



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2021 – 06:07 AM EDT

PDB ID : 1G7X
Title : ASPARTATE AMINOTRANSFERASE ACTIVE SITE MUTANT
N194A/R292L/R386L
Authors : Mizuguchi, H.; Hayashi, H.; Okada, K.; Miyahara, I.; Hirotsu, K.;
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Deposited on : 2000-11-15
Resolution : 2.20 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 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

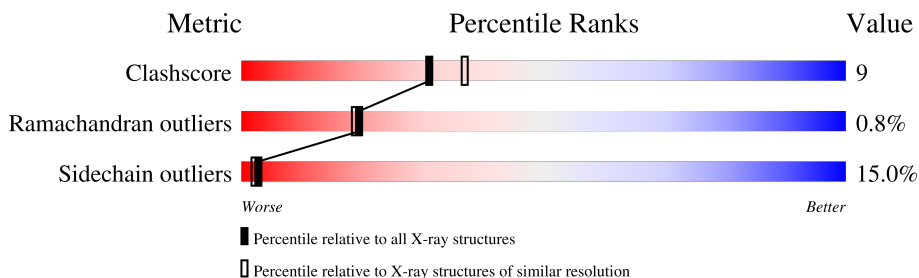
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3262 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.

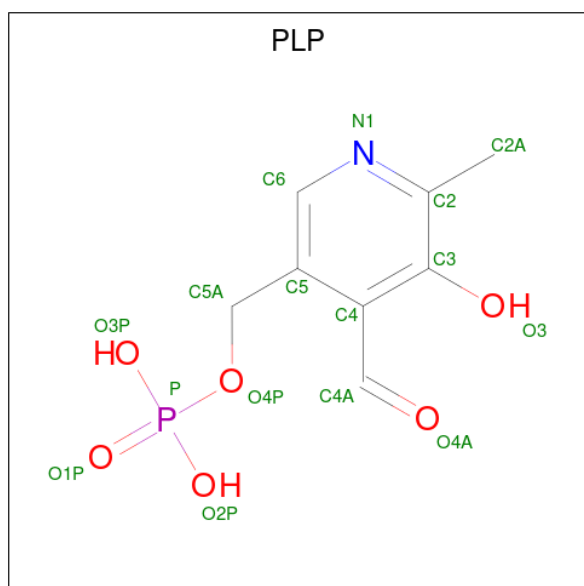
- Molecule 1 is a protein called ASPARTATE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3060	1935	529	583	13	4	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	ALA	ASN	engineered mutation	UNP P00509
A	282	ARG	LEU	engineered mutation	UNP P00509
A	386	LEU	ARG	engineered mutation	UNP P00509

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



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

- Molecule 3 is water.

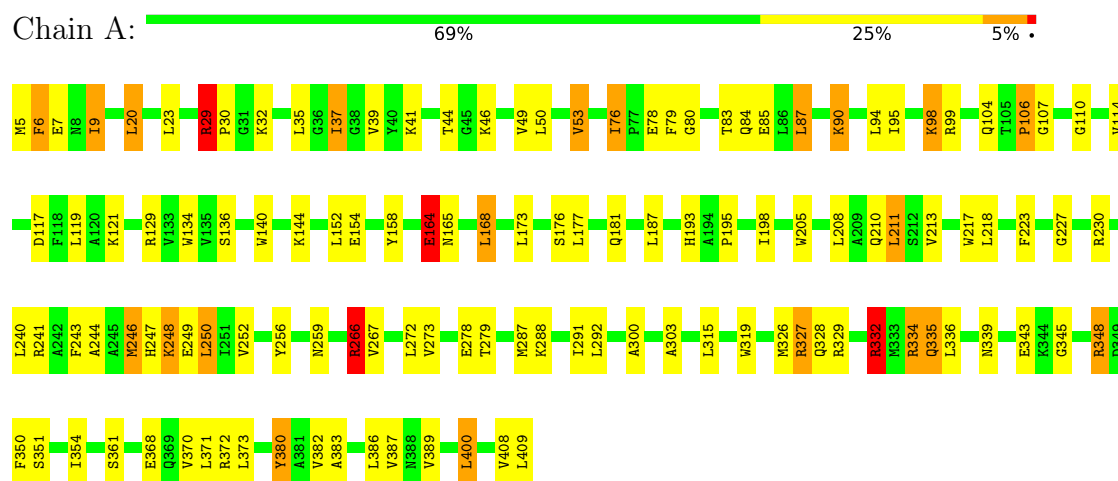
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	187	Total 187	O 187	0	0

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. 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. 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.

Note EDS was not executed.

• Molecule 1: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	155.39Å 89.29Å 79.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.229 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3262	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.70	0/3121	1.49	46/4230 (1.1%)

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	A	0	2

There are no bond length outliers.

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	ARG	NE-CZ-NH2	12.79	126.69	120.30
1	A	29	ARG	NE-CZ-NH1	-11.52	114.54	120.30
1	A	266	ARG	NH1-CZ-NH2	-10.30	108.07	119.40
1	A	217	TRP	CD1-CG-CD2	9.82	114.16	106.30
1	A	334	ARG	NE-CZ-NH2	9.57	125.09	120.30
1	A	217	TRP	CE2-CD2-CG	-8.89	100.19	107.30
1	A	319	TRP	CD1-CG-CD2	8.62	113.20	106.30
1	A	134	TRP	CD1-CG-CD2	8.43	113.05	106.30
1	A	140	TRP	CD1-CG-CD2	8.26	112.91	106.30
1	A	205	TRP	CD1-CG-CD2	7.82	112.56	106.30
1	A	205	TRP	CE2-CD2-CG	-7.79	101.07	107.30
1	A	140	TRP	CE2-CD2-CG	-7.64	101.19	107.30
1	A	134	TRP	CE2-CD2-CG	-7.55	101.26	107.30
1	A	334	ARG	NE-CZ-NH1	-7.53	116.53	120.30
1	A	319	TRP	CE2-CD2-CG	-7.51	101.29	107.30
1	A	327	ARG	NE-CZ-NH2	7.24	123.92	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	LEU	CA-CB-CG	7.04	131.50	115.30
1	A	266	ARG	NE-CZ-NH2	6.89	123.75	120.30
1	A	217	TRP	CG-CD2-CE3	6.84	140.06	133.90
1	A	266	ARG	NE-CZ-NH1	-6.42	117.09	120.30
1	A	80	GLY	CA-C-N	6.26	130.98	117.20
1	A	380	TYR	CB-CG-CD1	-6.00	117.40	121.00
1	A	217	TRP	CB-CG-CD1	-5.95	119.27	127.00
1	A	266	ARG	CA-CB-CG	5.84	126.26	113.40
1	A	164	GLU	CA-CB-CG	5.84	126.25	113.40
1	A	243	PHE	CA-C-N	5.77	129.89	117.20
1	A	327	ARG	NE-CZ-NH1	-5.77	117.42	120.30
1	A	6	PHE	CB-CG-CD1	-5.75	116.78	120.80
1	A	332	ARG	NE-CZ-NH2	5.71	123.16	120.30
1	A	205	TRP	CG-CD2-CE3	5.62	138.96	133.90
1	A	230	ARG	CB-CG-CD	-5.53	97.21	111.60
1	A	37	ILE	CA-C-N	5.48	127.16	116.20
1	A	80	GLY	O-C-N	-5.48	113.93	122.70
1	A	187	LEU	CA-CB-CG	5.43	127.79	115.30
1	A	292	LEU	CA-CB-CG	5.41	127.74	115.30
1	A	326	MET	CG-SD-CE	-5.37	91.61	100.20
1	A	84	GLN	CA-CB-CG	5.34	125.15	113.40
1	A	140	TRP	CG-CD2-CE3	5.33	138.70	133.90
1	A	319	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	A	250	LEU	CA-CB-CG	5.24	127.34	115.30
1	A	37	ILE	N-CA-C	5.21	125.08	111.00
1	A	329	ARG	NE-CZ-NH2	5.19	122.89	120.30
1	A	372	ARG	CA-CB-CG	5.17	124.78	113.40
1	A	134	TRP	CG-CD1-NE1	-5.16	104.94	110.10
1	A	246	MET	CA-CB-CG	5.12	122.01	113.30
1	A	87	LEU	CA-CB-CG	5.07	126.95	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	266	ARG	Sidechain
1	A	29	ARG	Sidechain

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	3060	0	3011	55	0
2	A	15	0	7	0	0
3	A	187	0	0	22	0
All	All	3262	0	3018	55	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 9.

All (55) 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:98:LYS:HA	1:A:98:LYS:HZ2	1.44	0.83
1:A:300:ALA:HA	3:A:507:HOH:O	1.85	0.77
1:A:107:GLY:HA3	1:A:266:ARG:NH1	1.98	0.77
1:A:107:GLY:HA3	1:A:266:ARG:HH11	1.50	0.77
1:A:106:PRO:HA	3:A:588:HOH:O	1.86	0.74
1:A:158:TYR:HB2	3:A:479:HOH:O	1.89	0.72
1:A:213:VAL:HB	3:A:580:HOH:O	1.88	0.72
1:A:152:LEU:HG	3:A:571:HOH:O	1.93	0.68
1:A:279:THR:HB	3:A:575:HOH:O	1.94	0.67
1:A:218:LEU:HG	3:A:583:HOH:O	1.95	0.64
1:A:50:LEU:HB2	1:A:53:VAL:HG13	1.77	0.64
1:A:247:HIS:N	3:A:498:HOH:O	2.34	0.61
1:A:20:LEU:HD12	1:A:380:TYR:HD1	1.65	0.60
1:A:37:ILE:HD13	1:A:41:LYS:HD2	1.83	0.59
1:A:79:PHE:HA	3:A:473:HOH:O	2.04	0.58
1:A:94:LEU:HD11	1:A:244:ALA:HB1	1.85	0.57
1:A:370:VAL:HG21	1:A:383:ALA:HA	1.85	0.56
1:A:95:ILE:O	1:A:98:LYS:HD2	2.05	0.56
1:A:287:MET:HG3	3:A:584:HOH:O	2.06	0.56
1:A:114:VAL:HB	3:A:513:HOH:O	2.06	0.54
1:A:241:ARG:HA	3:A:453:HOH:O	2.10	0.51
1:A:168:LEU:HD21	1:A:173:LEU:HD12	1.92	0.51
1:A:291:ILE:HG13	3:A:513:HOH:O	2.11	0.50
1:A:117:ASP:O	1:A:121:LYS:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:VAL:HB	3:A:584:HOH:O	2.11	0.49
1:A:246:MET:N	3:A:498:HOH:O	2.46	0.49
1:A:136:SER:OG	1:A:193:HIS:HE1	1.97	0.48
1:A:288:LYS:HG3	3:A:499:HOH:O	2.13	0.48
1:A:266:ARG:HA	1:A:266:ARG:HE	1.78	0.47
1:A:85:GLU:HG2	1:A:90:LYS:HA	1.95	0.47
1:A:227:GLY:O	1:A:327:ARG:HD3	2.15	0.47
1:A:303:ALA:HB3	3:A:507:HOH:O	2.16	0.46
1:A:30:PRO:HA	1:A:32:LYS:HG2	1.98	0.46
1:A:240:LEU:HB2	3:A:577:HOH:O	2.16	0.46
1:A:110:GLY:O	1:A:114:VAL:HG13	2.16	0.45
1:A:348:ARG:HB2	1:A:350:PHE:CD2	2.51	0.45
1:A:335:GLN:HA	1:A:354:ILE:HD11	1.97	0.45
1:A:334:ARG:HH12	1:A:361:SER:HB3	1.83	0.44
1:A:249:GLU:HB2	3:A:583:HOH:O	2.18	0.44
1:A:328:GLN:O	1:A:332:ARG:HD3	2.18	0.43
1:A:164:GLU:HG3	1:A:165:ASN:OD1	2.18	0.43
1:A:334:ARG:HG2	1:A:389:VAL:HG11	2.00	0.43
1:A:35:LEU:HD11	1:A:400:LEU:HD21	2.00	0.43
1:A:177:LEU:HD12	1:A:177:LEU:HA	1.91	0.43
1:A:6:PHE:O	1:A:9:ILE:HB	2.19	0.42
1:A:373:LEU:CD1	1:A:408:VAL:HG21	2.49	0.42
1:A:94:LEU:HD13	1:A:273:VAL:HG11	2.02	0.42
1:A:256:TYR:HB2	1:A:267:VAL:HB	2.02	0.42
1:A:144:LYS:HE3	3:A:452:HOH:O	2.19	0.41
1:A:248:LYS:HD3	1:A:248:LYS:HA	1.83	0.41
1:A:104:GLN:NE2	3:A:507:HOH:O	2.53	0.41
1:A:382:VAL:HB	1:A:386:LEU:HB3	2.02	0.41
1:A:129:ARG:HA	1:A:154:GLU:O	2.21	0.41
1:A:76:ILE:HD11	1:A:78:GLU:HB2	2.03	0.41
1:A:90:LYS:HD2	3:A:578:HOH:O	2.21	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	394/396 (100%)	373 (95%)	18 (5%)	3 (1%)	19	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ARG
1	A	345	GLY
1	A	106	PRO

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	319/319 (100%)	271 (85%)	48 (15%)	3	2

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	MET
1	A	7	GLU
1	A	9	ILE
1	A	20	LEU
1	A	23	LEU
1	A	29	ARG
1	A	39	VAL
1	A	44	THR
1	A	46	LYS
1	A	49	VAL
1	A	53	VAL
1	A	76	ILE
1	A	83	THR
1	A	87	LEU
1	A	90	LYS
1	A	98	LYS

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Mol	Chain	Res	Type
1	A	99	ARG
1	A	119	LEU
1	A	164	GLU
1	A	168	LEU
1	A	176	SER
1	A	181	GLN
1	A	195	PRO
1	A	198	ILE
1	A	208	LEU
1	A	210	GLN
1	A	211	LEU
1	A	223	PHE
1	A	248	LYS
1	A	250	LEU
1	A	252	VAL
1	A	259	ASN
1	A	266	ARG
1	A	272	LEU
1	A	278	GLU
1	A	315	LEU
1	A	332	ARG
1	A	335	GLN
1	A	336	LEU
1	A	339	ASN
1	A	343	GLU
1	A	348	ARG
1	A	351	SER
1	A	368	GLU
1	A	371	LEU
1	A	387	VAL
1	A	400	LEU
1	A	409	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	84	GLN
1	A	166	HIS
1	A	193	HIS
1	A	247	HIS
1	A	259	ASN

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Mol	Chain	Res	Type
1	A	356	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	PLP	A	413	1	15,15,16	1.42	1 (6%)	20,22,23	1.75	2 (10%)

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	413	1	-	5/6/6/8	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	413	PLP	C3-C2	-3.68	1.37	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	413	PLP	O4P-C5A-C5	6.15	121.08	109.35
2	A	413	PLP	O2P-P-O4P	-2.08	101.19	106.73

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	413	PLP	C4-C5-C5A-O4P
2	A	413	PLP	C6-C5-C5A-O4P
2	A	413	PLP	C5A-O4P-P-O1P
2	A	413	PLP	C5A-O4P-P-O2P
2	A	413	PLP	C5A-O4P-P-O3P

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.