Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:52 PM GMT

PDB ID	:	4ASL
Title	:	Structure of Epa1A in complex with the T-antigen (Gal-b1-3- GalNAc)
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Deposited on	:	2012-05-02
Resolution	:	1.24 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:

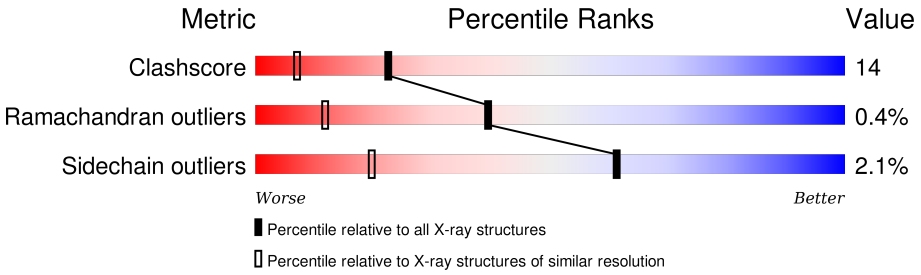
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	FAILED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.24 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	1327 (1.28-1.20)
Ramachandran outliers	100387	1274 (1.28-1.20)
Sidechain outliers	100360	1272 (1.28-1.20)

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. 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 <=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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	259	75% 12% • 12%

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	NGA	A	1270	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2484 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 EPA1P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	35	0
			2028	1324	314	379	11			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	SER	-	EXPRESSION TAG	UNP Q6VBJ0
A	14	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	15	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	16	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	17	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	18	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	19	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	20	SER	-	EXPRESSION TAG	UNP Q6VBJ0
A	21	SER	-	EXPRESSION TAG	UNP Q6VBJ0
A	22	GLY	-	EXPRESSION TAG	UNP Q6VBJ0
A	23	LEU	-	EXPRESSION TAG	UNP Q6VBJ0
A	24	VAL	-	EXPRESSION TAG	UNP Q6VBJ0
A	25	PRO	-	EXPRESSION TAG	UNP Q6VBJ0
A	26	ARG	-	EXPRESSION TAG	UNP Q6VBJ0
A	27	GLY	-	EXPRESSION TAG	UNP Q6VBJ0
A	28	SER	-	EXPRESSION TAG	UNP Q6VBJ0
A	29	HIS	-	EXPRESSION TAG	UNP Q6VBJ0
A	30	MET	-	EXPRESSION TAG	UNP Q6VBJ0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

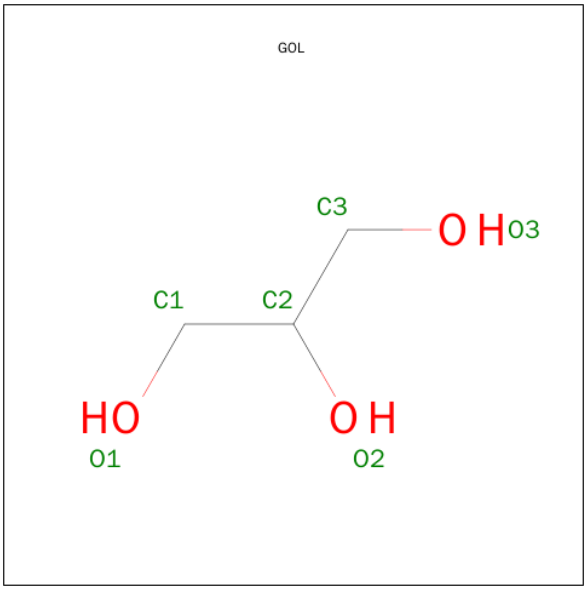
- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total C N O 26 14 1 11	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total Na 5 5	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	402	Total O 412 412	0	10

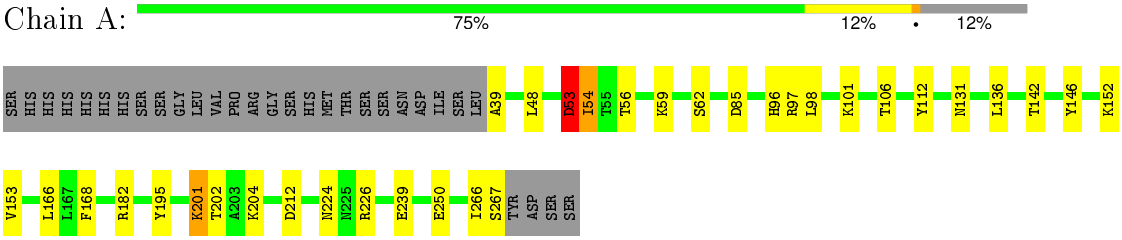
3 Residue-property plots (i)

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 failed to run properly.

- Molecule 1: EPA1P

Chain A:



4 Data and refinement statistics (i)

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	74.60Å 103.90Å 69.40Å 89.90° 90.00° 89.90°	Depositor
Resolution (Å)	10.00 – 1.24	Depositor
% Data completeness (in resolution range)	98.5 (10.00-1.24)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.117 , 0.155	Depositor
Wilson B-factor (Å^2)	12.3	Xtriage
Anisotropy	0.287	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 82969 reflections	Xtriage
Total number of atoms	2484	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CA, GAL, NGA, NA

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	0.64	0/2181	0.80	3/2962 (0.1%)

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
3	A	1	0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	53[A]	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	53[B]	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	226	ARG	NE-CZ-NH2	-5.10	117.75	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1270	NGA	C3

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	2028	0	1978	51	0
2	A	1	0	0	0	0
3	A	26	0	20	1	0
4	A	5	0	0	0	0
5	A	12	0	15	5	0
6	A	412	0	0	31	1
All	All	2484	0	2013	56	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 14.

All (56) 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:166[B]:LEU:HD11	1:A:168:PHE:CE1	1.63	1.31
1:A:112[B]:TYR:CE2	6:A:2201:HOH:O	1.84	1.27
5:A:1275:GOL:H11	6:A:2397:HOH:O	1.11	1.27
1:A:239[B]:GLU:HG2	6:A:2268:HOH:O	1.35	1.24
1:A:201[A]:LYS:NZ	6:A:2305:HOH:O	1.63	1.24
1:A:153[A]:VAL:HG12	6:A:2263:HOH:O	1.39	1.18
1:A:97[B]:ARG:NH1	6:A:2174:HOH:O	1.79	1.14
1:A:62[B]:SER:OG	6:A:2066:HOH:O	1.71	1.07
1:A:112[B]:TYR:CZ	6:A:2201:HOH:O	1.98	1.06
1:A:85[A]:ASP:OD2	6:A:2134:HOH:O	1.76	1.03
1:A:101[B]:LYS:NZ	1:A:146[B]:TYR:OH	1.92	1.02
1:A:166[B]:LEU:CD1	1:A:168:PHE:CE1	2.50	0.94
1:A:202[B]:THR:OG1	6:A:2316:HOH:O	1.91	0.87
3:A:1270:NGA:O7	6:A:2116:HOH:O	1.96	0.83
1:A:152[B]:LYS:NZ	1:A:250[B]:GLU:OE1	2.12	0.82
1:A:166[B]:LEU:HD11	1:A:168:PHE:CZ	2.15	0.81
1:A:239[B]:GLU:CG	6:A:2268:HOH:O	2.07	0.78
1:A:166[B]:LEU:HD11	1:A:168:PHE:CD1	2.19	0.78
1:A:212:ASP:OD2	1:A:266:ILE:HD11	1.85	0.75
5:A:1276:GOL:C1	6:A:2164:HOH:O	2.42	0.68
1:A:142:THR:OG1	1:A:224[B]:ASN:ND2	2.30	0.65
1:A:202[A]:THR:HG22	6:A:2316:HOH:O	1.99	0.62
1:A:204:LYS:NZ	6:A:2317:HOH:O	2.23	0.61
5:A:1276:GOL:H11	6:A:2164:HOH:O	2.02	0.59
1:A:202[A]:THR:CG2	6:A:2316:HOH:O	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59[B]:LYS:HE2	1:A:106:THR:HG21	1.85	0.59
1:A:182[B]:ARG:NH2	6:A:2291:HOH:O	2.36	0.58
1:A:101[A]:LYS:NZ	6:A:2066:HOH:O	2.36	0.56
1:A:202[A]:THR:HB	6:A:2316:HOH:O	2.06	0.55
1:A:146[A]:TYR:CZ	1:A:182[A]:ARG:CZ	2.90	0.55
1:A:204:LYS:CE	6:A:2317:HOH:O	2.55	0.53
1:A:202[B]:THR:CB	6:A:2316:HOH:O	2.54	0.52
1:A:56[A]:THR:HG22	6:A:2043:HOH:O	2.09	0.52
1:A:96[B]:HIS:CD2	6:A:2078:HOH:O	2.63	0.51
5:A:1275:GOL:O3	6:A:2342:HOH:O	2.19	0.51
1:A:202[B]:THR:CG2	6:A:2305:HOH:O	2.60	0.50
1:A:202[A]:THR:CB	6:A:2316:HOH:O	2.59	0.50
1:A:146[A]:TYR:CE1	1:A:182[A]:ARG:NE	2.80	0.49
1:A:131[B]:ASN:ND2	6:A:2250:HOH:O	2.25	0.49
1:A:39:ALA:HB2	1:A:48:LEU:HD12	1.94	0.49
1:A:39:ALA:CB	1:A:48:LEU:HD12	2.45	0.47
1:A:202[B]:THR:HG22	6:A:2305:HOH:O	2.15	0.47
1:A:201[B]:LYS:HG2	6:A:2170[B]:HOH:O	2.15	0.46
1:A:152[A]:LYS:HZ2	1:A:152[A]:LYS:HG2	1.60	0.43
1:A:195:TYR:CE1	1:A:202[B]:THR:HG21	2.53	0.43
1:A:201[B]:LYS:CE	1:A:201[B]:LYS:HA	2.49	0.43
1:A:54[B]:ILE:HD11	6:A:2049:HOH:O	2.18	0.42
1:A:168:PHE:CD1	1:A:195:TYR:HB2	2.54	0.42
1:A:62[B]:SER:HB3	1:A:146[B]:TYR:CE1	2.56	0.41
1:A:98:LEU:HB2	5:A:1276:GOL:H11	2.02	0.41
1:A:266:ILE:O	1:A:267:SER:HB2	2.21	0.41
1:A:131[B]:ASN:HA	1:A:131[B]:ASN:HD22	1.59	0.40

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)
6:A:2046:HOH:O	6:A:2202:HOH:O[8_455]	2.18	0.02

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	263/259 (102%)	253 (96%)	8 (3%)	2 (1%)	24 4

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53[A]	ASP
1	A	53[B]	ASP

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	229/224 (102%)	222 (97%)	7 (3%)	47 9

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53[A]	ASP
1	A	53[B]	ASP
1	A	54[A]	ILE
1	A	54[B]	ILE
1	A	136	LEU
1	A	201[A]	LYS
1	A	201[B]	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	HIS
1	A	170	ASN
1	A	191	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

2 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	$\#\|Z\| > 2$
3	GAL	A	1269	3,2	12,12,12	0.63	0	17,17,17	0.82	0
3	NGA	A	1270	3	14,14,15	25.61	1 (7%)	15,19,21	11.55	3 (20%)

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	GAL	A	1269	3,2	-	0/2/22/22	0/1/1/1
3	NGA	A	1270	3	1/1/5/7	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1270	NGA	O3-C3	95.82	3.72	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1270	NGA	O3-C3-C2	-44.06	21.83	109.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1270	NGA	O3-C3-C4	-6.41	95.90	110.34
3	A	1270	NGA	O5-C5-C6	2.23	112.18	107.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1270	NGA	C3

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1270	NGA	1	0

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 6 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	$\#\|Z\| > 2$
5	GOL	A	1275	-	5,5,5	0.56	0	5,5,5	0.41	0
5	GOL	A	1276	4	5,5,5	0.37	0	5,5,5	0.96	0

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	1275	-	-	0/4/4/4	0/0/0/0
5	GOL	A	1276	4	-	0/4/4/4	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.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1275	GOL	2	0
5	A	1276	GOL	3	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 failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers

EDS failed to run properly - this section will therefore be empty.