



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 26, 2026 – 07:38 AM UTC

PDB ID : 1MPX / pdb\_00001mpx  
Title : ALPHA-AMINO ACID ESTER HYDROLASE LABELED WITH SELENOMETHIONINE  
Authors : Barends, T.R.M.; Polderman-Tijmes, J.J.; Jekel, P.A.; Hensgens, C.M.H.; de Vries, E.J.; Janssen, D.B.; Dijkstra, B.W.  
Deposited on : 2002-09-13  
Resolution : 1.90 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

<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 : 4-5-2 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

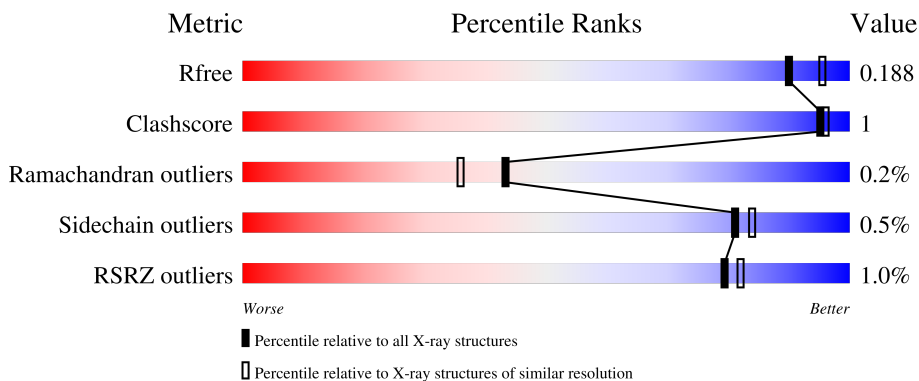
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	615	 96%
1	B	615	 96%
1	C	615	 95% 5%
1	D	615	 95%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 21702 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 alpha-amino acid ester hydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	614	4848	3099	832	897	2	18	0	0	0
1	B	614	4848	3099	832	897	2	18	0	0	0
1	C	614	4848	3099	832	897	2	18	0	0	0
1	D	614	4848	3099	832	897	2	18	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MSE	MET	modified residue	UNP Q8PK36
A	51	MSE	MET	modified residue	UNP Q8PK36
A	54	MSE	MET	modified residue	UNP Q8PK36
A	96	MSE	MET	modified residue	UNP Q8PK36
A	131	MSE	MET	modified residue	UNP Q8PK36
A	170	MSE	MET	modified residue	UNP Q8PK36
A	182	MSE	MET	modified residue	UNP Q8PK36
A	200	MSE	MET	modified residue	UNP Q8PK36
A	205	MSE	MET	modified residue	UNP Q8PK36
A	290	MSE	MET	modified residue	UNP Q8PK36
A	300	MSE	MET	modified residue	UNP Q8PK36
A	311	MSE	MET	modified residue	UNP Q8PK36
A	321	MSE	MET	modified residue	UNP Q8PK36
A	335	MSE	MET	modified residue	UNP Q8PK36
A	464	MSE	MET	modified residue	UNP Q8PK36
A	527	MSE	MET	modified residue	UNP Q8PK36
A	533	MSE	MET	modified residue	UNP Q8PK36
A	585	MSE	MET	modified residue	UNP Q8PK36
B	27	MSE	MET	modified residue	UNP Q8PK36
B	51	MSE	MET	modified residue	UNP Q8PK36
B	54	MSE	MET	modified residue	UNP Q8PK36

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Chain	Residue	Modelled	Actual	Comment	Reference
B	96	MSE	MET	modified residue	UNP Q8PK36
B	131	MSE	MET	modified residue	UNP Q8PK36
B	170	MSE	MET	modified residue	UNP Q8PK36
B	182	MSE	MET	modified residue	UNP Q8PK36
B	200	MSE	MET	modified residue	UNP Q8PK36
B	205	MSE	MET	modified residue	UNP Q8PK36
B	290	MSE	MET	modified residue	UNP Q8PK36
B	300	MSE	MET	modified residue	UNP Q8PK36
B	311	MSE	MET	modified residue	UNP Q8PK36
B	321	MSE	MET	modified residue	UNP Q8PK36
B	335	MSE	MET	modified residue	UNP Q8PK36
B	464	MSE	MET	modified residue	UNP Q8PK36
B	527	MSE	MET	modified residue	UNP Q8PK36
B	533	MSE	MET	modified residue	UNP Q8PK36
B	585	MSE	MET	modified residue	UNP Q8PK36
C	27	MSE	MET	modified residue	UNP Q8PK36
C	51	MSE	MET	modified residue	UNP Q8PK36
C	54	MSE	MET	modified residue	UNP Q8PK36
C	96	MSE	MET	modified residue	UNP Q8PK36
C	131	MSE	MET	modified residue	UNP Q8PK36
C	170	MSE	MET	modified residue	UNP Q8PK36
C	182	MSE	MET	modified residue	UNP Q8PK36
C	200	MSE	MET	modified residue	UNP Q8PK36
C	205	MSE	MET	modified residue	UNP Q8PK36
C	290	MSE	MET	modified residue	UNP Q8PK36
C	300	MSE	MET	modified residue	UNP Q8PK36
C	311	MSE	MET	modified residue	UNP Q8PK36
C	321	MSE	MET	modified residue	UNP Q8PK36
C	335	MSE	MET	modified residue	UNP Q8PK36
C	464	MSE	MET	modified residue	UNP Q8PK36
C	527	MSE	MET	modified residue	UNP Q8PK36
C	533	MSE	MET	modified residue	UNP Q8PK36
C	585	MSE	MET	modified residue	UNP Q8PK36
D	27	MSE	MET	modified residue	UNP Q8PK36
D	51	MSE	MET	modified residue	UNP Q8PK36
D	54	MSE	MET	modified residue	UNP Q8PK36
D	96	MSE	MET	modified residue	UNP Q8PK36
D	131	MSE	MET	modified residue	UNP Q8PK36
D	170	MSE	MET	modified residue	UNP Q8PK36
D	182	MSE	MET	modified residue	UNP Q8PK36
D	200	MSE	MET	modified residue	UNP Q8PK36
D	205	MSE	MET	modified residue	UNP Q8PK36

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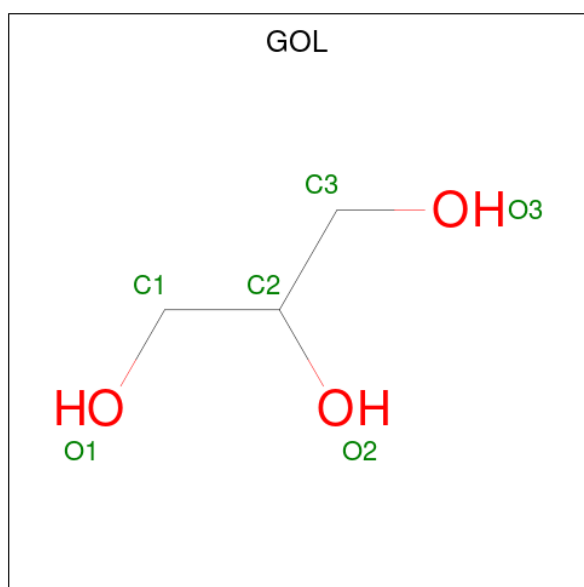
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Chain	Residue	Modelled	Actual	Comment	Reference
D	290	MSE	MET	modified residue	UNP Q8PK36
D	300	MSE	MET	modified residue	UNP Q8PK36
D	311	MSE	MET	modified residue	UNP Q8PK36
D	321	MSE	MET	modified residue	UNP Q8PK36
D	335	MSE	MET	modified residue	UNP Q8PK36
D	464	MSE	MET	modified residue	UNP Q8PK36
D	527	MSE	MET	modified residue	UNP Q8PK36
D	533	MSE	MET	modified residue	UNP Q8PK36
D	585	MSE	MET	modified residue	UNP Q8PK36

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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 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	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 6	C 3	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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	616	Total 616	O 616	0	0
4	B	628	Total 628	O 628	0	0
4	C	508	Total 508	O 508	0	0
4	D	494	Total 494	O 494	0	0

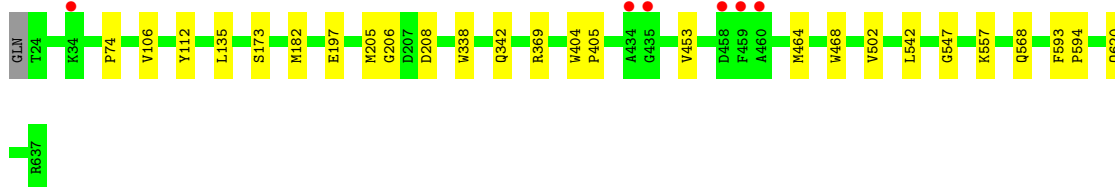
### 3 Residue-property plots [i](#)

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.

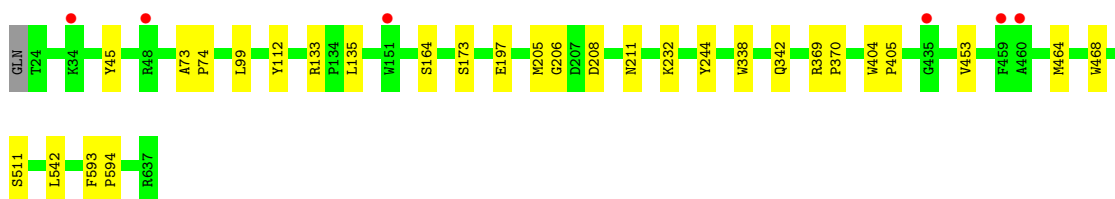
- Molecule 1: alpha-amino acid ester hydrolase



- Molecule 1: alpha-amino acid ester hydrolase



- Molecule 1: alpha-amino acid ester hydrolase



- Molecule 1: alpha-amino acid ester hydrolase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.77Å 126.02Å 132.29Å 90.00° 91.06° 90.00°	Depositor
Resolution (Å)	40.00 – 1.90 40.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	95.5 (40.00-1.90) 95.5 (40.00-1.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.149 , 0.178 0.160 , 0.188	Depositor DCC
$R_{free}$ test set	11129 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 37.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.013 for -h,l,k 0.018 for -h,-l,-k 0.136 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21702	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% 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, CA

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	0.86	2/4983 (0.0%)	0.81	3/6765 (0.0%)
1	B	0.87	2/4983 (0.0%)	0.81	2/6765 (0.0%)
1	C	0.82	1/4983 (0.0%)	0.80	2/6765 (0.0%)
1	D	0.83	0/4983	0.80	2/6765 (0.0%)
All	All	0.84	5/19932 (0.0%)	0.80	9/27060 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	205	MSE	SE-CE	-13.23	1.55	1.95
1	A	205	MSE	SE-CE	-8.88	1.68	1.95
1	A	533	MSE	SE-CE	-5.73	1.78	1.95
1	B	464	MSE	SE-CE	-5.45	1.79	1.95
1	C	205	MSE	SE-CE	-5.30	1.79	1.95

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ASP	N-CA-C	8.04	121.20	111.40
1	B	208	ASP	N-CA-C	7.80	121.30	111.24
1	C	208	ASP	N-CA-C	7.51	120.56	111.40
1	D	208	ASP	N-CA-C	7.35	120.37	111.40
1	D	244	TYR	N-CA-C	-5.47	105.22	111.07

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	4848	0	4663	11	0
1	B	4848	0	4663	12	0
1	C	4848	0	4663	13	0
1	D	4848	0	4663	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	18	0	24	0	0
3	B	18	0	24	0	0
3	C	12	0	16	0	0
3	D	12	0	16	0	0
4	A	616	0	0	0	0
4	B	628	0	0	0	0
4	C	508	0	0	0	0
4	D	494	0	0	0	0
All	All	21702	0	18732	47	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 1.

The worst 5 of 47 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:106:VAL:HB	1:B:369:ARG:HG2	1.78	0.63
1:A:593:PHE:CG	1:A:594:PRO:HA	2.50	0.47
1:C:593:PHE:CG	1:C:594:PRO:HA	2.49	0.47
1:A:338:TRP:HB3	1:A:342:GLN:HB3	1.96	0.46
1:A:40:ASP:HB2	1:A:43:ASN:ND2	2.30	0.46

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	612/615 (100%)	586 (96%)	25 (4%)	1 (0%)	43	36
1	B	612/615 (100%)	585 (96%)	26 (4%)	1 (0%)	43	36
1	C	612/615 (100%)	585 (96%)	26 (4%)	1 (0%)	43	36
1	D	612/615 (100%)	586 (96%)	25 (4%)	1 (0%)	43	36
All	All	2448/2460 (100%)	2342 (96%)	102 (4%)	4 (0%)	43	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	GLY
1	D	206	GLY
1	B	206	GLY
1	C	206	GLY

### 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	514/497 (103%)	512 (100%)	2 (0%)	84	87
1	B	514/497 (103%)	512 (100%)	2 (0%)	84	87
1	C	514/497 (103%)	510 (99%)	4 (1%)	73	75
1	D	514/497 (103%)	511 (99%)	3 (1%)	78	81
All	All	2056/1988 (103%)	2045 (100%)	11 (0%)	81	84

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	511	SER
1	D	48	ARG
1	D	372	PHE
1	D	211	ASN
1	C	135	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	219	ASN
1	C	495	GLN
1	C	436	GLN
1	C	563	GLN
1	B	217	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	D	3007	-	5,5,5	0.35	0	5,5,5	0.30	0
3	GOL	D	3010	-	5,5,5	0.43	0	5,5,5	0.28	0
3	GOL	A	3006	-	5,5,5	0.39	0	5,5,5	0.28	0
3	GOL	A	3002	-	5,5,5	0.49	0	5,5,5	0.32	0
3	GOL	A	3011	-	5,5,5	0.37	0	5,5,5	0.25	0
3	GOL	C	3001	-	5,5,5	0.42	0	5,5,5	0.23	0
3	GOL	B	3005	-	5,5,5	0.44	0	5,5,5	0.33	0
3	GOL	C	3008	-	5,5,5	0.41	0	5,5,5	0.26	0
3	GOL	B	3004	-	5,5,5	0.29	0	5,5,5	0.34	0
3	GOL	B	3009	-	5,5,5	0.40	0	5,5,5	0.26	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
3	GOL	D	3007	-	-	0/4/4/4	-
3	GOL	D	3010	-	-	2/4/4/4	-
3	GOL	A	3006	-	-	0/4/4/4	-
3	GOL	A	3002	-	-	0/4/4/4	-
3	GOL	A	3011	-	-	0/4/4/4	-
3	GOL	C	3001	-	-	0/4/4/4	-
3	GOL	B	3005	-	-	0/4/4/4	-
3	GOL	C	3008	-	-	0/4/4/4	-
3	GOL	B	3004	-	-	0/4/4/4	-
3	GOL	B	3009	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	3010	GOL	C1-C2-C3-O3
3	D	3010	GOL	O2-C2-C3-O3

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 [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	596/615 (96%)	-0.31	6 (1%) 79 82	11, 17, 32, 50	0
1	B	596/615 (96%)	-0.33	6 (1%) 79 82	11, 17, 32, 52	0
1	C	596/615 (96%)	-0.05	6 (1%) 79 82	13, 22, 37, 55	0
1	D	596/615 (96%)	-0.00	5 (0%) 82 85	13, 22, 37, 51	0
All	All	2384/2460 (96%)	-0.17	23 (0%) 79 82	11, 20, 35, 55	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	460	ALA	4.4
1	B	459	PHE	4.1
1	A	459	PHE	4.0
1	A	460	ALA	3.4
1	B	435	GLY	3.1

### 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 oligosaccharides 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( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	3011	6/6	0.87	0.14	26,41,44,47	0
3	GOL	C	3001	6/6	0.87	0.13	29,33,34,36	0
3	GOL	D	3010	6/6	0.92	0.13	24,32,38,39	0
3	GOL	A	3006	6/6	0.94	0.13	18,26,30,31	0
3	GOL	B	3009	6/6	0.95	0.08	16,26,29,30	0
3	GOL	C	3008	6/6	0.96	0.09	17,31,33,36	0
3	GOL	D	3007	6/6	0.97	0.06	15,18,24,25	0
3	GOL	B	3005	6/6	0.97	0.06	18,19,25,28	0
2	CA	C	638	1/1	0.98	0.04	19,19,19,19	0
3	GOL	A	3002	6/6	0.98	0.05	16,17,21,28	0
3	GOL	B	3004	6/6	0.98	0.04	17,18,23,25	0
2	CA	A	638	1/1	0.99	0.02	15,15,15,15	0
2	CA	D	638	1/1	0.99	0.04	21,21,21,21	0
2	CA	B	638	1/1	1.00	0.02	14,14,14,14	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.