-O2
3	B	2002	GOL	O1-C1-C2-O2
3	D	102	GOL	O1-C1-C2-C3
3	A	2001	GOL	O2-C2-C3-O3
3	A	2003	GOL	O1-C1-C2-C3
3	A	2003	GOL	C1-C2-C3-O3
3	A	2003	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2001	GOL	1	0
4	B	2004	FMT	0	1

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, 95th 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	301/303 (99%)	-0.29	4 (1%) 77 78	19, 35, 56, 81	4 (1%)
1	B	303/303 (100%)	-0.45	4 (1%) 77 78	18, 29, 53, 85	1 (0%)
2	C	76/76 (100%)	-0.16	0 100 100	26, 42, 62, 67	0
2	D	76/76 (100%)	-0.78	0 100 100	17, 26, 40, 46	0
All	All	756/758 (99%)	-0.39	8 (1%) 80 81	17, 32, 56, 85	5 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1908	LYS	3.3
1	A	1609	ASN	3.1
1	B	1609	ASN	2.9
1	A	1909	ASN	2.5
1	A	1654	ALA	2.4
1	A	1635	LYS	2.3
1	B	1911	LYS	2.3
1	B	1909	ASN	2.2

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 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, 95th 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(\AA^2)	Q<0.9
3	GOL	A	2001	6/6	0.77	0.14	40,51,52,55	0
4	FMT	A	2004	3/3	0.79	0.14	52,62,64,74	0
4	FMT	B	2004	3/3	0.79	0.15	64,64,77,77	0
3	GOL	A	2002	6/6	0.80	0.18	59,67,72,79	0
3	GOL	A	2003	6/6	0.84	0.22	47,58,70,70	0
3	GOL	B	2003	6/6	0.85	0.22	52,63,65,67	0
3	GOL	B	2002	6/6	0.90	0.11	36,50,57,58	0
3	GOL	C	102	6/6	0.91	0.10	40,59,76,77	0
3	GOL	B	2001	6/6	0.91	0.11	38,58,63,68	0
3	GOL	C	101	6/6	0.91	0.11	25,44,50,52	0
3	GOL	D	102	6/6	0.95	0.12	19,34,47,49	0
3	GOL	D	101	6/6	0.96	0.09	23,31,35,48	0
5	ZN	A	2005	1/1	0.97	0.06	27,27,27,27	1
5	ZN	B	2005	1/1	1.00	0.06	28,28,28,28	1

6.5 Other polymers [i](#)

There are no such residues in this entry.