



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:49 PM UTC

PDB ID : 1BF6 / pdb_00001bf6
Title : PHOSPHOTRIESTERASE HOMOLOGY PROTEIN FROM ES-
CHERICHIA COLI
Authors : Buchbinder, J.L.; Stephenson, R.C.; Scanlan, T.S.; Fletterick, R.J.
Deposited on : 1998-05-27
Resolution : 1.70 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

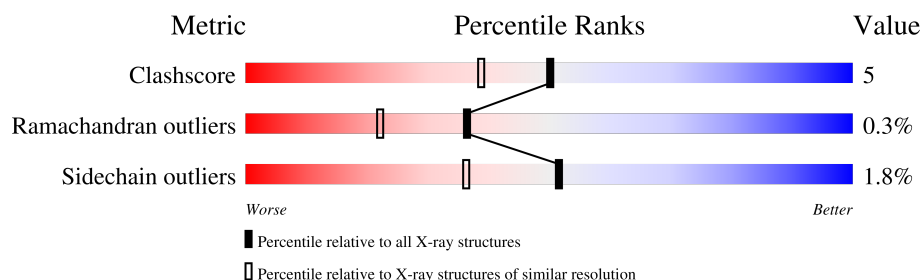
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)

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	291	 84% 14% •
1	B	291	 81% 17% •

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4911 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 PHOSPHOTRIESTERASE HOMOLOGUE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2297	1438	401	441	17			
1	B	291	Total	C	N	O	S	0	0	0
			2298	1438	401	442	17			

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

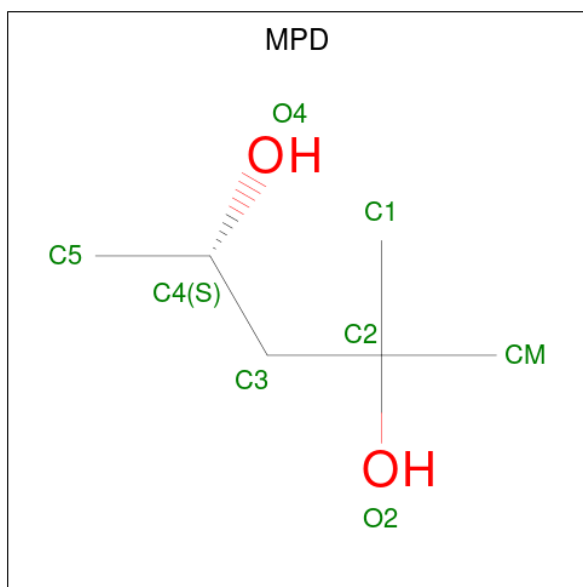
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is water.

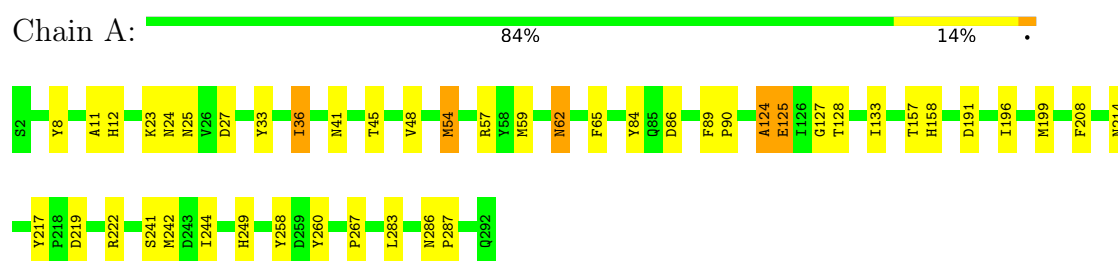
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	151	Total	O	0	0
			151	151		
6	B	137	Total	O	0	0
			137	137		

3 Residue-property plots

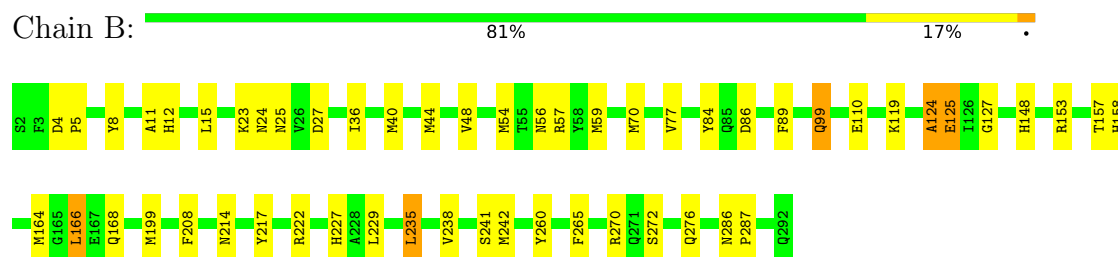
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: PHOSPHOTRIESTERASE HOMOLOGY PROTEIN



• Molecule 1: PHOSPHOTRIESTERASE HOMOLOGY PROTEIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.07 Å 80.80 Å 98.20 Å 90.00° 97.10° 90.00°	Depositor
Resolution (Å)	50.00 – 1.70	Depositor
% Data completeness (in resolution range)	98.0 (50.00-1.70)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.204 , 0.241	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4911	wwPDB-VP
Average B, all atoms (Å ²)	14.0	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: SO4, GOL, ZN, MPD

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	0.59	0/2337	1.06	17/3155 (0.5%)
1	B	0.55	0/2338	1.06	13/3156 (0.4%)
All	All	0.57	0/4675	1.06	30/6311 (0.5%)

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	GLU	OE1-CD-OE2	14.09	156.70	122.90
1	B	125	GLU	OE1-CD-OE2	11.17	149.71	122.90
1	B	124	ALA	O-C-N	-10.96	111.64	123.04
1	B	125	GLU	N-CA-CB	8.30	124.60	110.50
1	A	125	GLU	N-CA-CB	7.65	123.51	110.50
1	A	125	GLU	CG-CD-OE2	-7.60	100.93	118.40
1	A	124	ALA	O-C-N	-7.32	115.43	123.04
1	A	125	GLU	CG-CD-OE1	-7.07	102.14	118.40
1	B	125	GLU	CG-CD-OE2	-6.90	102.54	118.40
1	A	59	MET	N-CA-C	-6.52	104.96	113.17
1	A	33	TYR	N-CA-C	6.31	118.72	111.02
1	A	191	ASP	N-CA-C	-6.24	100.16	109.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	157	THR	N-CA-C	6.24	119.69	110.46
1	A	157	THR	N-CA-C	6.11	119.51	110.46
1	B	208	PHE	N-CA-C	-6.09	97.22	108.24
1	B	59	MET	N-CA-C	-6.05	105.19	113.30
1	B	11	ALA	N-CA-C	5.85	119.52	112.38
1	A	208	PHE	N-CA-C	-5.78	97.32	107.73
1	A	11	ALA	N-CA-C	5.54	119.66	113.01
1	B	265	PHE	N-CA-C	5.50	116.95	111.07
1	A	283	LEU	N-CA-C	5.49	119.15	112.23
1	A	90	PRO	N-CA-C	-5.34	103.39	111.41
1	B	124	ALA	CB-CA-C	-5.30	101.29	111.78
1	A	54	MET	N-CA-C	5.24	119.36	112.92
1	A	127	GLY	N-CA-C	5.22	121.60	112.10
1	B	222	ARG	N-CA-C	-5.21	105.69	111.36
1	A	222	ARG	N-CA-C	-5.18	105.71	111.36
1	B	127	GLY	N-CA-C	5.11	120.47	111.57
1	A	124	ALA	CA-C-O	-5.10	115.69	121.25
1	B	57	ARG	N-CA-C	5.05	119.65	111.37

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	ALA	Peptide
1	B	124	ALA	Peptide

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	2297	0	2243	20	0
1	B	2298	0	2246	28	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	10	0	0	0	0
4	A	8	0	14	0	0
5	A	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	151	0	0	0	0
6	B	137	0	0	2	0
All	All	4911	0	4511	48	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 5.

All (48) 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:B:270:ARG:HD3	1:B:276:GLN:NE2	2.12	0.65
1:A:125:GLU:OE1	1:A:158:HIS:HB2	1.99	0.62
1:B:148:HIS:HE1	6:B:372:HOH:O	1.86	0.59
1:B:148:HIS:HD2	1:B:153:ARG:O	1.88	0.56
1:B:227:HIS:HE1	1:B:272:SER:OG	1.88	0.56
1:B:242:MET:HE2	1:B:260:TYR:HB3	1.88	0.56
1:B:125:GLU:OE1	1:B:158:HIS:HB2	2.06	0.56
1:A:41:ASN:O	1:A:45:THR:HG23	2.07	0.55
1:B:270:ARG:HH11	1:B:276:GLN:HE22	1.54	0.55
1:B:40:MET:O	1:B:44:MET:HG3	2.05	0.55
1:A:214:ASN:ND2	1:A:219:ASP:H	2.05	0.54
1:A:23:LYS:O	1:A:24:ASN:HB2	2.08	0.53
1:B:286:ASN:HB2	1:B:287:PRO:HD3	1.89	0.53
1:B:270:ARG:HD3	1:B:276:GLN:HE22	1.74	0.53
1:B:164:MET:O	1:B:168:GLN:HG3	2.10	0.52
1:A:57:ARG:HH12	5:A:529:GOL:H31	1.76	0.51
1:B:23:LYS:O	1:B:24:ASN:HB2	2.10	0.50
1:A:286:ASN:HB2	1:A:287:PRO:HD3	1.94	0.50
1:A:12:HIS:CG	1:A:54:MET:HG3	2.47	0.49
1:A:214:ASN:HA	1:A:217:TYR:O	2.13	0.49
1:B:166:LEU:HD13	1:B:199:MET:HG3	1.93	0.49
1:A:62:ASN:HD22	1:A:62:ASN:C	2.22	0.48
1:B:8:TYR:HB2	1:B:48:VAL:HA	1.95	0.48
1:A:196:ILE:HA	1:A:199:MET:HE3	1.95	0.47
1:B:166:LEU:HD13	1:B:199:MET:CG	2.45	0.47
1:A:12:HIS:CD2	1:A:54:MET:HG3	2.50	0.47
1:B:25:ASN:ND2	1:B:27:ASP:H	2.13	0.47
1:B:15:LEU:O	1:B:36:ILE:HD13	2.14	0.46
1:B:229:LEU:HD13	1:B:238:VAL:HG21	1.98	0.45
1:B:12:HIS:CD2	1:B:54:MET:HG3	2.51	0.45
1:A:36:ILE:CD1	1:A:258:TYR:HE1	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ASN:HA	1:B:217:TYR:O	2.17	0.44
1:A:8:TYR:HB2	1:A:48:VAL:HA	2.00	0.44
1:B:86:ASP:HA	1:B:89:PHE:CD2	2.54	0.43
1:A:25:ASN:ND2	1:A:27:ASP:H	2.16	0.43
1:A:62:ASN:ND2	1:A:65:PHE:H	2.16	0.43
1:A:214:ASN:HD21	1:A:219:ASP:CG	2.27	0.43
1:B:12:HIS:CG	1:B:54:MET:HG3	2.54	0.43
1:A:128:THR:HG21	1:A:133:ILE:HG12	2.01	0.42
1:A:244:ILE:HD12	1:A:249:HIS:HB3	2.01	0.42
1:A:242:MET:HE2	1:A:260:TYR:HB3	2.01	0.41
1:A:86:ASP:HA	1:A:89:PHE:CD2	2.55	0.41
1:B:70:MET:HE2	1:B:77:VAL:HB	2.02	0.41
1:B:110:GLU:O	1:B:119:LYS:HE3	2.21	0.41
1:B:99:GLN:HE21	1:B:99:GLN:H	1.69	0.40
1:B:158:HIS:CD2	1:B:158:HIS:C	2.98	0.40
1:B:4:ASP:HA	1:B:5:PRO:HD2	1.97	0.40
1:B:235:LEU:HB2	6:B:347: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	289/291 (99%)	278 (96%)	10 (4%)	1 (0%)	36	22
1	B	289/291 (99%)	277 (96%)	11 (4%)	1 (0%)	36	22
All	All	578/582 (99%)	555 (96%)	21 (4%)	2 (0%)	36	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	84	TYR

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Mol	Chain	Res	Type
1	A	84	TYR

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	248/249 (100%)	244 (98%)	4 (2%)	55	41
1	B	249/249 (100%)	244 (98%)	5 (2%)	48	32
All	All	497/498 (100%)	488 (98%)	9 (2%)	51	36

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ILE
1	A	62	ASN
1	A	241	SER
1	A	267	PRO
1	B	56	ASN
1	B	99	GLN
1	B	166	LEU
1	B	235	LEU
1	B	241	SER

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

Mol	Chain	Res	Type
1	A	25	ASN
1	A	38	GLN
1	A	41	ASN
1	A	62	ASN
1	A	173	GLN
1	A	192	ASN
1	A	195	ASN
1	A	214	ASN

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Mol	Chain	Res	Type
1	A	268	GLN
1	B	25	ASN
1	B	32	GLN
1	B	56	ASN
1	B	99	GLN
1	B	148	HIS
1	B	150	GLN
1	B	227	HIS
1	B	253	ASN
1	B	268	GLN
1	B	276	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
3	SO4	A	295	-	4,4,4	0.89	0	6,6,6	0.40	0
3	SO4	A	294	-	4,4,4	0.92	0	6,6,6	0.38	0
5	GOL	A	529	-	5,5,5	1.01	0	5,5,5	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MPD	A	720	-	7,7,7	1.28	1 (14%)	9,10,10	3.04	4 (44%)

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
5	GOL	A	529	-	-	2/4/4/4	-
4	MPD	A	720	-	-	1/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	720	MPD	O2-C2	2.99	1.52	1.44

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	720	MPD	CM-C2-C1	7.70	127.86	110.63
4	A	720	MPD	O4-C4-C3	-2.78	100.29	111.35
4	A	720	MPD	O2-C2-CM	-2.77	99.34	107.99
4	A	720	MPD	O2-C2-C1	-2.68	99.64	107.99

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	529	GOL	O1-C1-C2-C3
5	A	529	GOL	O1-C1-C2-O2
4	A	720	MPD	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	529	GOL	1	0

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 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.