



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:42 PM EDT

PDB ID : 4K5N / pdb_00004k5n
Title : Phosphonic Arginine Mimetics as Inhibitors of the M1 Aminopeptidases from Plasmodium falciparum
Authors : McGowan, S.
Deposited on : 2013-04-15
Resolution : 1.91 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 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 Phenix2.0
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

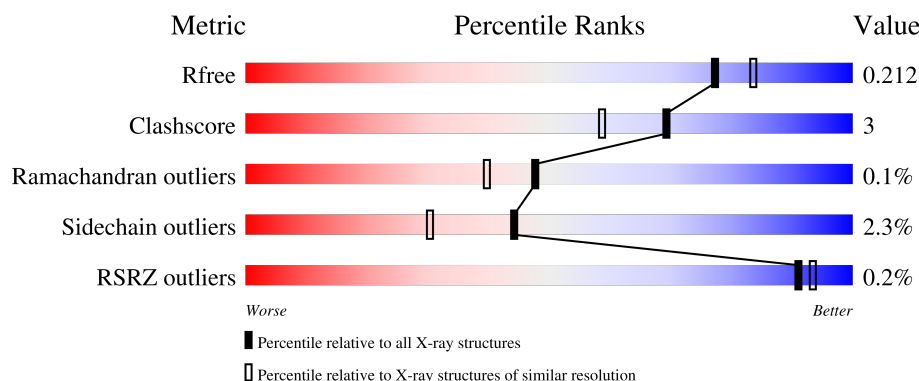
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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 $\leq 5\%$. 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	895	 89% 10% ..

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	1105	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8291 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 M1 family aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	889	Total	C	N	O	S	0	8	0
			7237	4662	1173	1373	29			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	213	GLN	ASN	engineered mutation	UNP O96935
A	223	GLN	ASN	engineered mutation	UNP O96935
A	378	PRO	HIS	engineered mutation	UNP O96935
A	501	GLN	ASN	engineered mutation	UNP O96935
A	745	GLN	ASN	engineered mutation	UNP O96935
A	795	GLN	ASN	engineered mutation	UNP O96935
A	1069	GLN	ASN	engineered mutation	UNP O96935
A	1085	HIS	-	expression tag	UNP O96935
A	1086	HIS	-	expression tag	UNP O96935
A	1087	HIS	-	expression tag	UNP O96935
A	1088	HIS	-	expression tag	UNP O96935
A	1089	HIS	-	expression tag	UNP O96935
A	1090	HIS	-	expression tag	UNP O96935

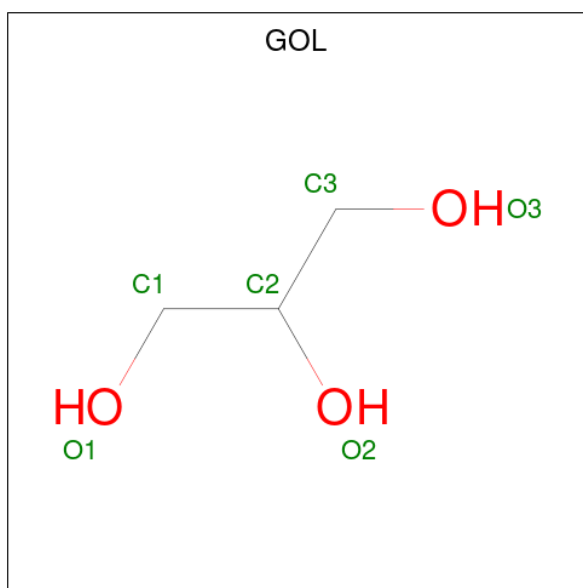
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

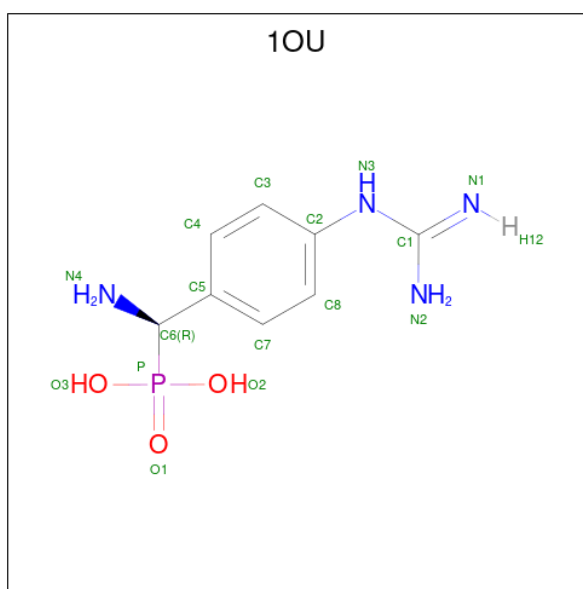
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Mg	0	0
			3	3		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is [(R)-amino(4-carbamimidamidophenyl)methyl]phosphonic acid (CCD ID: 1OU) (formula: $C_8H_{13}N_4O_3P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			16	8	4	3	1		

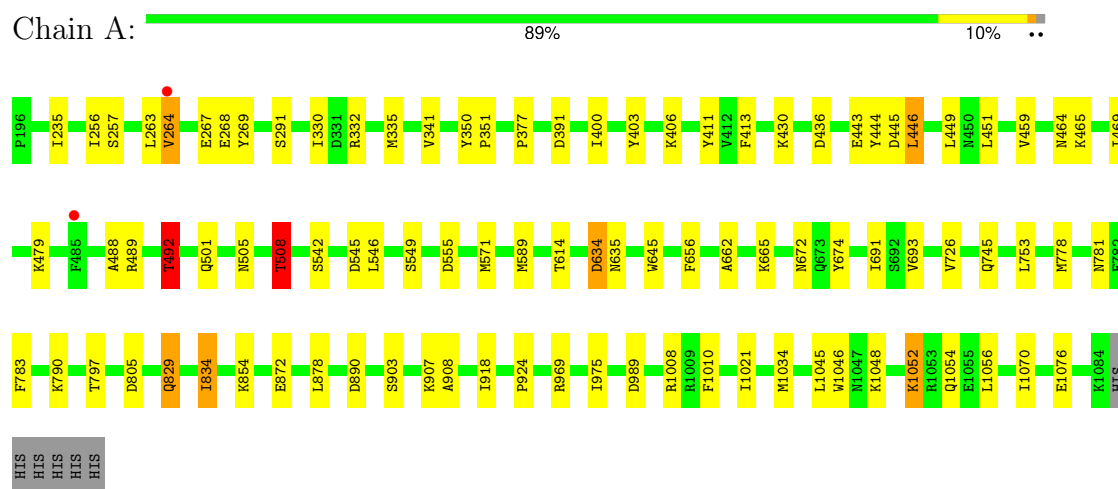
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1022	Total	O	0	0
			1022	1022		

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: M1 family aminopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.76Å 109.45Å 118.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.45 – 1.91 80.45 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.8 (80.45-1.91) 100.0 (80.45-1.91)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.161 , 0.210 0.163 , 0.212	Depositor DCC
R_{free} test set	3936 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8291	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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, 1OU, MG

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	1.36	17/7424 (0.2%)	1.13	12/10053 (0.1%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	549	SER	C-O	9.50	1.31	1.23
1	A	975	ILE	CA-CB	7.78	1.64	1.54
1	A	264	VAL	CA-CB	6.88	1.62	1.54
1	A	691	ILE	CA-CB	6.45	1.61	1.53
1	A	341	VAL	CA-CB	6.44	1.62	1.54
1	A	430	LYS	N-CA	6.43	1.54	1.46
1	A	918	ILE	CA-CB	6.30	1.62	1.54
1	A	330	ILE	CA-CB	6.11	1.61	1.53
1	A	693	VAL	N-CA	5.84	1.52	1.46
1	A	400	ILE	CA-CB	5.53	1.60	1.54
1	A	377	PRO	CA-C	5.36	1.57	1.52
1	A	1070	ILE	N-CA	5.27	1.52	1.46
1	A	469	ILE	CA-CB	5.24	1.61	1.54
1	A	783	PHE	C-O	5.23	1.30	1.24
1	A	542	SER	CA-C	5.16	1.59	1.52
1	A	464	ASN	N-CA	5.13	1.52	1.46
1	A	446	LEU	N-CA	5.06	1.52	1.45

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	508	THR	N-CA-CB	-8.68	97.49	110.85
1	A	1008	ARG	N-CA-C	7.01	118.92	111.28
1	A	377	PRO	N-CA-C	6.77	118.96	110.70
1	A	350	TYR	CA-C-N	6.68	126.62	119.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	350	TYR	C-N-CA	6.68	126.62	119.28
1	A	492	THR	N-CA-CB	-5.78	101.61	110.16
1	A	264	VAL	N-CA-C	5.45	115.71	107.80
1	A	634	ASP	CB-CA-C	5.40	117.86	110.94
1	A	235	ILE	N-CA-C	-5.37	100.69	108.36
1	A	492	THR	OG1-CB-CG2	5.31	119.92	109.30
1	A	508	THR	OG1-CB-CG2	5.29	119.88	109.30
1	A	829	GLN	CA-CB-CG	-5.15	103.80	114.10

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	7237	0	7101	50	0
2	A	1	0	0	0	0
3	A	3	0	0	0	0
4	A	12	0	15	0	0
5	A	16	0	11	0	0
6	A	1022	0	0	21	0
All	All	8291	0	7127	50	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 (50) 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:834:ILE:HB	6:A:1832:HOH:O	1.36	1.21
1:A:781[A]:ASN:ND2	6:A:2196:HOH:O	1.96	0.99
1:A:890[B]:ASP:OD1	6:A:2190:HOH:O	1.88	0.88
1:A:1034[B]:MET:HE2	6:A:1748:HOH:O	1.75	0.86
1:A:778[B]:MET:SD	1:A:797:THR:HG21	2.19	0.82
1:A:834:ILE:HG13	1:A:834:ILE:O	1.89	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:969:ARG:HD3	6:A:2058:HOH:O	1.91	0.70
1:A:805:ASP:OD1	6:A:2207:HOH:O	2.11	0.68
1:A:256:ILE:HD11	1:A:269:TYR:CD1	2.28	0.68
1:A:1076:GLU:OE2	6:A:2218:HOH:O	2.13	0.66
1:A:989:ASP:CB	6:A:1494:HOH:O	2.44	0.65
1:A:878:LEU:HD21	1:A:924:PRO:HG2	1.80	0.63
1:A:672:ASN:ND2	6:A:2192:HOH:O	2.33	0.62
1:A:656:PHE:O	1:A:745:GLN:HG3	2.00	0.61
1:A:263:LEU:HA	1:A:268:GLU:OE1	2.02	0.60
1:A:508:THR:HG22	1:A:614:THR:HG22	1.84	0.58
1:A:726:VAL:HG22	6:A:1725:HOH:O	2.04	0.57
1:A:1076:GLU:HG2	6:A:2193:HOH:O	2.05	0.56
1:A:488:ALA:O	1:A:492:THR:HB	2.08	0.53
1:A:781[A]:ASN:CG	6:A:2196:HOH:O	2.46	0.52
1:A:745:GLN:NE2	6:A:1395:HOH:O	2.42	0.52
1:A:508:THR:CG2	1:A:614:THR:HG22	2.40	0.52
1:A:403:TYR:N	1:A:443:GLU:OE2	2.36	0.51
1:A:778[B]:MET:HE2	6:A:2160:HOH:O	2.12	0.50
1:A:257:SER:HB2	1:A:291:SER:OG	2.13	0.48
1:A:1046:TRP:O	1:A:1054:GLN:HG2	2.14	0.48
1:A:501:GLN:NE2	1:A:505:ASN:HD22	2.12	0.48
1:A:1052:LYS:HE2	1:A:1056:LEU:HG	1.97	0.47
1:A:834:ILE:HD11	1:A:1048:LYS:HB3	1.97	0.47
1:A:351:PRO:HG2	1:A:391:ASP:HA	1.97	0.46
1:A:444:TYR:CE2	1:A:446:LEU:HB2	2.51	0.46
1:A:674:TYR:CD2	6:A:2069:HOH:O	2.56	0.46
1:A:1010:PHE:CE1	1:A:1021:ILE:HG13	2.51	0.45
1:A:489:ARG:O	1:A:492:THR:HG22	2.17	0.45
1:A:903:SER:O	1:A:907:LYS:HG3	2.17	0.45
1:A:589:MET:HE1	1:A:645:TRP:CE2	2.52	0.45
1:A:829:GLN:NE2	6:A:1994:HOH:O	2.51	0.44
1:A:790:LYS:HG2	6:A:2033:HOH:O	2.17	0.43
1:A:908:ALA:HA	6:A:2096:HOH:O	2.18	0.43
1:A:445:ASP:OD1	1:A:445:ASP:N	2.49	0.43
1:A:264:VAL:N	1:A:268:GLU:OE1	2.51	0.43
1:A:1052:LYS:HA	1:A:1052:LYS:HD2	1.83	0.43
1:A:1034[B]:MET:CE	6:A:1748:HOH:O	2.51	0.42
1:A:465:LYS:HE2	6:A:1581:HOH:O	2.19	0.42
1:A:501:GLN:HE21	1:A:501:GLN:HA	1.84	0.42
1:A:332:ARG:HG3	1:A:335:MET:HG2	2.00	0.42
1:A:264:VAL:CG2	1:A:267:GLU:HB3	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:TYR:HB3	1:A:413:PHE:CE2	2.56	0.41
1:A:546:LEU:CD1	6:A:2122:HOH:O	2.69	0.40
1:A:662:ALA:O	1:A:665:LYS:HD3	2.21	0.40

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	895/895 (100%)	878 (98%)	16 (2%)	1 (0%)	48 40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	459	VAL

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	799/827 (97%)	781 (98%)	18 (2%)	44 30

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	406	LYS
1	A	436	ASP
1	A	449	LEU
1	A	451	LEU
1	A	479	LYS
1	A	492	THR
1	A	508	THR
1	A	545	ASP
1	A	555	ASP
1	A	571	MET
1	A	634	ASP
1	A	635	ASN
1	A	753	LEU
1	A	834	ILE
1	A	854	LYS
1	A	872	GLU
1	A	1045	LEU
1	A	1052	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	HIS
1	A	312	ASN
1	A	464	ASN
1	A	501	GLN
1	A	527	ASN
1	A	621	ASN
1	A	626	GLN
1	A	659	ASN
1	A	666	GLN
1	A	775	GLN
1	A	779	ASN
1	A	829	GLN
1	A	915	ASN

5.3.3 RNA ⓘ

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 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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
4	GOL	A	1105	-	5,5,5	1.00	0	5,5,5	2.10	3 (60%)
5	1OU	A	1106	2	15,16,16	2.40	4 (26%)	19,23,23	1.72	5 (26%)
4	GOL	A	1104	-	5,5,5	0.40	0	5,5,5	1.27	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	GOL	A	1105	-	-	3/4/4/4	-
5	1OU	A	1106	2	-	5/13/14/14	0/1/1/1
4	GOL	A	1104	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1106	1OU	P-O3	5.80	1.64	1.54
5	A	1106	1OU	P-O2	5.72	1.63	1.54
5	A	1106	1OU	P-C6	-2.43	1.80	1.84
5	A	1106	1OU	C1-N3	-2.01	1.35	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1106	1OU	O2-P-O1	-4.21	102.89	113.45
4	A	1105	GOL	C3-C2-C1	2.97	122.69	111.80
5	A	1106	1OU	O3-P-O2	2.64	114.76	107.58
4	A	1105	GOL	O3-C3-C2	2.49	121.57	110.38
5	A	1106	1OU	C4-C5-C6	2.43	123.51	120.76
4	A	1105	GOL	O2-C2-C1	2.31	118.73	109.18
5	A	1106	1OU	C4-C3-C2	2.22	122.85	120.30
5	A	1106	1OU	O2-P-C6	2.02	113.32	106.33

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1104	GOL	O1-C1-C2-C3
4	A	1105	GOL	O1-C1-C2-C3
5	A	1106	1OU	C5-C6-P-O1
5	A	1106	1OU	C5-C6-P-O2
4	A	1105	GOL	O1-C1-C2-O2
4	A	1104	GOL	O1-C1-C2-O2
4	A	1105	GOL	C1-C2-C3-O3
5	A	1106	1OU	C5-C6-P-O3
5	A	1106	1OU	N4-C6-P-O2
5	A	1106	1OU	N4-C6-P-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, 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	889/895 (99%)	-0.52	2 (0%) 91 93	7, 19, 34, 49	8 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	485	PHE	2.4
1	A	264	VAL	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 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, 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(Å ²)	Q<0.9
3	MG	A	1107	1/1	0.94	0.07	41,41,41,41	0
4	GOL	A	1105	6/6	0.94	0.09	15,24,26,26	0
3	MG	A	1102	1/1	0.96	0.06	31,31,31,31	0
3	MG	A	1103	1/1	0.97	0.07	27,27,27,27	0
5	1OU	A	1106	16/16	0.97	0.06	13,21,28,30	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	1104	6/6	0.98	0.05	15,16,25,29	0
2	ZN	A	1101	1/1	1.00	0.02	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.