Full wwPDB X-ray Structure Validation Report ⓘ

Mar 19, 2025 – 01:27 PM EDT

PDB ID	:	1KNW
Title	:	Crystal structure of diaminopimelate decarboxylase
Authors	:	Levdikov, V.; Blagova, L.; Bose, N.; Momany, C.
Deposited on	:	2001-12-19
Resolution	:	2.10 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:

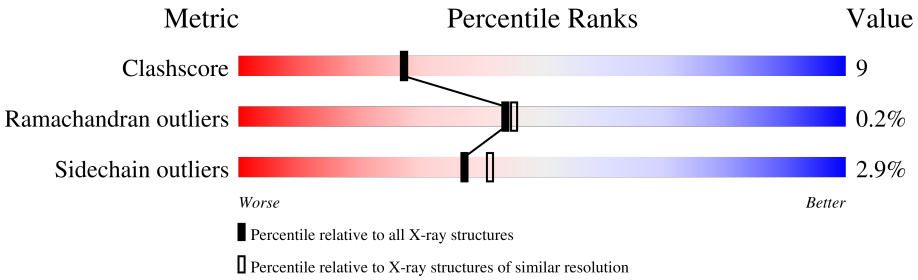
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

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 2.10 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	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	425	84% 13% ••

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3702 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.

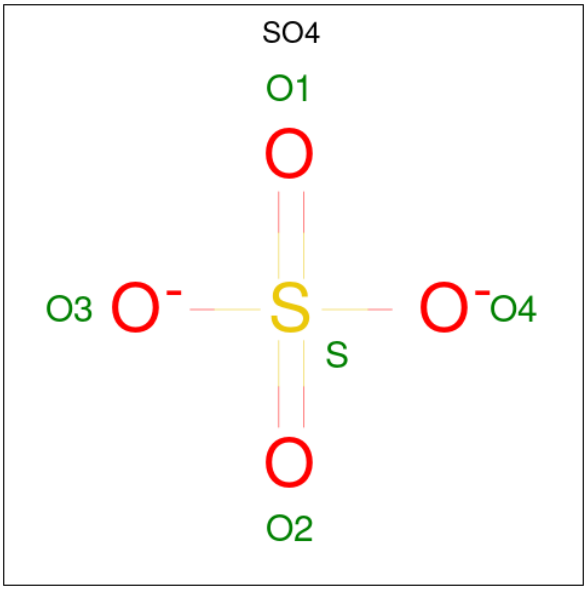
- Molecule 1 is a protein called Diaminopimelate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	421	3275	2055	595	613	12	0	2	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	421	HIS	-	expression tag	UNP P00861
A	422	HIS	-	expression tag	UNP P00861
A	423	HIS	-	expression tag	UNP P00861
A	424	HIS	-	expression tag	UNP P00861
A	425	HIS	-	expression tag	UNP P00861

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

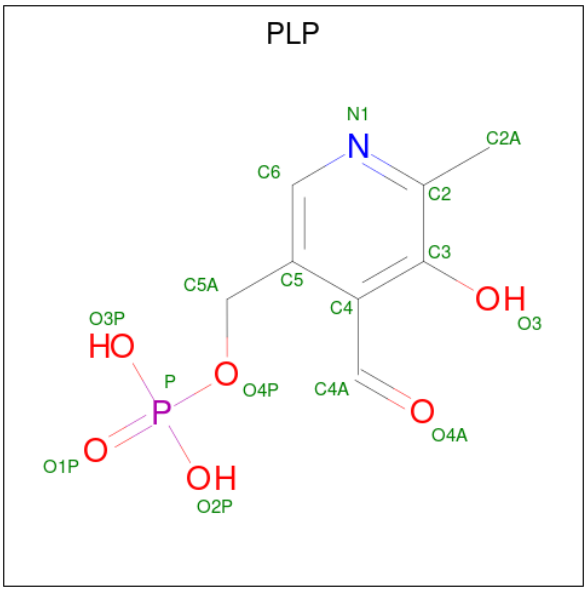


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	A	1	5	4	1		0	0

- Molecule 3 is LITHIUM ION (three-letter code: LI) (formula: Li).

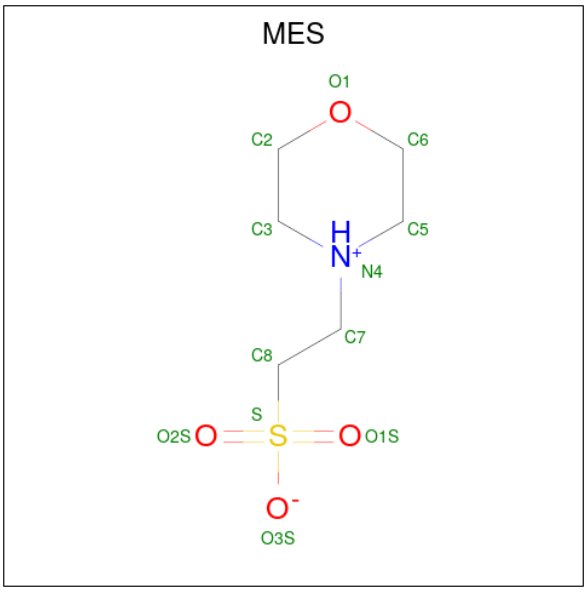
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Li 2 2	0	0

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 15 8 1 5 1	0	0

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 6 is water.

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

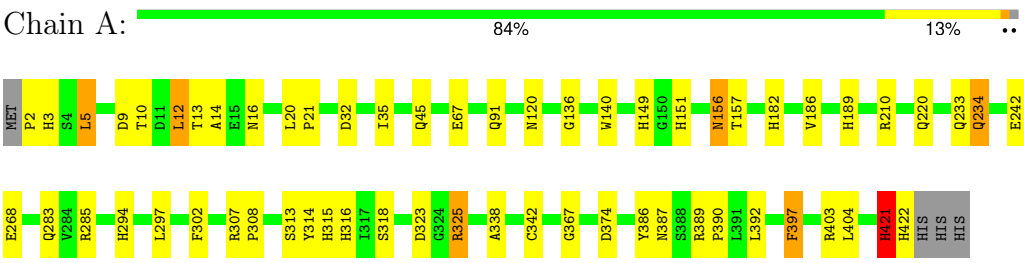
3 Residue-property plots (i)

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: Diaminopimelate decarboxylase

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	98.58Å 98.58Å 176.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.10	Depositor
% Data completeness (in resolution range)	98.0 (10.00-2.10)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.173 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3702	wwPDB-VP
Average B, all atoms (Å^2)	28.0	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, PLP, LI, MES

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	0.53	0/3355	0.70	0/4557

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	392	LEU	Mainchain
1	A	421	HIS	Mainchain

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	3275	0	3203	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5	0	0	0	0
3	A	2	0	0	0	0
4	A	15	0	6	1	0
5	A	12	0	12	0	0
6	A	393	0	0	8	0
All	All	3702	0	3221	59	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 9.

All (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:156:ASN:HD22	1:A:157:THR:H	1.12	0.93
1:A:149:HIS:H	1:A:156:ASN:HD21	1.28	0.80
1:A:156:ASN:HD22	1:A:157:THR:N	1.83	0.76
1:A:13:THR:HB	1:A:16:ASN:OD1	1.91	0.71
1:A:5:LEU:H	1:A:5:LEU:HD22	1.57	0.69
1:A:13:THR:HG22	1:A:14:ALA:H	1.60	0.67
1:A:283:GLN:HE21	1:A:367:GLY:HA2	1.65	0.62
1:A:5:LEU:HD21	1:A:318:SER:OG	2.00	0.61
1:A:307:ARG:HH11	1:A:315:HIS:CE1	2.19	0.61
1:A:421:HIS:O	1:A:422:HIS:HB2	2.02	0.59
1:A:186:VAL:HA	1:A:220[B]:GLN:NE2	2.17	0.59
1:A:13:THR:HG22	1:A:14:ALA:N	2.17	0.58
1:A:10:THR:HB	1:A:32:ASP:OD2	2.04	0.58
1:A:5:LEU:HD22	1:A:5:LEU:N	2.19	0.58
1:A:283:GLN:NE2	1:A:285:ARG:HH11	2.02	0.57
1:A:294:HIS:HE1	6:A:615:HOH:O	1.88	0.57
1:A:10:THR:HG21	1:A:35:ILE:HD11	1.86	0.56
1:A:323:ASP:OD1	1:A:325:ARG:HD2	2.06	0.56
1:A:3:HIS:NE2	1:A:12:LEU:HB3	2.21	0.55
1:A:2:PRO:HB3	1:A:374:ASP:OD2	2.08	0.54
1:A:2:PRO:HG3	1:A:316:HIS:CB	2.37	0.54
1:A:342:CYS:H	1:A:387:ASN:HD21	1.57	0.53
1:A:20:LEU:HD11	1:A:397:PHE:CE1	2.44	0.53
1:A:151:HIS:HB3	6:A:869:HOH:O	2.07	0.53
1:A:234:GLN:CD	1:A:234:GLN:H	2.12	0.53
1:A:67:GLU:HG3	6:A:757:HOH:O	2.08	0.53
1:A:233:GLN:HG2	1:A:314:TYR:CD2	2.44	0.52
1:A:20:LEU:N	1:A:21:PRO:HD2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:GLY:HA2	1:A:182:HIS:O	2.12	0.50
1:A:67:GLU:HB3	6:A:816:HOH:O	2.11	0.50
1:A:297:LEU:HD22	1:A:338:ALA:HB3	1.95	0.48
1:A:5:LEU:O	1:A:13:THR:HG23	2.13	0.48
1:A:16:ASN:O	1:A:20:LEU:HG	2.12	0.48
1:A:249:ASN:ND2	1:A:252:ARG:HE	2.10	0.48
1:A:2:PRO:HB2	6:A:907:HOH:O	2.14	0.47
1:A:20:LEU:HD11	1:A:397:PHE:HE1	1.81	0.44
1:A:120:ASN:HA	1:A:140:TRP:HB2	2.00	0.44
1:A:189:HIS:HE1	1:A:268:GLU:OE2	1.99	0.44
1:A:210:ARG:NH2	6:A:751:HOH:O	2.47	0.44
1:A:2:PRO:HA	6:A:642:HOH:O	2.17	0.44
1:A:2:PRO:HG3	1:A:316:HIS:HB2	2.00	0.43
1:A:249:ASN:HD22	1:A:252:ARG:HH11	1.65	0.43
1:A:249:ASN:HD22	1:A:252:ARG:HE	1.66	0.43
1:A:249:ASN:ND2	1:A:252:ARG:HH11	2.16	0.43
1:A:45:GLN:HE22	1:A:242:GLU:HA	1.84	0.43
1:A:186:VAL:HA	1:A:220[B]:GLN:HE22	1.83	0.43
1:A:342:CYS:H	1:A:387:ASN:ND2	2.16	0.42
1:A:307:ARG:HB2	1:A:308:PRO:HD3	2.01	0.42
1:A:307:ARG:HB3	1:A:313:SER:HB2	2.02	0.42
1:A:323:ASP:OD2	1:A:325:ARG:NH1	2.53	0.42
1:A:283:GLN:NE2	1:A:367:GLY:HA2	2.33	0.41
1:A:389:ARG:HA	1:A:390:PRO:HD3	1.70	0.41
1:A:5:LEU:H	1:A:5:LEU:CD2	2.30	0.41
1:A:3:HIS:HE2	1:A:12:LEU:HB3	1.86	0.41
1:A:268:GLU:OE2	4:A:554:PLP:N1	2.54	0.41
1:A:386:TYR:O	1:A:387:ASN:HB2	2.21	0.41
1:A:403:ARG:HG2	6:A:919:HOH:O	2.20	0.40
1:A:13:THR:CG2	1:A:14:ALA:N	2.85	0.40
1:A:283:GLN:NE2	1:A:285:ARG:NH1	2.67	0.40

There are no symmetry-related clashes.

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	421/425 (99%)	414 (98%)	6 (1%)	1 (0%)	44 45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	421	HIS

5.3.2 Protein sidechains (i)

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	348/350 (99%)	338 (97%)	10 (3%)	37 41

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	9	ASP
1	A	12	LEU
1	A	91	GLN
1	A	156	ASN
1	A	234	GLN
1	A	302	PHE
1	A	325	ARG
1	A	397	PHE
1	A	404	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	GLN
1	A	91	GLN
1	A	116	GLN

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Mol	Chain	Res	Type
1	A	156	ASN
1	A	189	HIS
1	A	211	GLN
1	A	249	ASN
1	A	283	GLN
1	A	289	GLN
1	A	294	HIS
1	A	315	HIS
1	A	373	HIS
1	A	387	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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
4	PLP	A	554	1	15,15,16	1.70	5 (33%)	21,22,23	1.86	7 (33%)
2	SO4	A	520	-	4,4,4	0.71	0	6,6,6	0.11	0
5	MES	A	510	-	12,12,12	2.70	5 (41%)	15,16,16	3.08	7 (46%)

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
4	PLP	A	554	1	-	0/6/6/8	0/1/1/1
5	MES	A	510	-	-	1/6/14/14	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	510	MES	C8-S	-7.23	1.67	1.77
5	A	510	MES	C3-C2	-3.72	1.36	1.50
4	A	554	PLP	O3-C3	-2.97	1.30	1.36
4	A	554	PLP	C2A-C2	2.64	1.54	1.50
4	A	554	PLP	C5-C4	2.49	1.43	1.40
5	A	510	MES	C3-N4	-2.34	1.40	1.46
4	A	554	PLP	C4A-C4	-2.22	1.47	1.51
4	A	554	PLP	C2-N1	2.17	1.37	1.33
5	A	510	MES	C7-C8	-2.13	1.46	1.52
5	A	510	MES	C5-C6	-2.09	1.42	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	510	MES	C2-C3-N4	5.53	118.53	110.12
5	A	510	MES	C5-N4-C3	5.11	119.86	108.84
5	A	510	MES	O1-C2-C3	4.96	122.45	111.77
5	A	510	MES	C6-C5-N4	4.81	117.43	110.12
4	A	554	PLP	C4A-C4-C5	-3.69	117.14	120.94
5	A	510	MES	C7-N4-C5	3.39	120.28	111.24
4	A	554	PLP	C5-C6-N1	-3.31	118.45	123.83
5	A	510	MES	O1-C6-C5	3.30	118.89	111.77
5	A	510	MES	C7-N4-C3	3.19	119.74	111.24
4	A	554	PLP	C6-C5-C4	3.08	120.62	118.10
4	A	554	PLP	C6-N1-C2	2.95	124.56	119.20
4	A	554	PLP	C4A-C4-C3	2.90	125.35	120.52
4	A	554	PLP	C2A-C2-C3	2.86	124.15	120.80
4	A	554	PLP	C3-C2-N1	-2.25	118.12	120.96

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	510	MES	C8-C7-N4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	554	PLP	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

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.