



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:30 PM GMT

PDB ID : 1B4X
Title : ASPARTATE AMINOTRANSFERASE FROM E. COLI, C191S MUTATION,
WITH BOUND MALEATE
Authors : Jeffery, C.J.; Gloss, L.M.; Petsko, G.A.; Ringe, D.
Deposited on : 1998-12-30
Resolution : 2.45 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

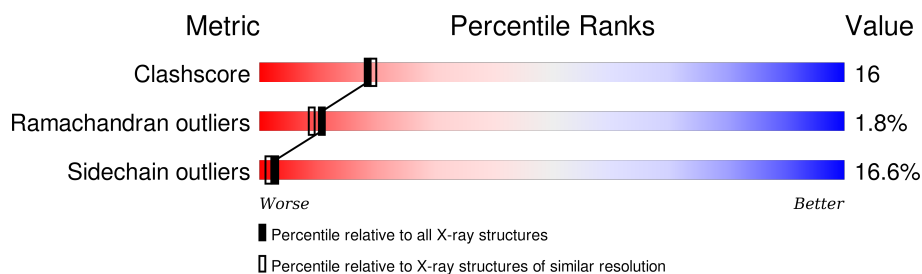
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3118 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	3069	1936	536	585	12	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	SER	CYS	ENGINEERED	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 MALEIC ACID (three-letter code: MAE) (formula: C₄H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is water.

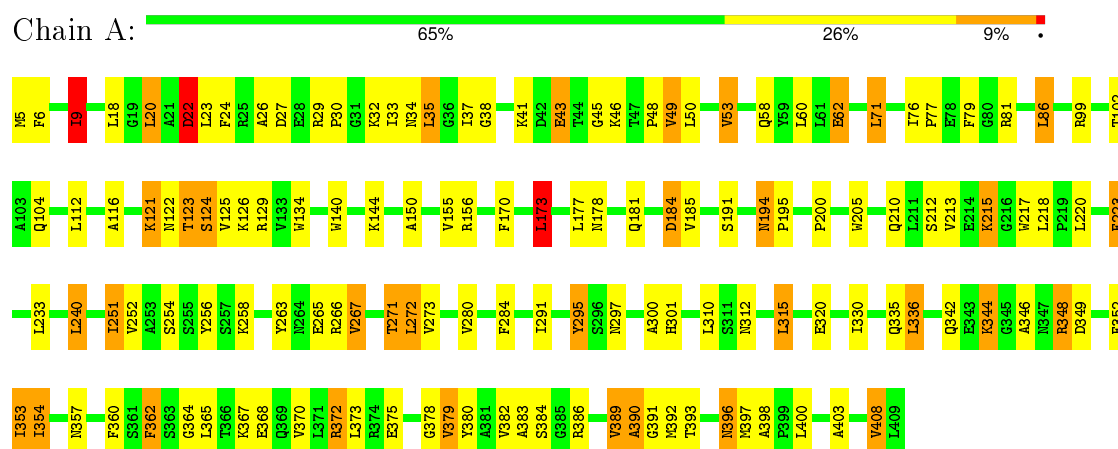
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	26	Total	O	0	0
			26	26		

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.

Note EDS was not executed.

• Molecule 1: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	157.13 Å 86.69 Å 79.87 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.45	Depositor
% Data completeness (in resolution range)	86.0 (10.00-2.45)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.207 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3118	wwPDB-VP
Average B, all atoms (Å ²)	41.0	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: MAE, 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	0.41	0/3130	0.83	4/4240 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	LEU	CA-CB-CG	6.66	130.63	115.30
1	A	173	LEU	CA-CB-CG	6.54	130.35	115.30
1	A	295	TYR	N-CA-C	-6.14	94.43	111.00
1	A	346	ALA	N-CA-C	5.18	124.98	111.00

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	3069	0	3016	95	0
2	A	15	0	7	4	0
3	A	8	0	2	0	0
4	A	26	0	0	1	0
All	All	3118	0	3025	95	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 16.

All (95) 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:123:THR:HG22	1:A:125:VAL:HG12	1.57	0.85
1:A:50:LEU:HB2	1:A:53:VAL:HG13	1.62	0.81
1:A:348:ARG:NH2	1:A:364:GLY:HA3	1.95	0.80
1:A:336:LEU:HD12	1:A:397:MET:HG2	1.64	0.79
1:A:382:VAL:HG13	1:A:384:SER:HB3	1.69	0.74
1:A:58:GLN:O	1:A:62:GLU:HG2	1.87	0.74
1:A:23:LEU:O	1:A:27:ASP:HB2	1.87	0.74
1:A:200:PRO:HG2	1:A:205:TRP:CE2	2.27	0.70
1:A:123:THR:CG2	1:A:125:VAL:HG12	2.23	0.69
1:A:22:ASP:O	1:A:26:ALA:HB3	1.93	0.68
1:A:396:ASN:HD22	1:A:396:ASN:C	2.00	0.65
1:A:397:MET:HE1	1:A:400:LEU:HD23	1.78	0.64
1:A:38:GLY:HA3	1:A:360:PHE:HZ	1.64	0.63
1:A:29:ARG:HH11	1:A:378:GLY:HA2	1.64	0.62
1:A:195:PRO:HB3	1:A:386:ARG:HD3	1.83	0.61
1:A:389:VAL:HG12	1:A:392:MET:SD	2.41	0.61
1:A:6:PHE:HA	1:A:9:ILE:HG13	1.81	0.61
1:A:396:ASN:HD22	1:A:397:MET:N	1.98	0.61
1:A:27:ASP:HB3	1:A:32:LYS:HE2	1.83	0.61
1:A:24:PHE:CE2	1:A:32:LYS:HB3	2.36	0.60
1:A:185:VAL:HG22	1:A:218:LEU:HD23	1.83	0.59
1:A:312:ASN:ND2	1:A:315:LEU:HB2	2.18	0.58
1:A:144:LYS:HA	1:A:155:VAL:HG21	1.85	0.58
1:A:256:TYR:HD2	1:A:267:VAL:HG22	1.69	0.57
1:A:370:VAL:HG11	1:A:383:ALA:HA	1.85	0.57
1:A:382:VAL:CG1	1:A:386:ARG:HB3	2.35	0.56
1:A:271:THR:HG23	4:A:770:HOH:O	2.04	0.56
1:A:212:SER:HA	1:A:217:TRP:CE3	2.41	0.56
1:A:41:LYS:HG2	1:A:45:GLY:HA2	1.87	0.56
1:A:266:ARG:NH2	2:A:458:PLP:O2P	2.39	0.55
1:A:123:THR:HG23	1:A:124:SER:N	2.22	0.54
1:A:210:GLN:HA	1:A:213:VAL:HG12	1.90	0.54
1:A:258:LYS:HG3	1:A:263:TYR:HE1	1.72	0.53
1:A:220:LEU:HG	1:A:251:ILE:HG12	1.91	0.53
1:A:37:ILE:HG13	1:A:38:GLY:N	2.24	0.53
1:A:312:ASN:HD22	1:A:315:LEU:HB2	1.74	0.52
1:A:200:PRO:HG2	1:A:205:TRP:CZ2	2.45	0.52
1:A:33:ILE:HG22	1:A:35:LEU:HD13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:ASN:CB	2:A:458:PLP:H2A1	2.41	0.51
1:A:178:ASN:ND2	1:A:215:LYS:HE2	2.25	0.51
1:A:372:ARG:HB3	1:A:408:VAL:CG2	2.41	0.51
1:A:397:MET:CE	1:A:400:LEU:HD23	2.41	0.51
1:A:170:PHE:O	1:A:173:LEU:HB3	2.10	0.51
1:A:181:GLN:O	1:A:184:ASP:HB2	2.12	0.49
1:A:348:ARG:HH21	1:A:364:GLY:HA3	1.74	0.49
1:A:223:PHE:HE2	1:A:240:LEU:HD12	1.77	0.49
1:A:266:ARG:HH22	2:A:458:PLP:P	2.35	0.49
1:A:34:ASN:O	1:A:380:TYR:O	2.31	0.48
1:A:49:VAL:HG23	1:A:53:VAL:HG22	1.95	0.47
1:A:362:PHE:HE1	1:A:384:SER:HG	1.59	0.47
1:A:24:PHE:CZ	1:A:32:LYS:HD3	2.49	0.47
1:A:352:PHE:CE1	1:A:353:ILE:HG22	2.50	0.47
1:A:335:GLN:CA	1:A:354:ILE:HD11	2.45	0.47
1:A:123:THR:CG2	1:A:124:SER:N	2.77	0.46
1:A:389:VAL:C	1:A:391:GLY:H	2.19	0.46
1:A:348:ARG:NH1	1:A:348:ARG:HG3	2.31	0.45
1:A:373:LEU:HD22	1:A:403:ALA:HB1	1.98	0.45
1:A:116:ALA:HB1	1:A:150:ALA:HB2	1.99	0.44
1:A:121:LYS:NZ	1:A:122:ASN:HD21	2.16	0.44
1:A:177:LEU:O	1:A:217:TRP:HZ2	1.99	0.44
1:A:49:VAL:HG23	1:A:53:VAL:CG2	2.47	0.44
1:A:20:LEU:HD11	1:A:380:TYR:HB3	1.98	0.44
1:A:79:PHE:CZ	1:A:256:TYR:HE2	2.35	0.44
1:A:86:LEU:HD23	1:A:86:LEU:HA	1.88	0.44
1:A:393:THR:O	1:A:397:MET:HB2	2.18	0.43
1:A:24:PHE:CE1	1:A:32:LYS:HD3	2.53	0.43
1:A:373:LEU:HB3	1:A:379:VAL:HG13	2.00	0.43
1:A:185:VAL:HG22	1:A:218:LEU:HB3	1.99	0.43
1:A:116:ALA:HB1	1:A:150:ALA:CB	2.48	0.43
1:A:29:ARG:NH1	1:A:378:GLY:HA2	2.32	0.43
1:A:20:LEU:HA	1:A:23:LEU:HD12	1.99	0.43
1:A:396:ASN:C	1:A:396:ASN:ND2	2.71	0.43
1:A:71:LEU:HD22	1:A:300:ALA:HB2	2.01	0.43
1:A:38:GLY:HA3	1:A:360:PHE:CZ	2.50	0.42
1:A:140:TRP:HB2	2:A:458:PLP:H2A3	2.01	0.42
1:A:280:VAL:O	1:A:284:PHE:HB2	2.18	0.42
1:A:223:PHE:O	1:A:254:SER:HA	2.19	0.42
1:A:177:LEU:HD12	1:A:177:LEU:HA	1.84	0.41
1:A:330:ILE:HG12	1:A:390:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ILE:HA	1:A:77:PRO:HD3	1.86	0.41
1:A:86:LEU:HD21	1:A:233:LEU:HD13	2.03	0.41
1:A:29:ARG:O	1:A:32:LYS:HE3	2.20	0.41
1:A:291:ILE:HG23	1:A:295:TYR:CE1	2.56	0.41
1:A:76:ILE:H	1:A:104:GLN:NE2	2.19	0.41
1:A:134:TRP:HA	1:A:156:ARG:O	2.20	0.41
1:A:46:LYS:O	1:A:48:PRO:HD3	2.19	0.41
1:A:382:VAL:CG1	1:A:384:SER:HB3	2.46	0.41
1:A:344:LYS:HZ3	1:A:398:ALA:HA	1.86	0.41
1:A:99:ARG:O	1:A:273:VAL:HA	2.21	0.41
1:A:367:LYS:HG2	1:A:368:GLU:OE2	2.21	0.40
1:A:315:LEU:HA	1:A:315:LEU:HD12	1.93	0.40
1:A:380:TYR:CD1	1:A:380:TYR:N	2.88	0.40
1:A:312:ASN:HD22	1:A:315:LEU:HD22	1.86	0.40
1:A:348:ARG:HH11	1:A:348:ARG:CG	2.35	0.40
1:A:354:ILE:HA	1:A:354:ILE:HD13	1.89	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	394/396 (100%)	359 (91%)	28 (7%)	7 (2%)	11	9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ILE
1	A	35	LEU
1	A	30	PRO
1	A	22	ASP
1	A	301	HIS

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Mol	Chain	Res	Type
1	A	390	ALA
1	A	43	GLU

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	320/320 (100%)	267 (83%)	53 (17%)	3 1

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	MET
1	A	9	ILE
1	A	18	LEU
1	A	20	LEU
1	A	22	ASP
1	A	43	GLU
1	A	49	VAL
1	A	53	VAL
1	A	60	LEU
1	A	62	GLU
1	A	71	LEU
1	A	81	ARG
1	A	86	LEU
1	A	102	THR
1	A	112	LEU
1	A	121	LYS
1	A	123	THR
1	A	124	SER
1	A	126	LYS
1	A	129	ARG
1	A	173	LEU
1	A	184	ASP
1	A	191	SER
1	A	194	ASN

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Mol	Chain	Res	Type
1	A	215	LYS
1	A	223	PHE
1	A	240	LEU
1	A	251	ILE
1	A	252	VAL
1	A	265	GLU
1	A	267	VAL
1	A	271	THR
1	A	272	LEU
1	A	297	ASN
1	A	310	LEU
1	A	315	LEU
1	A	320	GLU
1	A	336	LEU
1	A	342	GLN
1	A	344	LYS
1	A	348	ARG
1	A	349	ASP
1	A	353	ILE
1	A	354	ILE
1	A	357	ASN
1	A	362	PHE
1	A	365	LEU
1	A	372	ARG
1	A	375	GLU
1	A	379	VAL
1	A	389	VAL
1	A	396	ASN
1	A	408	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	GLN
1	A	122	ASN
1	A	178	ASN
1	A	194	ASN
1	A	226	GLN
1	A	297	ASN
1	A	312	ASN
1	A	328	GLN
1	A	331	GLN

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Mol	Chain	Res	Type
1	A	339	ASN
1	A	342	GLN
1	A	396	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	$\# Z > 2$
3	MAE	A	410	-	1,7,7	1.19	0	0,8,8	0.00	-
2	PLP	A	458	1	15,15,16	2.63	4 (26%)	21,22,23	2.33	6 (28%)

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	MAE	A	410	-	-	0/0/5/5	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLP	A	458	1	-	0/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	458	PLP	C3-C2	-8.55	1.34	1.40
2	A	458	PLP	P-O3P	-2.80	1.44	1.54
2	A	458	PLP	P-O1P	-2.19	1.44	1.51
2	A	458	PLP	C2A-C2	2.97	1.56	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	458	PLP	O2P-P-O4P	-2.77	98.60	106.56
2	A	458	PLP	C5-C6-N1	-2.02	120.36	123.86
2	A	458	PLP	C5A-C5-C4	2.00	124.31	121.65
2	A	458	PLP	C4A-C4-C5	2.20	123.17	120.88
2	A	458	PLP	O3P-P-O1P	2.86	119.80	110.58
2	A	458	PLP	O4P-C5A-C5	8.10	122.39	108.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	458	PLP	4	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.