



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:55 PM GMT

PDB ID : 1PPI
Title : THE ACTIVE CENTER OF A MAMMALIAN ALPHA-AMYLASE. THE
STRUCTURE OF THE COMPLEX OF A PANCREATIC ALPHA-
AMYLASE WITH A CARBOHYDRATE INHIBITOR REFINED TO 2.2
ANGSTROMS RESOLUTION
Authors : Qian, M.; Haser, R.; Payan, F.
Deposited on : 1994-02-22
Resolution : 2.20 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>

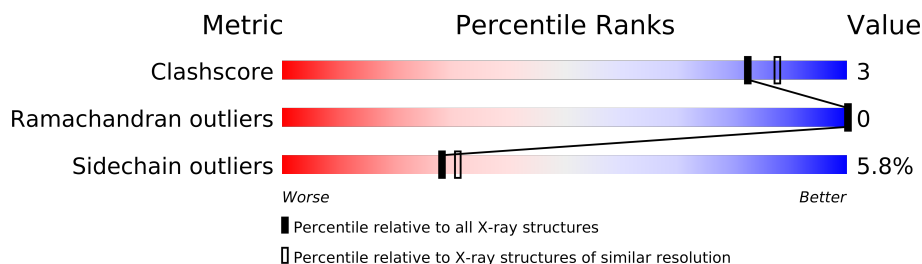
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **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 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	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	496	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4358 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 ALPHA-AMYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			3908	2469	687	731	21			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	VAL	ILE	CONFLICT	UNP P00690
A	243	LYS	GLN	CONFLICT	UNP P00690
A	310	SER	ALA	CONFLICT	UNP P00690

- Molecule 2 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	4	Total	C	N	O	0	0
			55	31	1	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	VAL	ILE	CONFLICT	UNP P00690
A	243	LYS	GLN	CONFLICT	UNP P00690
A	310	SER	ALA	CONFLICT	UNP P00690

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	393	Total 393	O 393	0	0

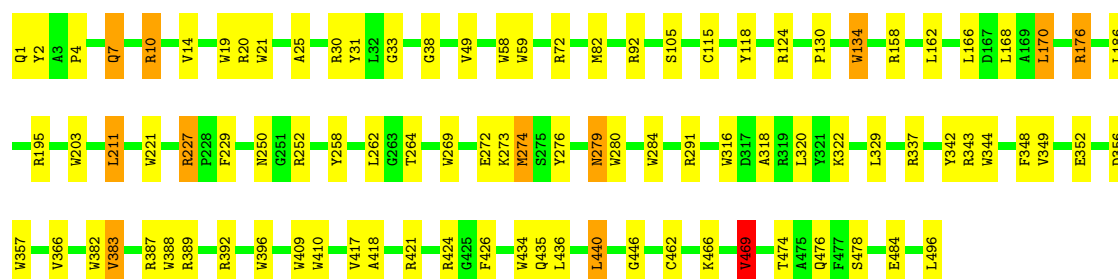
3 Residue-property plots

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: ALPHA-AMYLASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.30Å 87.80Å 103.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.153 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4358	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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: GLC, DAF, BGC, CA, CL

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	0.94	6/4018 (0.1%)	1.68	92/5459 (1.7%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2	TYR	CE1-CZ	-6.35	1.30	1.38
1	A	383	VAL	CA-CB	5.84	1.67	1.54
1	A	258	TYR	CE1-CZ	-5.24	1.31	1.38
1	A	469	VAL	CA-CB	5.14	1.65	1.54
1	A	276	TYR	CG-CD2	-5.12	1.32	1.39
1	A	434	TRP	CG-CD1	-5.11	1.29	1.36

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	343	ARG	NE-CZ-NH2	-18.81	110.90	120.30
1	A	72	ARG	NE-CZ-NH2	-15.34	112.63	120.30
1	A	343	ARG	NE-CZ-NH1	15.04	127.82	120.30
1	A	195	ARG	NE-CZ-NH1	13.80	127.20	120.30
1	A	72	ARG	NE-CZ-NH1	13.50	127.05	120.30
1	A	176	ARG	NE-CZ-NH1	12.67	126.64	120.30
1	A	252	ARG	NE-CZ-NH2	-11.94	114.33	120.30
1	A	195	ARG	NE-CZ-NH2	-11.30	114.65	120.30
1	A	252	ARG	NE-CZ-NH1	11.29	125.95	120.30
1	A	176	ARG	NE-CZ-NH2	-11.23	114.69	120.30
1	A	10	ARG	NE-CZ-NH1	9.81	125.20	120.30
1	A	434	TRP	CD1-CG-CD2	9.78	114.12	106.30
1	A	227	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	A	344	TRP	CD1-CG-CD2	9.38	113.80	106.30
1	A	337	ARG	NE-CZ-NH1	9.34	124.97	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280	TRP	CD1-CG-CD2	9.33	113.76	106.30
1	A	19	TRP	CD1-CG-CD2	9.25	113.70	106.30
1	A	58	TRP	CD1-CG-CD2	8.94	113.45	106.30
1	A	221	TRP	CD1-CG-CD2	8.79	113.33	106.30
1	A	203	TRP	CD1-CG-CD2	8.67	113.23	106.30
1	A	389	ARG	NE-CZ-NH1	8.45	124.53	120.30
1	A	134	TRP	CD1-CG-CD2	8.12	112.79	106.30
1	A	316	TRP	CD1-CG-CD2	8.10	112.78	106.30
1	A	10	ARG	NE-CZ-NH2	-8.01	116.30	120.30
1	A	382	TRP	CD1-CG-CD2	7.95	112.66	106.30
1	A	227	ARG	NE-CZ-NH1	7.95	124.27	120.30
1	A	284	TRP	CD1-CG-CD2	7.95	112.66	106.30
1	A	280	TRP	CE2-CD2-CG	-7.79	101.07	107.30
1	A	434	TRP	CE2-CD2-CG	-7.74	101.11	107.30
1	A	124	ARG	NE-CZ-NH2	-7.73	116.44	120.30
1	A	410	TRP	CD1-CG-CD2	7.65	112.42	106.30
1	A	409	TRP	CD1-CG-CD2	7.61	112.39	106.30
1	A	388	TRP	CD1-CG-CD2	7.59	112.37	106.30
1	A	316	TRP	CG-CD2-CE3	7.58	140.72	133.90
1	A	344	TRP	CE2-CD2-CG	-7.53	101.28	107.30
1	A	203	TRP	CE2-CD2-CG	-7.51	101.29	107.30
1	A	2	TYR	CB-CG-CD1	-7.48	116.51	121.00
1	A	284	TRP	CE2-CD2-CG	-7.45	101.34	107.30
1	A	59	TRP	CD1-CG-CD2	7.43	112.24	106.30
1	A	269	TRP	CD1-CG-CD2	7.42	112.24	106.30
1	A	221	TRP	CE2-CD2-CG	-7.39	101.38	107.30
1	A	316	TRP	CE2-CD2-CG	-7.35	101.42	107.30
1	A	389	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	A	134	TRP	CE2-CD2-CG	-7.32	101.44	107.30
1	A	59	TRP	CE2-CD2-CG	-7.28	101.47	107.30
1	A	58	TRP	CE2-CD2-CG	-7.21	101.53	107.30
1	A	19	TRP	CE2-CD2-CG	-7.17	101.56	107.30
1	A	396	TRP	CD1-CG-CD2	7.13	112.01	106.30
1	A	424	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	A	410	TRP	CE2-CD2-CG	-6.87	101.80	107.30
1	A	316	TRP	CB-CG-CD1	-6.84	118.11	127.00
1	A	21	TRP	CE2-CD2-CG	-6.83	101.83	107.30
1	A	21	TRP	CD1-CG-CD2	6.78	111.72	106.30
1	A	30	ARG	NE-CZ-NH2	-6.77	116.92	120.30
1	A	124	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	A	382	TRP	CE2-CD2-CG	-6.74	101.91	107.30
1	A	20	ARG	NE-CZ-NH1	6.73	123.66	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	396	TRP	CE2-CD2-CG	-6.72	101.92	107.30
1	A	409	TRP	CE2-CD2-CG	-6.70	101.94	107.30
1	A	357	TRP	CD1-CG-CD2	6.43	111.45	106.30
1	A	269	TRP	CE2-CD2-CG	-6.35	102.22	107.30
1	A	357	TRP	CE2-CD2-CG	-6.34	102.23	107.30
1	A	421	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	A	21	TRP	CG-CD2-CE3	6.15	139.44	133.90
1	A	342	TYR	CB-CG-CD2	-6.15	117.31	121.00
1	A	382	TRP	CG-CD2-CE3	6.14	139.43	133.90
1	A	30	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	59	TRP	CB-CG-CD1	-5.91	119.32	127.00
1	A	417	VAL	N-CA-CB	-5.87	98.58	111.50
1	A	388	TRP	CE2-CD2-CG	-5.87	102.61	107.30
1	A	14	VAL	CB-CA-C	-5.84	100.30	111.40
1	A	134	TRP	CB-CG-CD1	-5.81	119.44	127.00
1	A	356	ASP	CB-CG-OD1	5.78	123.51	118.30
1	A	280	TRP	CB-CG-CD1	-5.76	119.51	127.00
1	A	280	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	A	118	TYR	CB-CG-CD2	-5.61	117.64	121.00
1	A	284	TRP	CG-CD2-CE3	5.54	138.89	133.90
1	A	382	TRP	CB-CG-CD1	-5.46	119.90	127.00
1	A	410	TRP	CB-CG-CD1	-5.43	119.94	127.00
1	A	58	TRP	CB-CG-CD1	-5.37	120.02	127.00
1	A	59	TRP	CG-CD2-CE3	5.30	138.67	133.90
1	A	476	GLN	CB-CG-CD	5.29	125.35	111.60
1	A	410	TRP	CG-CD2-CE3	5.27	138.64	133.90
1	A	387	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	A	274	MET	CG-SD-CE	-5.21	91.87	100.20
1	A	357	TRP	CG-CD1-NE1	-5.14	104.96	110.10
1	A	134	TRP	CG-CD2-CE3	5.12	138.51	133.90
1	A	273	LYS	CB-CG-CD	-5.12	98.29	111.60
1	A	203	TRP	CG-CD1-NE1	-5.09	105.01	110.10
1	A	58	TRP	CG-CD2-CE3	5.08	138.47	133.90
1	A	158	ARG	CA-CB-CG	-5.06	102.27	113.40
1	A	280	TRP	CG-CD1-NE1	-5.01	105.09	110.10

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	3908	0	3687	23	0
2	A	55	0	45	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	393	0	0	0	0
All	All	4358	0	3732	24	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 (24) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:446:GLY:HA2	1:A:469:VAL:HG22	1.67	0.76
1:A:170:LEU:O	1:A:176:ARG:HD2	1.92	0.70
1:A:7:GLN:HB3	1:A:10:ARG:HD3	1.84	0.59
1:A:7:GLN:HE21	1:A:10:ARG:HD2	1.68	0.57
1:A:279:ASN:H	1:A:279:ASN:HD22	1.55	0.55
1:A:10:ARG:HB3	1:A:38:GLY:HA2	1.88	0.55
1:A:31:TYR:OH	1:A:392:ARG:HG3	2.07	0.53
2:A:992:DAF:H3H	2:A:992:DAF:H6	1.91	0.52
1:A:1:GLN:HG3	1:A:250:ASN:O	2.11	0.51
1:A:4:PRO:HA	1:A:229:PHE:CG	2.47	0.50
1:A:436:LEU:O	1:A:478:SER:HA	2.13	0.48
1:A:105:SER:HB3	1:A:166:LEU:HD21	1.99	0.45
1:A:318:ALA:O	1:A:322:LYS:HE3	2.18	0.44
1:A:10:ARG:HH22	1:A:33:GLY:HA2	1.83	0.44
1:A:25:ALA:HB2	1:A:82:MET:HA	1.99	0.43
1:A:10:ARG:NH2	1:A:33:GLY:HA2	2.33	0.43
1:A:440:LEU:O	1:A:474:THR:HA	2.19	0.43
1:A:348:PHE:HA	1:A:352:GLU:O	2.18	0.43
1:A:1:GLN:NE2	1:A:211:LEU:HG	2.33	0.42
1:A:291:ARG:HA	1:A:291:ARG:HD3	1.80	0.42
1:A:274:MET:HB3	1:A:274:MET:HE2	1.96	0.42
1:A:418:ALA:HB1	1:A:426:PHE:CZ	2.54	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:264:THR:HG22	1:A:272:GLU:HG3	2.02	0.41
1:A:462:CYS:SG	1:A:466:LYS:HG2	2.60	0.41

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	494/496 (100%)	483 (98%)	11 (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	413/413 (100%)	389 (94%)	24 (6%)	28	31

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	49	VAL
1	A	92	ARG
1	A	115	CYS
1	A	130	PRO
1	A	134	TRP
1	A	162	LEU
1	A	168	LEU

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Mol	Chain	Res	Type
1	A	170	LEU
1	A	186	LEU
1	A	211	LEU
1	A	227	ARG
1	A	262	LEU
1	A	279	ASN
1	A	320	LEU
1	A	329	LEU
1	A	349	VAL
1	A	366	VAL
1	A	383	VAL
1	A	435	GLN
1	A	440	LEU
1	A	469	VAL
1	A	484	GLU
1	A	496	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	53	ASN
1	A	75	ASN
1	A	279	ASN
1	A	373	ASN
1	A	399	ASN

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 ⓘ

4 carbohydrates 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	$\# Z > 2$
2	GLC	A	990	2	10,11,12	0.83	0	11,15,17	1.02	0
2	GLC	A	991	2	10,11,12	0.63	0	11,15,17	1.26	1 (9%)
2	DAF	A	992	2	21,22,23	4.71	9 (42%)	28,32,34	2.87	9 (32%)
2	BGC	A	993	2	12,12,12	0.82	0	17,17,17	1.33	3 (17%)

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	GLC	A	990	2	-	0/2/19/22	0/1/1/1
2	GLC	A	991	2	-	0/2/19/22	0/1/1/1
2	DAF	A	992	2	-	2/6/43/46	0/2/2/2
2	BGC	A	993	2	-	0/2/22/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	992	DAF	C6-C5	12.63	1.49	1.31
2	A	992	DAF	O4H-C4H	11.71	1.43	1.22
2	A	992	DAF	O7H-C7H	9.29	1.43	1.22
2	A	992	DAF	O5-C5	6.03	1.43	1.36
2	A	992	DAF	C1H-C6H	3.15	1.54	1.50
2	A	992	DAF	C5H-C4H	3.04	1.53	1.45
2	A	992	DAF	C7H-C5H	2.61	1.52	1.45
2	A	992	DAF	C3H-C4H	2.10	1.55	1.52
2	A	992	DAF	C4-C5	2.05	1.53	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	992	DAF	O7H-C7H-C5H	-8.23	107.04	125.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	992	DAF	O4H-C4H-C5H	-8.04	107.32	122.90
2	A	992	DAF	O4H-C4H-C3H	-6.32	111.41	119.76
2	A	992	DAF	C6H-C1H-N4	3.34	116.02	111.19
2	A	993	BGC	O4-C4-C3	-3.17	103.25	110.35
2	A	992	DAF	O5-C5-C6	-2.90	107.50	118.30
2	A	991	GLC	C4-C3-C2	-2.59	107.03	110.50
2	A	992	DAF	C4-C5-C6	-2.53	111.07	123.11
2	A	993	BGC	C4-C3-C2	-2.42	106.35	110.82
2	A	993	BGC	C1-C2-C3	-2.41	106.72	110.53
2	A	992	DAF	C6H-C5H-C4H	2.29	123.99	118.76
2	A	992	DAF	O2H-C2H-C1H	2.28	113.87	109.09
2	A	992	DAF	O2-C2-C3	-2.01	105.83	110.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	992	DAF	O7H-C7H-C5H-C6H
2	A	992	DAF	O7H-C7H-C5H-C4H

There are no ring outliers.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.