



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 06:28 PM GMT

PDB ID : 1PYM  
Title : PHOSPHOENOLPYRUVATE MUTASE FROM MOLLUSK IN WITH  
BOUND MG2-OXALATE  
Authors : Huang, K.; Li, Z.; Herzberg, O.  
Deposited on : 1999-02-25  
Resolution : 1.80 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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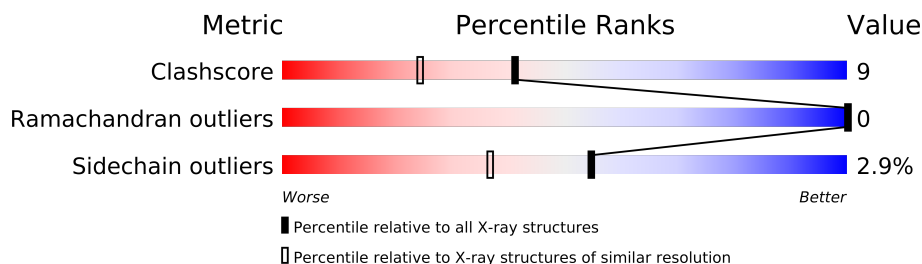
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
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 1.80 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	79885	4461 (1.80-1.80)
Ramachandran outliers	78287	4404 (1.80-1.80)
Sidechain outliers	78261	4403 (1.80-1.80)

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  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	295	
1	B	295	

## 2 Entry composition i

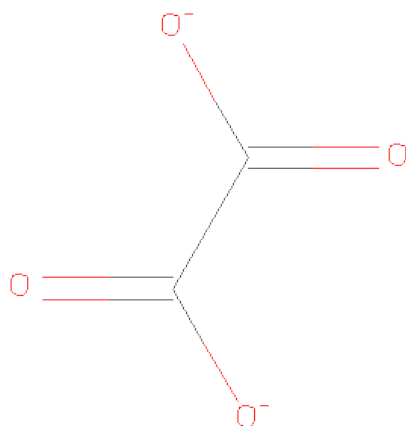
There are 4 unique types of molecules in this entry. The entry contains 5158 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PROTEIN (PHOSPHOENOLPYRUVATE MUTASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	Se	0	3	0
			2286	1434	398	444	3	7			
1	B	289	Total	C	N	O	S	Se	0	3	0
			2268	1424	394	440	3	7			

- Molecule 2 is OXALATE ION (three-letter code: OXL) (formula:  $C_2O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	2	4		
2	B	1	Total	C	O	0	0
			6	2	4		

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

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

- Molecule 4 is water.

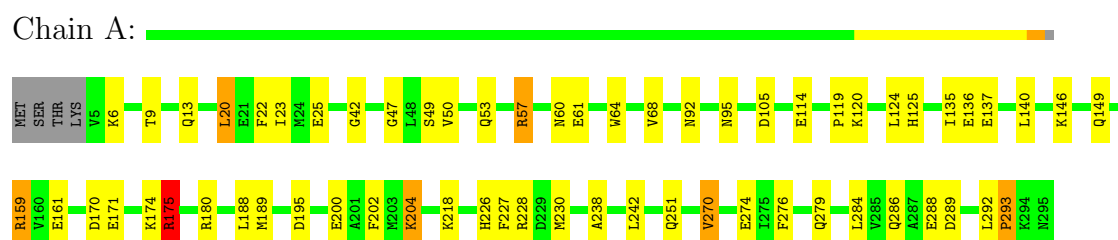
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	304	Total 304	O 304	0	0
4	B	286	Total 286	O 286	0	0

### 3 Residue-property plots i

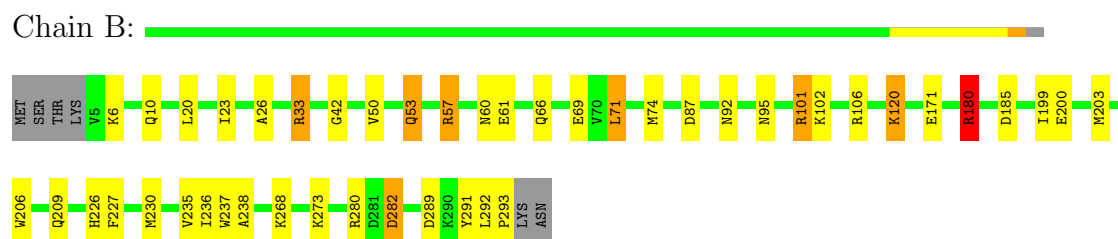
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: PROTEIN (PHOSPHOENOLPYRUVATE MUTASE)



#### • Molecule 1: PROTEIN (PHOSPHOENOLPYRUVATE MUTASE)



## 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, $\alpha$ , $\beta$ , $\gamma$	90.40Å 131.10Å 90.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.80	Depositor
% Data completeness (in resolution range)	88.6 (8.00-1.80)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.188 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5158	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	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: OXL, 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	0.96	1/2333 (0.0%)	1.02	6/3138 (0.2%)
1	B	0.98	2/2316 (0.1%)	1.04	15/3119 (0.5%)
All	All	0.97	3/4649 (0.1%)	1.03	21/6257 (0.3%)

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	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	69	GLU	CD-OE1	-6.50	1.18	1.25
1	A	204	LYS	CD-CE	6.15	1.66	1.51
1	B	282	ASP	CB-CG	5.14	1.62	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	57	ARG	NE-CZ-NH2	-12.77	113.91	120.30
1	A	175	ARG	NE-CZ-NH2	-11.89	114.35	120.30
1	A	57	ARG	NE-CZ-NH2	-9.72	115.44	120.30
1	A	175	ARG	NE-CZ-NH1	9.60	125.10	120.30
1	B	57	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	B	180	ARG	NE-CZ-NH2	-7.69	116.45	120.30
1	B	71	LEU	CA-CB-CG	-7.57	97.88	115.30
1	A	57	ARG	NE-CZ-NH1	7.21	123.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	ALA	N-CA-C	6.73	129.16	111.00
1	B	238	ALA	N-CA-C	6.28	127.95	111.00
1	B	33	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	B	106	ARG	NE-CZ-NH1	6.01	123.30	120.30
1	B	106	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	B	282	ASP	CB-CG-OD1	5.74	123.47	118.30
1	B	102	LYS	CD-CE-NZ	-5.69	98.61	111.70
1	B	180	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	B	101	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	A	159	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	B	237	TRP	N-CA-C	-5.28	96.75	111.00
1	B	33	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	B	291	TYR	N-CA-C	5.11	124.80	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	175	ARG	Sidechain

## 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	2286	0	2265	53	0
1	B	2268	0	2246	35	0
2	A	6	0	0	0	0
2	B	6	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	304	0	0	11	0
4	B	286	0	0	11	0
All	All	5158	0	4511	84	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 9.

All (84) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:293:PRO:HB3	4:A:1264:HOH:O	1.78	0.83
1:B:33:ARG:HD2	1:B:280:ARG:NH2	2.01	0.76
1:A:92:ASN:H	1:A:95:ASN:HD22	1.33	0.76
1:B:227:PHE:HA	1:B:230:MSE:HE3	1.66	0.75
1:A:171:GLU:O	1:A:175:ARG:HG2	1.88	0.74
1:A:137:GLU:HG2	4:A:1263:HOH:O	1.87	0.73
1:A:146:LYS:NZ	1:A:149:GLN:HE22	1.86	0.73
1:A:200:GLU:O	1:A:204:LYS:HG3	1.89	0.71
4:A:1025:HOH:O	1:B:101:ARG:HD2	1.93	0.67
1:A:125:HIS:HE1	4:A:1168:HOH:O	1.78	0.66
1:B:282:ASP:HB3	4:B:1204:HOH:O	1.96	0.66
1:A:137:GLU:HA	1:B:293:PRO:HG3	1.78	0.66
1:B:66:GLN:HA	4:B:1283:HOH:O	1.94	0.65
1:A:146:LYS:CE	1:A:149:GLN:HE22	2.09	0.65
1:B:33:ARG:HD2	1:B:280:ARG:CZ	2.30	0.62
1:B:280:ARG:NE	4:B:1070:HOH:O	2.31	0.62
1:B:120:LYS:C	1:B:120:LYS:HD3	2.20	0.62
1:A:146:LYS:HE2	1:A:149:GLN:HE22	1.64	0.61
1:A:159:ARG:HG3	1:A:188:LEU:HD22	1.83	0.61
1:A:200:GLU:OE2	1:A:226:HIS:HE1	1.83	0.61
1:B:199:ILE:O	1:B:203:MSE:HG2	2.01	0.60
1:A:286:GLN:O	1:A:289:ASP:HB3	2.00	0.60
1:B:33:ARG:HD3	4:B:1284:HOH:O	2.01	0.59
1:A:146:LYS:HE2	1:A:149:GLN:NE2	2.16	0.59
1:B:92:ASN:H	1:B:95:ASN:HD22	1.51	0.58
1:B:268:LYS:HD2	4:B:1258:HOH:O	2.04	0.57
1:A:227:PHE:HA	1:A:230:MSE:HE3	1.87	0.57
1:A:114:GLU:HB3	1:A:159:ARG:HD2	1.86	0.57
1:A:57:ARG:HD2	1:A:61:GLU:OE2	2.04	0.57
1:A:159:ARG:HD3	1:A:161:GLU:OE2	2.05	0.56
1:B:57:ARG:HD2	1:B:61:GLU:OE2	2.05	0.56
1:A:20:LEU:HD13	1:A:22:PHE:CZ	2.42	0.55
1:A:137:GLU:CA	1:B:293:PRO:HG3	2.36	0.55
1:A:228:ARG:NH2	4:A:1207:HOH:O	2.38	0.54
1:A:135:ILE:HD11	1:A:175:ARG:HD2	1.90	0.53
1:A:226:HIS:HD2	4:A:1208:HOH:O	1.91	0.53
1:A:92:ASN:N	1:A:95:ASN:HD22	2.06	0.52
1:B:200:GLU:OE2	1:B:226:HIS:HE1	1.92	0.52
1:A:293:PRO:HG2	4:B:1169:HOH:O	2.09	0.52
1:A:286:GLN:CG	4:A:1285:HOH:O	2.57	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:140:LEU:HD12	1:B:293:PRO:HB3	1.92	0.51
1:A:50:VAL:O	1:A:53:GLN:HG3	2.10	0.51
1:A:286:GLN:HG2	4:A:1285:HOH:O	2.09	0.51
1:A:170:ASP:O	1:A:174:LYS:HG3	2.10	0.51
1:A:200:GLU:HB3	1:A:204:LYS:HE3	1.93	0.50
1:A:284:LEU:O	1:A:288:GLU:HG3	2.11	0.50
1:A:189:MSE:HE3	1:A:202:PHE:CE1	2.48	0.49
1:A:136:GLU:HG2	1:B:293:PRO:HB3	1.95	0.49
1:A:251:GLN:HG3	4:A:1275:HOH:O	2.12	0.48
1:A:9:THR:O	1:A:13:GLN:HG3	2.13	0.48
1:A:49:SER:HA	1:A:242:LEU:HD22	1.96	0.47
1:A:23:ILE:HG22	1:A:42:GLY:HA3	1.97	0.47
1:B:10:GLN:NE2	4:B:1211:HOH:O	2.46	0.47
1:B:20:LEU:HD11	1:B:235:VAL:HG23	1.96	0.47
1:A:124:LEU:HD22	1:A:218:LYS:HE2	1.97	0.46
1:B:273:LYS:HG3	4:B:1042:HOH:O	2.15	0.46
1:A:146:LYS:HZ1	1:A:149:GLN:HE22	1.60	0.46
1:B:206:TRP:O	1:B:209:GLN:HG3	2.16	0.46
1:B:292:LEU:HD23	1:B:292:LEU:HA	1.74	0.46
1:A:60:ASN:HD22	1:A:119:PRO:HA	1.82	0.45
1:B:60:ASN:HD21	1:B:120:LYS:HG3	1.81	0.45
1:A:114:GLU:HA	1:A:159:ARG:HB3	1.99	0.45
1:B:6:LYS:NZ	4:B:1216:HOH:O	2.40	0.45
1:B:26:ALA:HB3	1:B:74:MSE:HE3	1.99	0.45
1:B:50:VAL:O	1:B:53:GLN:HG3	2.17	0.45
1:A:105:ASP:HB3	4:B:1022:HOH:O	2.17	0.44
1:B:23:ILE:HD11	1:B:236:ILE:HG12	1.99	0.44
1:A:6:LYS:HE2	1:A:6:LYS:HB2	1.76	0.42
1:A:175:ARG:H	1:A:175:ARG:HG2	1.72	0.42
1:B:60:ASN:ND2	1:B:120:LYS:HG3	2.35	0.42
1:A:64:TRP:O	1:A:68:VAL:HG23	2.19	0.42
1:B:280:ARG:HA	1:B:280:ARG:HD3	1.94	0.42
1:A:180:ARG:HD2	1:A:180:ARG:HA	1.90	0.42
1:A:189:MSE:HE3	1:A:202:PHE:CD1	2.54	0.42
1:B:180:ARG:HH22	1:B:185:ASP:C	2.23	0.41
1:B:226:HIS:CD2	4:B:1136:HOH:O	2.73	0.41
1:B:23:ILE:HG22	1:B:42:GLY:HA3	2.02	0.41
1:A:47:GLY:HA3	4:A:1158:HOH:O	2.19	0.41
1:B:6:LYS:O	1:B:10:GLN:HG3	2.21	0.41
1:B:87:ASP:OD1	1:B:120:LYS:HE2	2.20	0.41
1:A:114:GLU:CB	1:A:159:ARG:HD2	2.50	0.40
1:A:226:HIS:CD2	4:A:1208:HOH:O	2.71	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:270:VAL:HG22	1:A:274:GLU:HG2	2.04	0.40
1:A:276:PHE:HA	1:A:279:GLN:HE21	1.87	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	292/295 (99%)	280 (96%)	12 (4%)	0	100	100
1	B	290/295 (98%)	280 (97%)	10 (3%)	0	100	100
All	All	582/590 (99%)	560 (96%)	22 (4%)	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	248/242 (102%)	240 (97%)	8 (3%)	51	32
1	B	246/242 (102%)	240 (98%)	6 (2%)	61	44
All	All	494/484 (102%)	480 (97%)	14 (3%)	55	38

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	25	GLU

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Mol	Chain	Res	Type
1	A	120	LYS
1	A	175	ARG
1	A	195	ASP
1	A	270	VAL
1	A	292	LEU
1	A	293	PRO
1	B	53	GLN
1	B	71	LEU
1	B	120	LYS
1	B	171	GLU
1	B	180	ARG
1	B	289	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	16	ASN
1	A	60	ASN
1	A	95	ASN
1	A	125	HIS
1	A	149	GLN
1	A	190	HIS
1	A	226	HIS
1	A	279	GLN
1	A	295	ASN
1	B	10	GLN
1	B	13	GLN
1	B	53	GLN
1	B	60	ASN
1	B	95	ASN
1	B	130	GLN
1	B	149	GLN
1	B	190	HIS
1	B	226	HIS

### 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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	OXL	A	1001	3	0,5,5	0.00	-	0,6,6	0.00	-
2	OXL	B	1002	3	0,5,5	0.00	-	0,6,6	0.00	-

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	OXL	A	1001	3	-	0/0/4/4	0/0/0/0
2	OXL	B	1002	3	-	0/0/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

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.