



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:52 AM GMT

PDB ID : 2BIE
Title : RADIATION DAMAGE OF THE SCHIFF BASE IN PHOSPHOSERINE
AMINOTRANSFERASE (STRUCTURE H)
Authors : Dubnovitsky, A.P.; Ravelli, R.B.G.; Popov, A.N.; Papageorgiou, A.C.
Deposited on : 2005-01-21
Resolution : 1.30 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

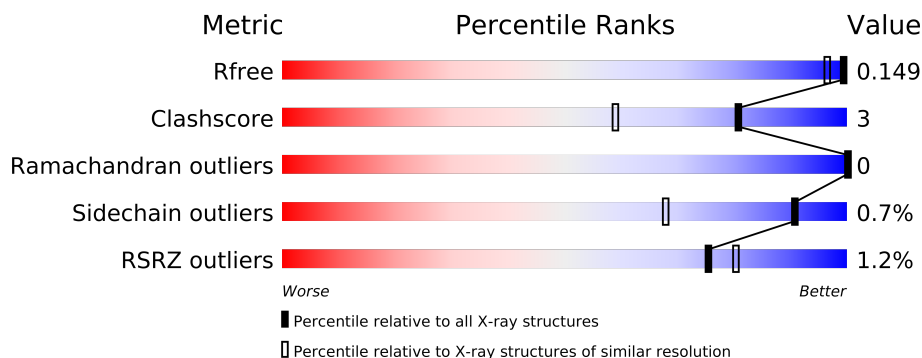
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.30 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}	66092	1025 (1.34-1.26)
Clashscore	79885	1140 (1.34-1.26)
Ramachandran outliers	78287	1093 (1.34-1.26)
Sidechain outliers	78261	1092 (1.34-1.26)
RSRZ outliers	66119	1025 (1.34-1.26)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	361	
1	B	361	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	1363	-	X
3	MG	B	1363	-	X
5	PGE	A	1366	-	X
6	PEG	A	1367	-	X

2 Entry composition i

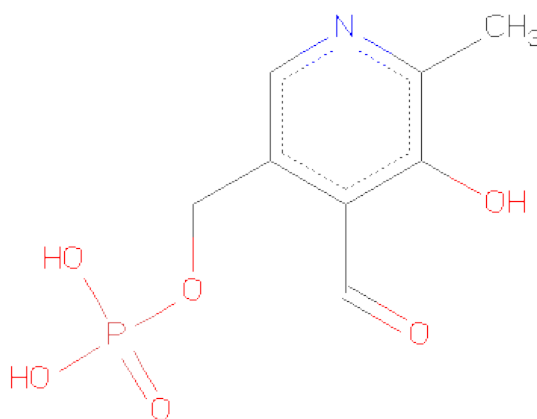
There are 7 unique types of molecules in this entry. The entry contains 6613 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PHOSPHOSERINE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	17	0
			2871	1821	487	548	15			
1	B	355	Total	C	N	O	S	0	14	0
			2836	1801	480	541	14			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

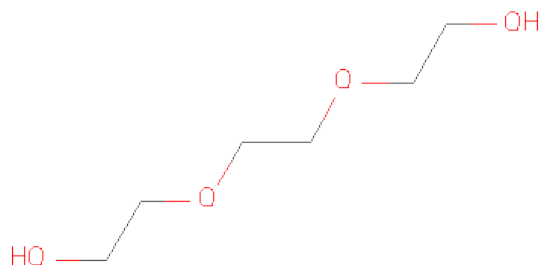
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Mg	0	1
			4	4		
3	A	2	Total	Mg	0	0
			2	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

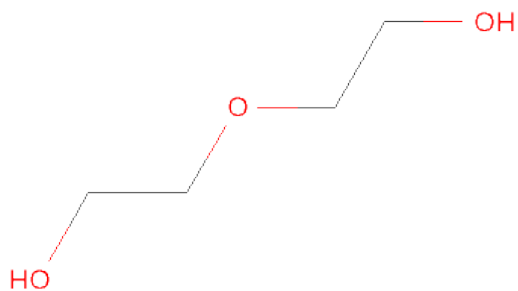
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Cl	0	0
			2	2		
4	A	2	Total	Cl	0	0
			2	2		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is water.

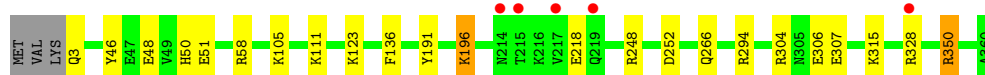
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	410	Total	O	0	0
			410	410		
7	B	432	Total	O	0	0
			432	432		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

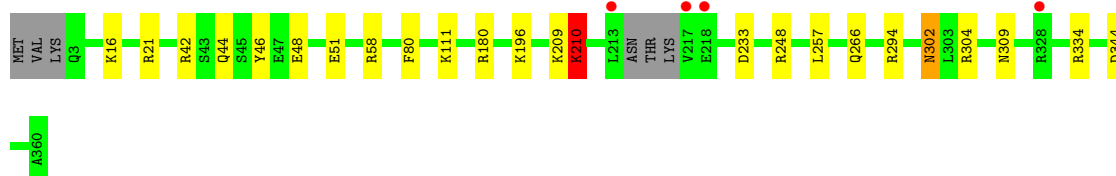
• Molecule 1: PHOSPHOSERINE AMINOTRANSFERASE

Chain A: 



• Molecule 1: PHOSPHOSERINE AMINOTRANSFERASE

Chain B: 



A360

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.73Å 84.27Å 67.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 1.30 11.98 – 1.30	Depositor EDS
% Data completeness (in resolution range)	96.2 (12.00-1.30) 96.2 (11.98-1.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 1.30Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.130 , 0.164 0.144 , 0.149	Depositor DCC
R_{free} test set	9361 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , 71.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 192460 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	6613	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: PEG, MG, PGE, CL, PLP

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	0.63	0/3006	1.20	21/4063 (0.5%)
1	B	0.63	0/2950	1.24	20/3990 (0.5%)
All	All	0.63	0/5956	1.22	41/8053 (0.5%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	42	ARG	NE-CZ-NH1	-15.91	112.35	120.30
1	B	42	ARG	NE-CZ-NH2	14.73	127.67	120.30
1	A	350	ARG	NE-CZ-NH1	10.64	125.62	120.30
1	A	248	ARG	NE-CZ-NH2	-10.16	115.22	120.30
1	B	58	ARG	NE-CZ-NH1	10.10	125.35	120.30
1	B	248	ARG	NE-CZ-NH2	-9.41	115.59	120.30
1	A	350	ARG	NE-CZ-NH2	-9.09	115.75	120.30
1	B	233	ASP	CB-CG-OD2	-8.25	110.88	118.30
1	B	248	ARG	NE-CZ-NH1	8.20	124.40	120.30
1	A	191	TYR	CG-CD1-CE1	7.33	127.16	121.30
1	A	58	ARG	NE-CZ-NH2	6.99	123.79	120.30
1	B	304	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	A	307	GLU	OE1-CD-OE2	-6.92	115.00	123.30
1	A	350	ARG	CD-NE-CZ	6.79	133.11	123.60
1	B	180	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	A	304	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	21	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	A	136	PHE	CB-CG-CD2	-6.41	116.31	120.80
1	A	51	GLU	OE1-CD-OE2	-6.35	115.68	123.30
1	A	218	GLU	O-C-N	6.35	132.85	122.70
1	B	210	LYS	CA-CB-CG	6.16	126.96	113.40
1	A	46	TYR	CB-CG-CD1	-6.13	117.32	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	344	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	A	136	PHE	CB-CG-CD1	5.80	124.86	120.80
1	A	294	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	B	46	TYR	CA-CB-CG	-5.66	102.66	113.40
1	A	51	GLU	CG-CD-OE2	5.65	129.59	118.30
1	A	50[A]	HIS	CA-CB-CG	5.53	123.00	113.60
1	A	50[B]	HIS	CA-CB-CG	5.53	123.00	113.60
1	B	334	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	306	GLU	OE1-CD-OE2	5.42	129.81	123.30
1	B	294	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	B	302[A]	ASN	CA-CB-CG	5.34	125.16	113.40
1	B	302[B]	ASN	CA-CB-CG	5.34	125.16	113.40
1	B	42	ARG	CB-CG-CD	5.31	125.40	111.60
1	B	51	GLU	CG-CD-OE1	5.30	128.91	118.30
1	A	48	GLU	CA-CB-CG	5.16	124.74	113.40
1	A	248	ARG	NH1-CZ-NH2	5.15	125.06	119.40
1	A	252	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	B	257	LEU	CA-CB-CG	5.08	126.98	115.30
1	B	80	PHE	CB-CG-CD2	5.01	124.31	120.80

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2871	0	0	8	0
1	B	2836	0	0	10	0
2	A	15	0	0	1	0
2	B	15	0	0	1	0
3	A	2	0	0	0	0
3	B	4	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	10	0	0	1	0
6	A	7	0	0	0	0
6	B	7	0	0	0	0
7	A	410	0	0	6	0
7	B	432	0	0	8	0
All	All	6613	0	0	19	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (19) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:266[B]:GLN:NE2	7:A:2291:HOH:O	2.34	0.60
1:B:266[A]:GLN:NE2	7:B:2322:HOH:O	2.49	0.46
1:B:44:GLN:NE2	1:B:48:GLU:OE2	2.49	0.46
1:A:123[A]:LYS:NZ	7:A:2171:HOH:O	2.49	0.46
1:A:105[B]:LYS:NZ	7:A:2138:HOH:O	2.50	0.45
1:B:210:LYS:NZ	7:B:2274:HOH:O	2.49	0.45
1:B:210:LYS:NZ	7:B:2272:HOH:O	2.50	0.45
1:A:123[B]:LYS:NZ	5:A:1366:PGE:O3	2.49	0.45
1:B:209:LYS:NZ	7:B:2271:HOH:O	2.50	0.45
1:A:196:LYS:NZ	2:A:1361:PLP:O3	2.50	0.44
1:B:266[B]:GLN:NE2	7:B:2320:HOH:O	2.49	0.44
1:A:111:LYS:NZ	7:A:2153:HOH:O	2.50	0.44
1:B:196:LYS:NZ	2:B:1361:PLP:O3	2.50	0.44
1:A:350:ARG:NH1	7:A:2393:HOH:O	2.50	0.44
1:B:111:LYS:NZ	7:B:2178:HOH:O	2.50	0.44
1:B:16[A]:LYS:NZ	7:B:2033:HOH:O	2.51	0.43
1:B:302[A]:ASN:ND2	1:B:309:ASN:ND2	2.67	0.43
1:A:315:LYS:NZ	7:A:2362:HOH:O	2.54	0.41
4:B:1366:CL:CL	7:B:2020:HOH:O	2.59	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	373/361 (103%)	367 (98%)	6 (2%)	0	100	100
1	B	365/361 (101%)	359 (98%)	6 (2%)	0	100	100
All	All	738/722 (102%)	726 (98%)	12 (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	321/310 (104%)	318 (99%)	3 (1%)	87	60
1	B	317/310 (102%)	316 (100%)	1 (0%)	96	82
All	All	638/620 (103%)	634 (99%)	4 (1%)	91	72

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	196	LYS
1	A	328	ARG
1	B	210	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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	PLP	A	1361	1	14,15,16	1.53	1 (7%)	20,22,23	0.91	1 (5%)
5	PGE	A	1366	-	9,9,9	0.78	0	8,8,8	2.23	2 (25%)
6	PEG	A	1367	-	6,6,6	0.50	0	5,5,5	1.56	1 (20%)
2	PLP	B	1361	1	14,15,16	1.45	3 (21%)	20,22,23	1.09	1 (5%)
6	PEG	B	1367	-	6,6,6	0.59	0	5,5,5	0.60	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
2	PLP	A	1361	1	-	0/6/6/8	0/1/1/1
5	PGE	A	1366	-	-	0/7/7/7	0/0/0/0
6	PEG	A	1367	-	-	0/4/4/4	0/0/0/0
2	PLP	B	1361	1	-	0/6/6/8	0/1/1/1
6	PEG	B	1367	-	-	0/4/4/4	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1361	PLP	C3-C2	-4.94	1.37	1.40
2	B	1361	PLP	C3-C2	-3.33	1.38	1.40
2	B	1361	PLP	C6-N1	2.10	1.39	1.34
2	B	1361	PLP	C5A-C5	2.03	1.56	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1366	PGE	C3-O2-C2	4.74	134.20	113.38
6	A	1367	PEG	C3-O2-C2	3.31	127.92	113.38
5	A	1366	PGE	C5-O3-C4	3.21	127.50	113.38
2	B	1361	PLP	C5-C6-N1	-2.77	118.87	123.86
2	A	1361	PLP	C5-C6-N1	-2.13	120.02	123.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	358/361 (99%)	-0.63	5 (1%) 72 77	9, 14, 31, 55	0
1	B	355/361 (98%)	-0.57	4 (1%) 77 82	9, 13, 32, 64	0
All	All	713/722 (98%)	-0.60	9 (1%) 75 79	9, 13, 31, 64	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	LEU	2.8
1	B	328	ARG	2.8
1	B	218	GLU	2.8
1	B	217	VAL	2.6
1	A	328	ARG	2.5
1	A	215	THR	2.3
1	A	217	VAL	2.2
1	A	214	ASN	2.2
1	A	219	GLN	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	PGE	A	1366	10/10	0.14	22.58	43,54,58,58	0
3	MG	A	1363	1/1	0.09	19.91	15,15,15,15	0
3	MG	B	1363	1/1	0.16	10.16	26,26,26,26	1
6	PEG	A	1367	7/7	0.09	4.63	26,26,41,44	0
3	MG	B	1364[A]	1/1	0.10	1.39	26,26,26,26	1
6	PEG	B	1367	7/7	0.07	1.38	24,26,34,36	0
3	MG	A	1362	1/1	0.10	1.20	16,16,16,16	0
3	MG	B	1364[B]	1/1	0.10	1.13	26,26,26,26	1
3	MG	B	1362	1/1	0.06	0.61	11,11,11,11	1
2	PLP	B	1361	15/16	0.03	-0.64	9,9,12,13	0
2	PLP	A	1361	15/16	0.03	-1.07	8,9,12,16	0
4	CL	A	1364	1/1	0.03	-1.18	11,11,11,11	0
4	CL	B	1366	1/1	0.03	-1.26	21,21,21,21	0
4	CL	B	1365	1/1	0.02	-1.87	11,11,11,11	0
4	CL	A	1365	1/1	0.01	-2.53	18,18,18,18	0

6.5 Other polymers ⓘ

There are no such residues in this entry.