



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 17, 2024 – 11:37 AM EST

PDB ID : 3SLA  
Title : X-ray structure of first four repeats of human beta-catenin  
Authors : Gupta, D.; Bienz, M.  
Deposited on : 2011-06-24  
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)

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<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (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 : 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

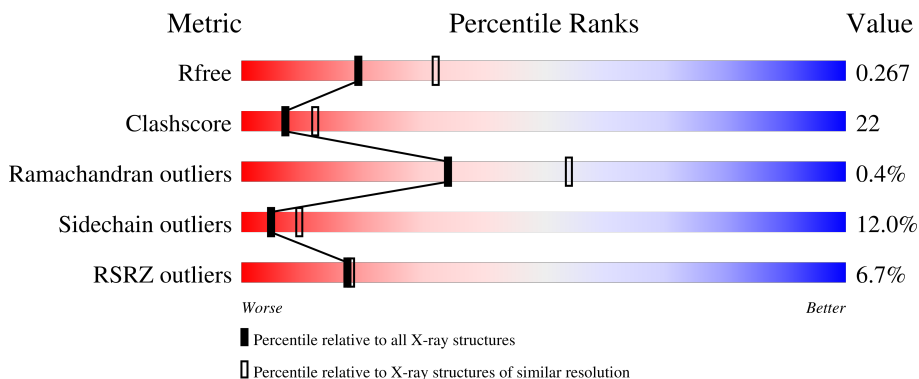
# 1 Overall quality at a glance

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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	168	
1	B	168	
1	C	168	
1	D	168	
1	E	168	

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	GOL	A	7	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6074 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 Catenin beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	166	1256	790	226	231	9	0	0	0
1	B	156	1166	734	213	210	9	0	0	0
1	C	153	1061	667	193	194	7	0	0	0
1	D	164	1236	778	221	228	9	0	0	0
1	E	162	1219	768	222	220	9	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	139	GLY	-	expression tag	UNP P35222
A	140	SER	-	expression tag	UNP P35222
B	139	GLY	-	expression tag	UNP P35222
B	140	SER	-	expression tag	UNP P35222
C	139	GLY	-	expression tag	UNP P35222
C	140	SER	-	expression tag	UNP P35222
D	139	GLY	-	expression tag	UNP P35222
D	140	SER	-	expression tag	UNP P35222
E	139	GLY	-	expression tag	UNP P35222
E	140	SER	-	expression tag	UNP P35222

- Molecule 2 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
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	D	1	Total C O 6 3 3	0	0
2	D	1	Total C O 6 3 3	0	0
2	E	1	Total C O 6 3 3	0	0
2	E	1	Total C O 6 3 3	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	2	Total Na 2 2	0	0

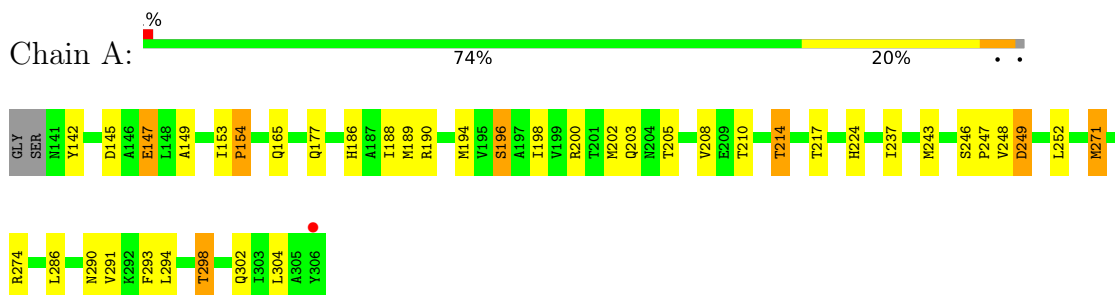
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	18	Total O 18 18	0	0
4	B	17	Total O 17 17	0	0
4	C	2	Total O 2 2	0	0
4	D	21	Total O 21 21	0	0
4	E	28	Total O 28 28	0	0

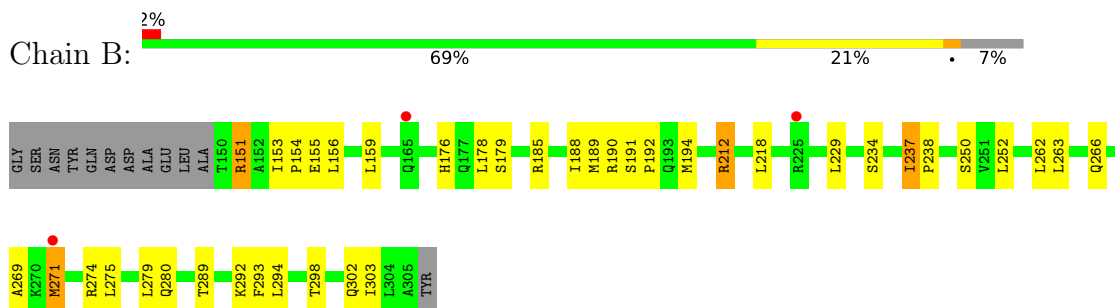
### 3 Residue-property plots [i](#)

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.

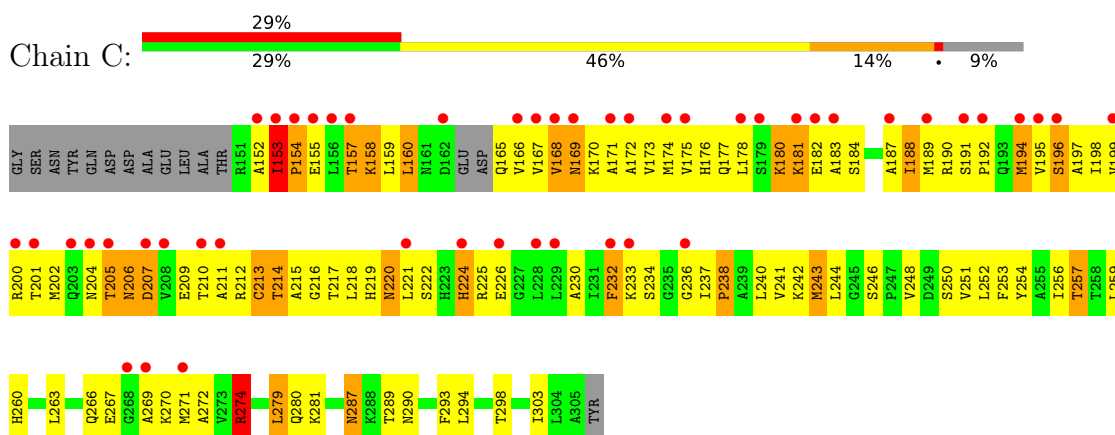
- Molecule 1: Catenin beta-1



- Molecule 1: Catenin beta-1

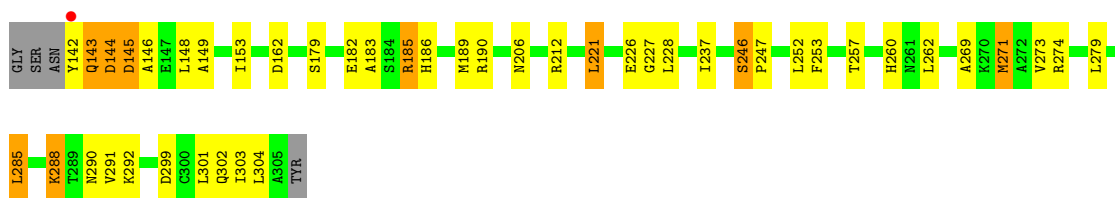


- Molecule 1: Catenin beta-1

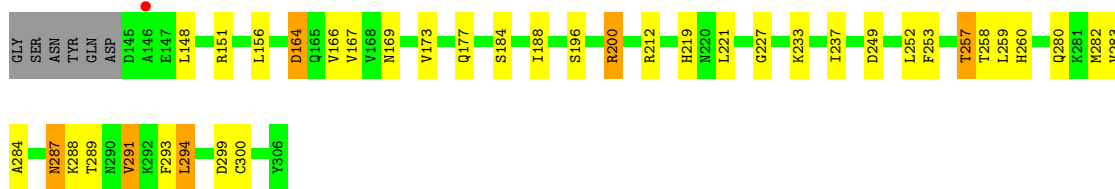
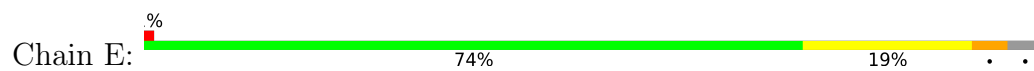


- Molecule 1: Catenin beta-1





- Molecule 1: Catenin beta-1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.79Å 90.79Å 364.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.71 – 2.50 40.71 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (40.71-2.50) 99.0 (40.71-2.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.218 , 0.277 0.212 , 0.267	Depositor DCC
$R_{free}$ test set	2719 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.4	Xtrriage
Anisotropy	0.001	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6074	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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, NA

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	0.95	1/1271 (0.1%)	0.95	1/1720 (0.1%)
1	B	0.85	0/1180	0.89	1/1600 (0.1%)
1	C	1.02	2/1072 (0.2%)	0.89	2/1456 (0.1%)
1	D	0.89	0/1251	0.91	2/1695 (0.1%)
1	E	0.94	1/1233 (0.1%)	0.94	1/1668 (0.1%)
All	All	0.93	4/6007 (0.1%)	0.92	7/8139 (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	C	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	154	PRO	N-CD	10.55	1.62	1.47
1	C	207	ASP	CA-CB	6.42	1.68	1.53
1	E	291	VAL	CB-CG1	-5.88	1.40	1.52
1	A	147	GLU	CG-CD	5.03	1.59	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	212	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	E	164	ASP	CB-CG-OD2	5.62	123.36	118.30
1	D	185	ARG	NE-CZ-NH2	-5.45	117.57	120.30
1	D	221	LEU	CB-CG-CD1	-5.33	101.94	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	ASP	CB-CG-OD2	-5.23	113.59	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	159	LEU	Peptide

## 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	1256	0	1305	34	0
1	B	1166	0	1214	29	0
1	C	1061	0	1029	156	0
1	D	1236	0	1281	37	0
1	E	1219	0	1282	23	0
2	A	24	0	32	7	0
2	D	12	0	16	2	0
2	E	12	0	16	1	0
3	E	2	0	0	0	0
4	A	18	0	0	1	0
4	B	17	0	0	1	0
4	C	2	0	0	0	0
4	D	21	0	0	3	0
4	E	28	0	0	2	0
All	All	6074	0	6175	273	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 22.

The worst 5 of 273 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:C:154:PRO:HB2	1:C:157:THR:OG1	1.41	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:197:ALA:O	1:C:201:THR:HG23	1.44	1.18
1:C:160:LEU:CB	1:C:168:VAL:HA	1.73	1.16
1:C:152:ALA:C	1:C:154:PRO:HD3	1.73	1.10
1:C:219:HIS:O	1:C:222:SER:HB3	1.55	1.05

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	164/168 (98%)	161 (98%)	3 (2%)	0	100	100
1	B	154/168 (92%)	150 (97%)	4 (3%)	0	100	100
1	C	149/168 (89%)	126 (85%)	20 (13%)	3 (2%)	7	12
1	D	162/168 (96%)	161 (99%)	1 (1%)	0	100	100
1	E	160/168 (95%)	158 (99%)	2 (1%)	0	100	100
All	All	789/840 (94%)	756 (96%)	30 (4%)	3 (0%)	34	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	153	ILE
1	C	160	LEU
1	C	225	ARG

### 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	136/140 (97%)	126 (93%)	10 (7%)	13	27
1	B	126/140 (90%)	115 (91%)	11 (9%)	10	20
1	C	99/140 (71%)	70 (71%)	29 (29%)	0	0
1	D	134/140 (96%)	121 (90%)	13 (10%)	8	16
1	E	132/140 (94%)	120 (91%)	12 (9%)	9	18
All	All	627/700 (90%)	552 (88%)	75 (12%)	5	9

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	271	MET
1	E	257	THR
1	D	288	LYS
1	E	166	VAL
1	C	168	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	287	ASN
1	E	280	GLN
1	E	302	GLN
1	E	287	ASN
1	E	260	HIS

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
2	GOL	A	1	-	5,5,5	0.54	0	5,5,5	0.54	0
2	GOL	D	5	-	5,5,5	0.32	0	5,5,5	0.61	0
2	GOL	A	7	-	5,5,5	0.48	0	5,5,5	1.14	1 (20%)
2	GOL	E	8	-	5,5,5	0.66	0	5,5,5	0.76	0
2	GOL	D	3	-	5,5,5	0.37	0	5,5,5	0.37	0
2	GOL	A	4	-	5,5,5	0.54	0	5,5,5	0.68	0
2	GOL	A	2	-	5,5,5	0.50	0	5,5,5	0.81	0
2	GOL	E	6	-	5,5,5	0.36	0	5,5,5	0.43	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	1	-	-	2/4/4/4	-
2	GOL	D	5	-	-	4/4/4/4	-
2	GOL	A	7	-	-	2/4/4/4	-
2	GOL	E	8	-	-	2/4/4/4	-
2	GOL	D	3	-	-	2/4/4/4	-
2	GOL	A	4	-	-	3/4/4/4	-
2	GOL	A	2	-	-	2/4/4/4	-
2	GOL	E	6	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	7	GOL	O3-C3-C2	2.09	120.20	110.20

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	4	GOL	O1-C1-C2-C3
2	A	7	GOL	C1-C2-C3-O3
2	D	5	GOL	O1-C1-C2-C3
2	E	6	GOL	C1-C2-C3-O3
2	E	6	GOL	O2-C2-C3-O3

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	5	GOL	1	0
2	A	7	GOL	3	0
2	E	8	GOL	1	0
2	D	3	GOL	1	0
2	A	4	GOL	1	0
2	A	2	GOL	3	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	166/168 (98%)	-0.07	1 (0%) 89 90	33, 48, 77, 122	0
1	B	156/168 (92%)	0.09	3 (1%) 66 69	39, 57, 83, 95	0
1	C	153/168 (91%)	1.39	48 (31%) 0 0	40, 95, 127, 137	0
1	D	164/168 (97%)	-0.02	1 (0%) 89 90	34, 50, 85, 121	0
1	E	162/168 (96%)	0.01	1 (0%) 89 90	32, 44, 74, 107	0
All	All	801/840 (95%)	0.27	54 (6%) 17 18	32, 54, 111, 137	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	192	PRO	7.3
1	C	152	ALA	5.5
1	C	168	VAL	5.0
1	C	157	THR	4.9
1	C	233	LYS	4.8

### 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	GOL	A	2	6/6	0.73	0.19	74,87,90,90	0
2	GOL	A	7	6/6	0.73	0.43	69,77,80,98	0
2	GOL	D	3	6/6	0.75	0.18	93,103,107,108	0
2	GOL	A	1	6/6	0.80	0.19	72,74,76,81	0
2	GOL	D	5	6/6	0.80	0.34	77,83,88,89	0
2	GOL	A	4	6/6	0.84	0.24	67,72,77,79	0
2	GOL	E	8	6/6	0.85	0.44	62,69,72,73	0
2	GOL	E	6	6/6	0.90	0.20	85,92,98,103	0
3	NA	E	1	1/1	0.94	0.14	54,54,54,54	0
3	NA	E	2	1/1	0.94	0.16	68,68,68,68	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.