



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 05:54 PM EDT

PDB ID : 4HKM / pdb\_00004hkm  
Title : Crystal Structure of an Anthranilate Phosphoribosyltransferase (target ID NYSGRC-016600) from Xanthomonas campestris  
Authors : Ghosh, A.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRC)  
Deposited on : 2012-10-15  
Resolution : 1.95 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](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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

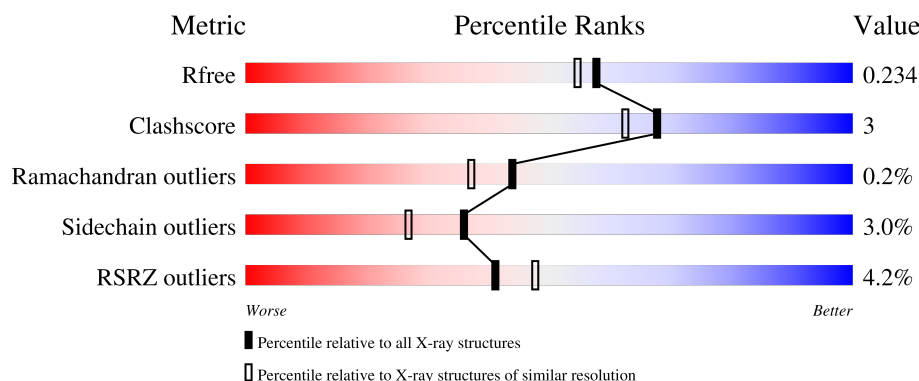
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


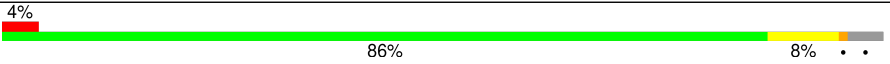
The reported resolution of this entry is 1.95 Å.

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))
$R_{free}$	164625	3187 (1.96-1.96)
Clashscore	180529	3412 (1.96-1.96)
Ramachandran outliers	177936	3390 (1.96-1.96)
Sidechain outliers	177891	3390 (1.96-1.96)
RSRZ outliers	164620	3186 (1.96-1.96)

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	346	
1	B	346	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5155 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.

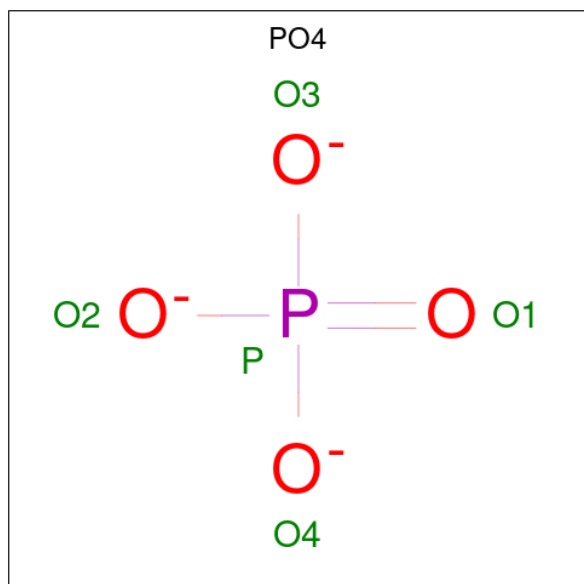
- Molecule 1 is a protein called Anthranilate phosphoribosyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	Se	0	2	0
			2374	1488	425	444	2	15			
1	B	331	Total	C	N	O	S	Se	0	2	0
			2477	1547	449	464	2	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q8PD71
B	0	SER	-	expression tag	UNP Q8PD71

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



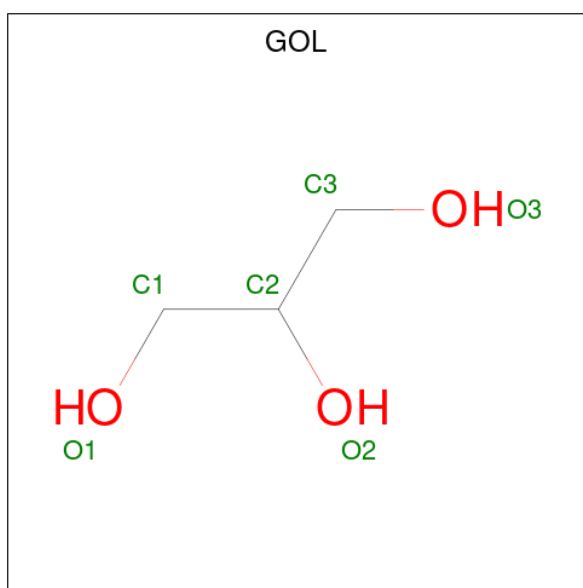
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		

*Continued on next page...*

Continued from previous page...

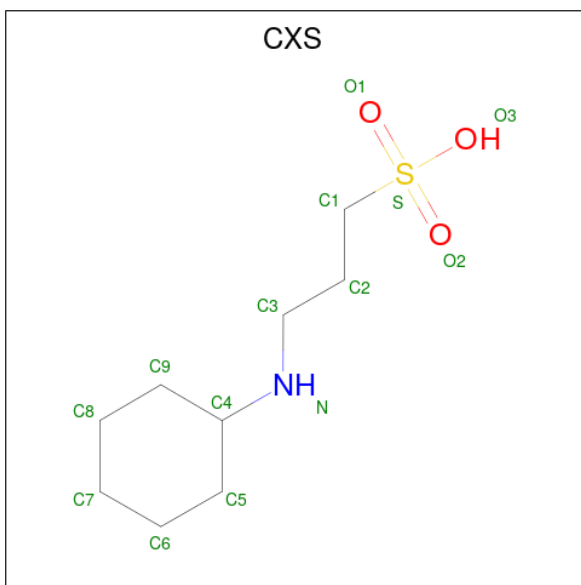
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

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



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

- Molecule 4 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (CCD ID: CXS) (formula:  $C_9H_{19}NO_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			14	9	1	3	1		

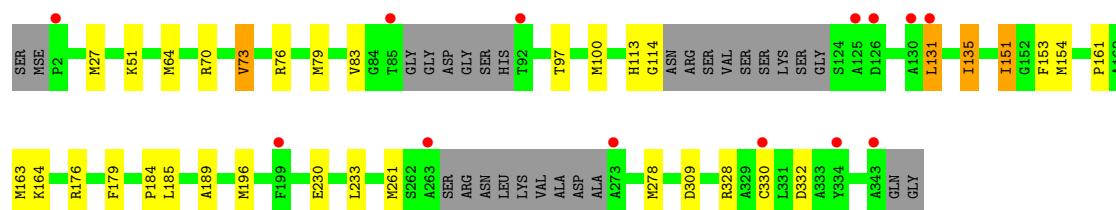
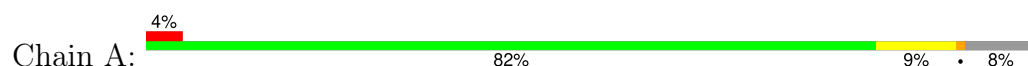
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	116	Total	O	0	1
			117	117		
5	B	130	Total	O	0	1
			131	131		

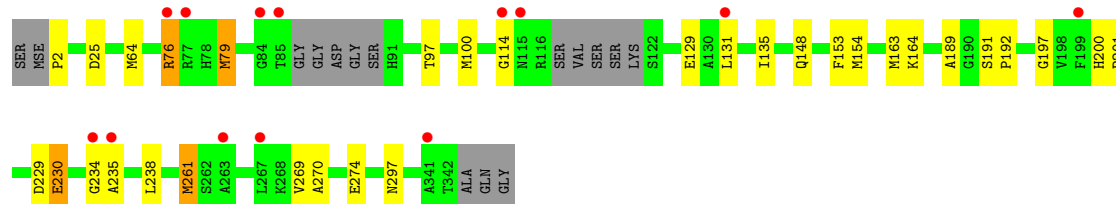
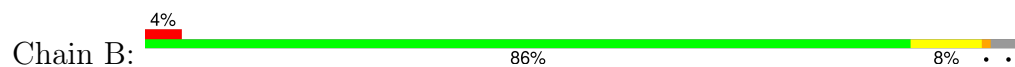
### 3 Residue-property plots [i](#)

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: Anthranilate phosphoribosyltransferase



- Molecule 1: Anthranilate phosphoribosyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.25Å 161.13Å 56.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.41 – 1.95 43.41 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.6 (43.41-1.95) 98.6 (43.41-1.95)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, $R_{free}$	0.187 , 0.227 0.196 , 0.234	Depositor DCC
$R_{free}$ test set	2538 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.7	Xtriage
Anisotropy	0.697	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5155	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.05% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, GOL, CXS

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	0.57	3/2399 (0.1%)	0.77	1/3225 (0.0%)
1	B	0.54	2/2504 (0.1%)	0.77	0/3367
All	All	0.55	5/4903 (0.1%)	0.77	1/6592 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	79	MSE	SE-CE	-5.93	1.77	1.95
1	B	261	MSE	SE-CE	-5.35	1.79	1.95
1	A	79	MSE	SE-CE	-5.25	1.79	1.95
1	A	261	MSE	SE-CE	-5.25	1.79	1.95
1	A	278	MSE	SE-CE	-5.12	1.80	1.95

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	LEU	N-CA-C	-5.27	106.62	114.64

There are no chirality outliers.

There are no planarity outliers.

### 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	2374	0	2401	17	0
1	B	2477	0	2501	17	0
2	A	10	0	0	0	0
2	B	20	0	0	0	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
4	B	14	0	19	0	0
5	A	117	0	0	2	0
5	B	131	0	0	0	0
All	All	5155	0	4937	34	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 3.

All (34) 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:154:MSE:HE1	1:A:189:ALA:HB2	1.54	0.87
1:A:100:MSE:HE2	1:A:151:ILE:HG23	1.63	0.81
1:A:64:MSE:HE1	1:A:163:MSE:SE	2.47	0.65
1:A:70:ARG:NH1	5:A:542:HOH:O	2.39	0.56
1:B:114:GLY:HA3	1:B:153:PHE:CZ	2.40	0.56
1:B:64:MSE:HE1	1:B:163:MSE:SE	2.56	0.56
1:B:270:ALA:H	1:B:274:GLU:CD	2.14	0.54
1:A:97:THR:O	1:A:100:MSE:HG2	2.08	0.54
1:B:154:MSE:HE1	1:B:189:ALA:HB2	1.91	0.52
1:B:235:ALA:HA	1:B:261:MSE:SE	2.59	0.52
1:A:176:ARG:HB3	3:A:403:GOL:H11	1.93	0.50
1:A:27[B]:MSE:HE1	1:A:179:PHE:CZ	2.46	0.50
1:A:328:ARG:NH1	1:A:332:ASP:OD1	2.45	0.50
1:B:76:ARG:HD2	1:B:79:MSE:HE1	1.93	0.50
1:B:129:GLU:HB3	1:B:135:ILE:HG12	1.95	0.49
1:A:83:VAL:HG21	1:A:184:PRO:HA	1.95	0.48
1:A:73:VAL:HG22	1:A:76:ARG:HG2	1.94	0.48
1:A:161:PRO:O	1:A:164:LYS:NZ	2.38	0.48
1:B:97:THR:HA	1:B:100:MSE:HE2	1.95	0.48
1:A:114:GLY:HA3	1:A:153:PHE:CZ	2.49	0.47
1:B:269:VAL:HB	1:B:274:GLU:HG3	1.96	0.47
1:A:163:MSE:HE3	5:A:503:HOH:O	2.16	0.46
1:B:197:GLY:HA3	1:B:229:ASP:O	2.16	0.46
1:B:2:PRO:HB2	1:B:25[A]:ASP:CG	2.42	0.45
1:B:230:GLU:HB2	1:B:297:ASN:OD1	2.18	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:GLY:HA2	1:B:261:MSE:SE	2.68	0.43
1:A:135:ILE:HD12	1:A:135:ILE:HA	1.87	0.43
1:B:200:HIS:CG	1:B:201:PRO:HD2	2.54	0.42
1:A:27[A]:MSE:HE3	1:A:27[A]:MSE:HB3	1.94	0.42
1:B:76:ARG:HA	1:B:79:MSE:HE2	2.01	0.42
1:A:185:LEU:HD23	1:A:196:MSE:HE1	2.02	0.42
1:B:234:GLY:HA2	1:B:235:ALA:HA	1.54	0.41
1:A:64:MSE:CE	1:A:163:MSE:SE	3.18	0.41
1:B:191:SER:HA	1:B:192:PRO:HD3	1.91	0.41

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	312/346 (90%)	306 (98%)	5 (2%)	1 (0%)	37	29
1	B	327/346 (94%)	321 (98%)	6 (2%)	0	100	100
All	All	639/692 (92%)	627 (98%)	11 (2%)	1 (0%)	44	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51	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	244/248 (98%)	235 (96%)	9 (4%)	29	19
1	B	255/248 (103%)	249 (98%)	6 (2%)	44	37
All	All	499/496 (101%)	484 (97%)	15 (3%)	36	27

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	VAL
1	A	113	HIS
1	A	131	LEU
1	A	135	ILE
1	A	151	ILE
1	A	230	GLU
1	A	233	LEU
1	A	309	ASP
1	A	330	CYS
1	B	76	ARG
1	B	131	LEU
1	B	148	GLN
1	B	164	LYS
1	B	230	GLU
1	B	238	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	193	ASN
1	B	248	HIS
1	B	266	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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

9 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	PO4	B	405	-	4,4,4	0.93	0	6,6,6	0.51	0
2	PO4	B	404	-	4,4,4	0.90	0	6,6,6	0.52	0
2	PO4	B	403	-	4,4,4	0.84	0	6,6,6	0.57	0
2	PO4	A	401	-	4,4,4	0.94	0	6,6,6	0.43	0
3	GOL	A	403	-	5,5,5	0.31	0	5,5,5	0.37	0
3	GOL	B	406	-	5,5,5	0.32	0	5,5,5	0.32	0
2	PO4	B	402	-	4,4,4	0.92	0	6,6,6	0.45	0
4	CXS	B	401	-	14,14,14	0.70	0	18,18,18	1.60	4 (22%)
2	PO4	A	402	-	4,4,4	0.89	0	6,6,6	0.49	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
4	CXS	B	401	-	-	1/8/16/16	0/1/1/1
3	GOL	B	406	-	-	2/4/4/4	-
3	GOL	A	403	-	-	4/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	CXS	C6-C5-C4	3.05	116.56	111.09

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	CXS	C9-C4-C5	2.71	115.49	110.80
4	B	401	CXS	C8-C9-C4	2.65	115.85	111.09
4	B	401	CXS	O2-S-C1	2.20	110.05	106.73

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	GOL	O1-C1-C2-C3
3	B	406	GOL	O1-C1-C2-C3
4	B	401	CXS	C9-C4-N-C3
3	A	403	GOL	C1-C2-C3-O3
3	A	403	GOL	O1-C1-C2-O2
3	B	406	GOL	O1-C1-C2-O2
3	A	403	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	GOL	1	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 ⓘ

### 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<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	304/346 (87%)	0.29	13 (4%)	40 47	14, 34, 68, 89	1 (0%)
1	B	317/346 (91%)	0.27	13 (4%)	42 49	14, 33, 62, 90	1 (0%)
All	All	621/692 (89%)	0.28	26 (4%)	41 48	14, 33, 65, 90	2 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	ALA	4.7
1	A	126	ASP	3.9
1	B	234	GLY	3.4
1	B	263	ALA	3.4
1	A	92	THR	3.3
1	A	2	PRO	3.3
1	B	114	GLY	3.1
1	B	235	ALA	2.9
1	A	131	LEU	2.9
1	B	115	ASN	2.9
1	A	343	ALA	2.9
1	B	85	THR	2.8
1	B	76	ARG	2.8
1	B	131	LEU	2.6
1	B	77	ARG	2.6
1	B	84	GLY	2.5
1	A	334	TYR	2.5
1	A	263	ALA	2.3
1	A	199	PHE	2.2
1	A	125	ALA	2.2
1	A	330	CYS	2.2
1	B	341	ALA	2.1
1	B	267	LEU	2.1
1	A	130	ALA	2.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	199	PHE	2.0
1	A	85	THR	2.0

## 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	PO4	A	402	5/5	0.66	0.11	86,87,87,87	0
2	PO4	A	401	5/5	0.67	0.16	103,105,107,109	0
3	GOL	A	403	6/6	0.74	0.15	29,34,45,56	0
2	PO4	B	405	5/5	0.78	0.09	87,89,90,92	0
2	PO4	B	402	5/5	0.79	0.15	66,67,72,77	0
2	PO4	B	403	5/5	0.81	0.15	51,57,67,71	0
3	GOL	B	406	6/6	0.86	0.10	42,57,60,62	0
4	CXS	B	401	14/14	0.87	0.13	34,45,51,51	0
2	PO4	B	404	5/5	0.92	0.17	48,49,50,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.