



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:17 PM UTC

PDB ID : 1CSS / pdb_00001css
Title : ALPHA-FLUORO ACID AND ALPHA-FLUORO AMIDE ANALOGS OF ACETYL-COA AS INHIBITORS OF OF CITRATE SYNTHASE: EFFECT OF PKA MATCHING ON BINDING AFFINITY AND HYDROGEN BOND LENGTH
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Deposited on : 1995-08-04
Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

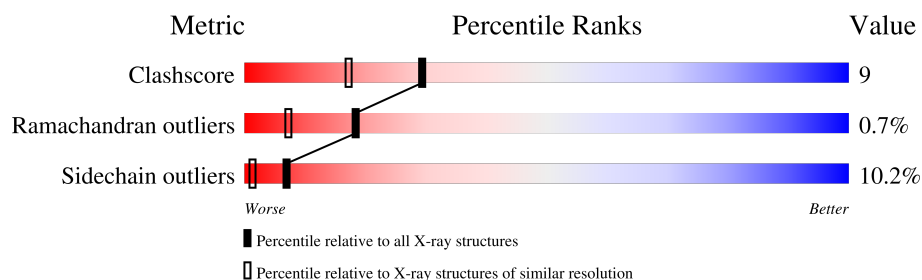
1 Overall quality at a glance

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	435	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FCX	A	700[2]	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3603 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.

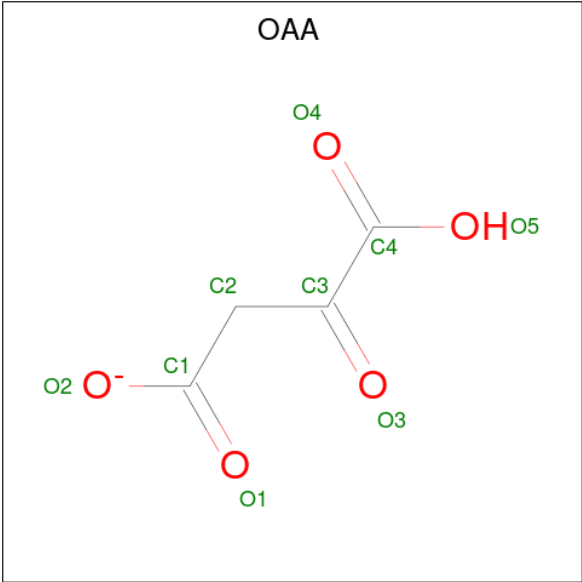
- Molecule 1 is a protein called CITRATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	0	0
			3391	2167	583	625	16			

There are 25 discrepancies between the modelled and reference sequences:

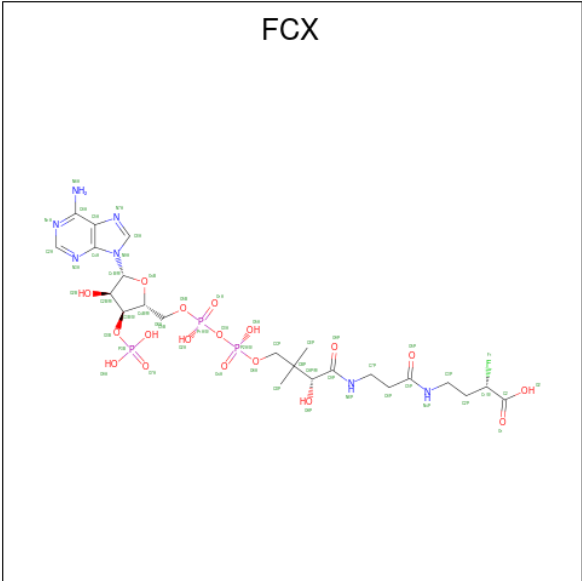
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	VAL	ILE	conflict	UNP P23007
A	12	SER	ASP	conflict	UNP P23007
A	32	ALA	VAL	conflict	UNP P23007
A	41	SER	MET	conflict	UNP P23007
A	52	ILE	VAL	conflict	UNP P23007
A	69	PHE	TYR	conflict	UNP P23007
A	77	LEU	MET	conflict	UNP P23007
A	82	GLY	LYS	conflict	UNP P23007
A	104	PRO	GLU	conflict	UNP P23007
A	110	VAL	LEU	conflict	UNP P23007
A	163	ASN	HIS	conflict	UNP P23007
A	170	PHE	LEU	conflict	UNP P23007
A	171	VAL	ILE	conflict	UNP P23007
A	175	ALA	CYS	conflict	UNP P23007
A	196	ALA	GLU	conflict	UNP P23007
A	222	PRO	ALA	conflict	UNP P23007
A	283	LEU	VAL	conflict	UNP P23007
A	286	SER	THR	conflict	UNP P23007
A	291	ASP	GLU	conflict	UNP P23007
A	292	LEU	VAL	conflict	UNP P23007
A	294	ALA	LYS	conflict	UNP P23007
A	296	ALA	VAL	conflict	UNP P23007
A	343	SER	HIS	conflict	UNP P23007
A	428	ALA	ASP	conflict	UNP P23007
A	431	GLU	ILE	conflict	UNP P23007

- Molecule 2 is OXALOACETATE ION (CCD ID: OAA) (formula: C₄H₃O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			9	4	5		

- Molecule 3 is ALPHA-FLUORO-CARBOXYMETHYLDETHIA COENZYME A COM-
PLEX (CCD ID: FCX) (formula: $C_{23}H_{37}FN_7O_{18}P_3$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	P	0	1
			58	26	2	7	20	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	145	Total 145	O 145	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: CITRATE SYNTHASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	104.39Å 78.43Å 58.47Å 90.00° 78.86° 90.00°	Depositor
Resolution (Å)	25.00 – 1.70	Depositor
% Data completeness (in resolution range)	86.0 (25.00-1.70)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.165 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3603	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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: OAA, FCX

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	1.19	1/3476 (0.0%)	1.80	68/4721 (1.4%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	61	ASP	CG-OD1	5.19	1.35	1.25

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	356	ILE	N-CA-C	11.49	121.21	111.90
1	A	64	ILE	N-CA-C	9.44	122.05	109.21
1	A	236	SER	N-CA-C	9.38	122.37	111.11
1	A	315	VAL	N-CA-C	-9.28	99.11	107.56
1	A	54	GLU	N-CA-C	8.83	123.36	112.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	ASP	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	3391	0	3370	59	0
2	A	9	0	2	0	0
3	A	58	0	10	1	0
4	A	145	0	0	1	1
All	All	3603	0	3382	59	1

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.

The worst 5 of 59 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:136:HIS:HD2	1:A:138:MET:H	1.19	0.88
1:A:350:VAL:HG21	1:A:380:VAL:HG21	1.59	0.84
1:A:204:ASP:H	1:A:212:ASN:HD21	1.35	0.74
1:A:136:HIS:CD2	1:A:138:MET:H	2.04	0.74
1:A:40:MET:HE2	1:A:48:MET:HG2	1.69	0.74

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:566:HOH:O	4:A:566:HOH:O[2_555]	0.88	1.32

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	433/435 (100%)	421 (97%)	9 (2%)	3 (1%)	18 7

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	ALA
1	A	435	ALA
1	A	293	GLY

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	361/361 (100%)	324 (90%)	37 (10%)	7 1

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	346	MET
1	A	425	MET
1	A	348	LYS
1	A	368	LYS
1	A	193	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	289	GLN
1	A	391	ASN
1	A	364	GLN
1	A	192	ASN
1	A	278	ASN

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](#)

3 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	FCX	A	700[2]	-	51,54,54	1.04	3 (5%)	71,81,81	1.34	9 (12%)
3	FCX	A	700[1]	-	51,54,54	0.94	2 (3%)	71,81,81	1.36	9 (12%)
2	OAA	A	702	-	8,8,8	0.58	0	8,10,10	1.98	2 (25%)

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	FCX	A	700[2]	-	1/1/13/15	3/54/70/70	0/3/3/3
3	FCX	A	700[1]	-	-	6/54/70/70	0/3/3/3
2	OAA	A	702	-	-	2/8/8/8	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	700[2]	FCX	C1-C2	-3.47	1.48	1.52
3	A	700[1]	FCX	P3B-O3B	2.65	1.64	1.59
3	A	700[2]	FCX	P3B-O3B	2.65	1.64	1.59
3	A	700[1]	FCX	C5P-N4P	2.34	1.38	1.33
3	A	700[2]	FCX	C5P-N4P	2.34	1.38	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	702	OAA	O3-C3-C2	3.77	126.22	120.41
3	A	700[1]	FCX	O4B-C1B-C2B	-3.72	98.66	106.62
3	A	700[2]	FCX	O4B-C1B-C2B	-3.72	98.66	106.62
3	A	700[1]	FCX	C2B-C1B-N9A	-3.38	104.90	113.30
3	A	700[2]	FCX	C2B-C1B-N9A	-3.38	104.90	113.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	700[2]	FCX	C1

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	700[1]	FCX	F1-C1-C2P-C3P
3	A	700[1]	FCX	C2-C1-C2P-C3P
3	A	700[1]	FCX	F1-C1-C2-O1
3	A	700[1]	FCX	F1-C1-C2-O2
3	A	700[2]	FCX	F1-C1-C2-O1

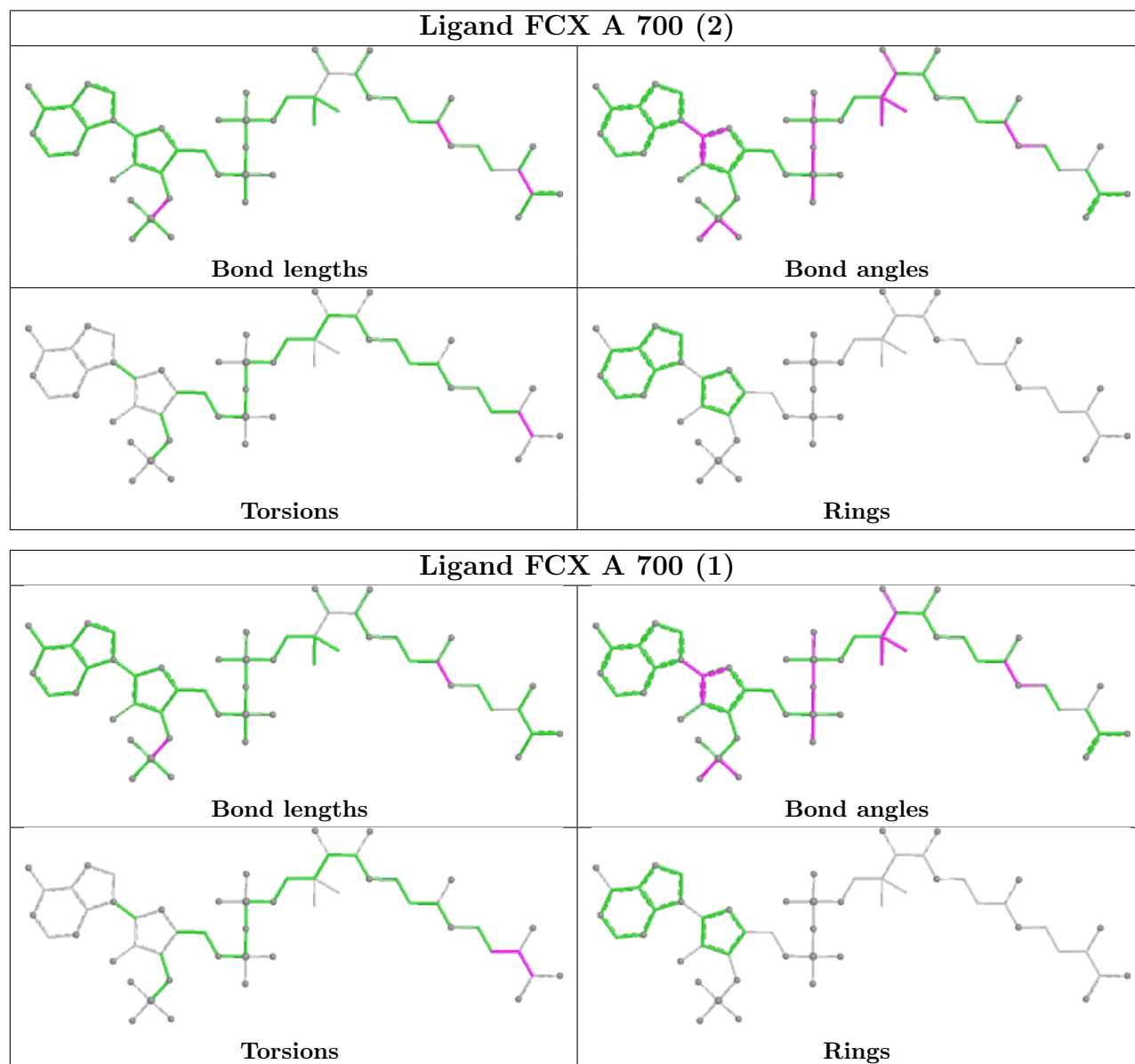
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	700[1]	FCX	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.