



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:05 AM GMT

PDB ID : 1XRC
Title : CRYSTAL STRUCTURE OF S-ADENOSYLMETHIONINE SYNTHETASE
Authors : Takusagawa, F.; Kamitori, S.; Misaki, S.; Markham, G.D.
Deposited on : 1995-10-26
Resolution : 3.00 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>

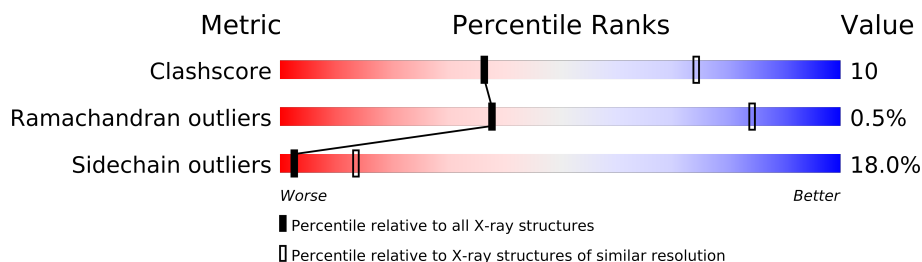
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.00 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	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)

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	383	

2 Entry composition i

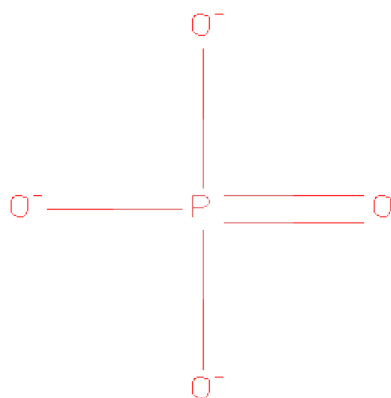
There are 4 unique types of molecules in this entry. The entry contains 3544 atoms, of which 632 are hydrogens and 0 are deuterium.

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 S-ADENOSYLMETHIONINE SYNTHETASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	377	Total	C	H	N	O	S	632	0	0
			3530	1830	632	495	560	13			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co).

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

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	K	0	0
			2	2		

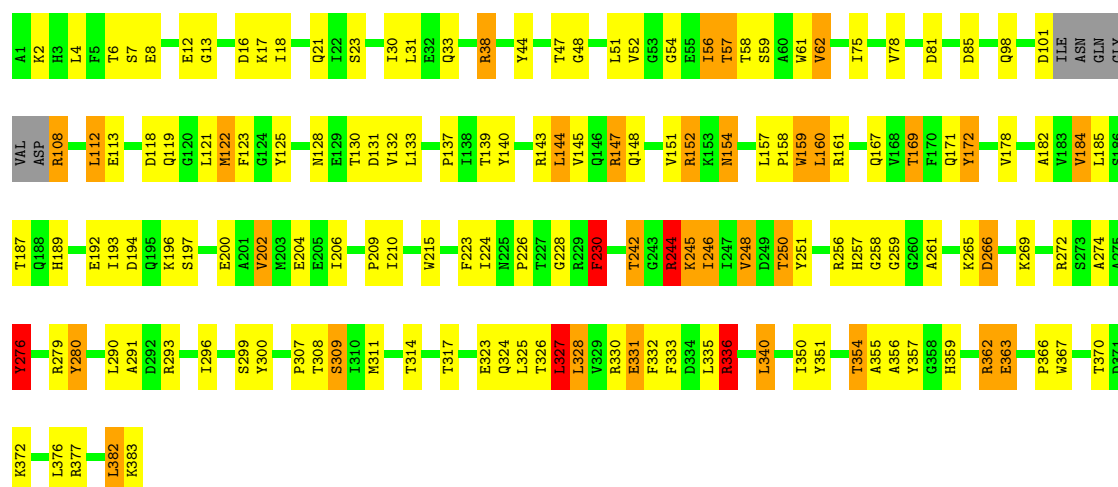
3 Residue-property plots

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: S-ADENOSYLMETHIONINE SYNTHETASE

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 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	128.90Å 128.90Å 139.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 3.00	Depositor
% Data completeness (in resolution range)	96.8 (10.00-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.197 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3544	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: K, CO, PO4

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	0.93	0/2956	1.72	52/4005 (1.3%)

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	19

There are no bond length outliers.

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	THR	CA-CB-CG2	9.86	126.20	112.40
1	A	161	ARG	NE-CZ-NH2	-9.69	115.45	120.30
1	A	215	TRP	CD1-CG-CD2	9.26	113.70	106.30
1	A	250	THR	N-CA-CB	-9.04	93.12	110.30
1	A	362	ARG	NE-CZ-NH2	-8.95	115.83	120.30
1	A	61	TRP	CD1-CG-CD2	8.40	113.02	106.30
1	A	159	TRP	CD1-CG-CD2	8.12	112.80	106.30
1	A	159	TRP	CE2-CD2-CG	-7.99	100.91	107.30
1	A	159	TRP	CG-CD2-CE3	7.70	140.83	133.90
1	A	61	TRP	CE2-CD2-CG	-7.57	101.25	107.30
1	A	159	TRP	CB-CG-CD1	-7.55	117.18	127.00
1	A	16	ASP	CB-CG-OD1	7.53	125.08	118.30
1	A	276	TYR	CB-CG-CD2	-7.52	116.49	121.00
1	A	8	GLU	CA-CB-CG	7.44	129.78	113.40
1	A	382	LEU	CA-CB-CG	7.29	132.06	115.30
1	A	336	ARG	NE-CZ-NH2	-7.21	116.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	TRP	CE2-CD2-CG	-7.20	101.54	107.30
1	A	327	LEU	CA-CB-CG	7.01	131.44	115.30
1	A	161	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	A	152	ARG	NE-CZ-NH2	-6.97	116.82	120.30
1	A	279	ARG	NE-CZ-NH2	-6.83	116.88	120.30
1	A	367	TRP	CD1-CG-CD2	6.57	111.55	106.30
1	A	331	GLU	OE1-CD-OE2	-6.40	115.61	123.30
1	A	367	TRP	CE2-CD2-CG	-6.40	102.18	107.30
1	A	108	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	A	362	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	A	230	PHE	CB-CG-CD2	-6.32	116.38	120.80
1	A	244	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	A	38	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	215	TRP	CG-CD1-NE1	-6.25	103.85	110.10
1	A	314	THR	N-CA-C	-6.25	94.13	111.00
1	A	293	ARG	NE-CZ-NH1	6.23	123.41	120.30
1	A	147	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	A	251	TYR	CB-CG-CD2	-5.89	117.47	121.00
1	A	261	ALA	CB-CA-C	-5.88	101.27	110.10
1	A	172	TYR	CB-CG-CD2	-5.87	117.48	121.00
1	A	256	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	A	160	LEU	CA-CB-CG	5.72	128.46	115.30
1	A	331	GLU	N-CA-CB	5.61	120.70	110.60
1	A	118	ASP	CB-CG-OD1	5.58	123.32	118.30
1	A	363	GLU	N-CA-C	5.47	125.76	111.00
1	A	78	VAL	N-CA-CB	-5.31	99.81	111.50
1	A	61	TRP	CG-CD1-NE1	-5.28	104.82	110.10
1	A	85	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	280	TYR	CA-C-N	5.19	128.61	117.20
1	A	159	TRP	CG-CD1-NE1	-5.13	104.97	110.10
1	A	61	TRP	CB-CG-CD1	-5.09	120.38	127.00
1	A	161	ARG	CA-C-N	5.08	131.32	117.10
1	A	172	TYR	CA-CB-CG	5.08	123.05	113.40
1	A	377	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	A	161	ARG	CB-CG-CD	5.07	124.77	111.60
1	A	351	TYR	CA-C-N	5.06	128.32	117.20

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	123	PHE	Sidechain

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Mol	Chain	Res	Type	Group
1	A	125	TYR	Peptide
1	A	140	TYR	Sidechain
1	A	194	ASP	Peptide
1	A	228	GLY	Peptide
1	A	230	PHE	Sidechain
1	A	244	ARG	Sidechain
1	A	259	GLY	Peptide
1	A	272	ARG	Sidechain
1	A	276	TYR	Sidechain
1	A	280	TYR	Sidechain
1	A	332	PHE	Sidechain
1	A	333	PHE	Sidechain
1	A	336	ARG	Sidechain
1	A	356	ALA	Peptide
1	A	362	ARG	Peptide
1	A	44	TYR	Sidechain
1	A	48	GLY	Peptide
1	A	54	GLY	Peptide

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	2898	632	2234	53	0
2	A	10	0	0	0	0
3	A	2	0	0	0	0
4	A	2	0	0	0	0
All	All	2912	632	2234	53	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 10.

All (53) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:265:LYS:HB3	1:A:269:LYS:HG3	1.60	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:257:HIS:HD2	1:A:258:GLY:O	1.69	0.76
1:A:23:SER:OG	1:A:242:THR:HG21	1.91	0.70
1:A:57:THR:HB	1:A:98:GLN:HB3	1.74	0.69
1:A:151:VAL:HA	1:A:154:ASN:ND2	2.09	0.66
1:A:56:ILE:HG23	1:A:58:THR:HG22	1.79	0.63
1:A:354:THR:HG23	1:A:359:HIS:NE2	2.13	0.62
1:A:324:GLN:O	1:A:328:LEU:HD23	2.01	0.61
1:A:244:ARG:O	1:A:246:ILE:HG22	2.03	0.59
1:A:204:GLU:O	1:A:209:PRO:HD3	2.02	0.59
1:A:245:LYS:HB3	1:A:248:VAL:HG13	1.86	0.58
1:A:324:GLN:O	1:A:327:LEU:HB3	2.06	0.56
1:A:30:ILE:HD11	1:A:56:ILE:HD11	1.86	0.56
1:A:130:THR:HG22	1:A:132:VAL:N	2.21	0.55
1:A:122:MET:HG3	1:A:274:ALA:HB3	1.89	0.55
1:A:328:LEU:HD12	1:A:376:LEU:HG	1.92	0.52
1:A:266:ASP:OD1	1:A:269:LYS:NZ	2.44	0.50
1:A:144:LEU:HD13	1:A:210:ILE:HG21	1.92	0.50
1:A:6:THR:OG1	1:A:169:THR:HB	2.11	0.50
1:A:223:PHE:HB3	1:A:226:PRO:HG3	1.93	0.49
1:A:147:ARG:HG2	1:A:206:ILE:HA	1.96	0.48
1:A:159:TRP:CE3	1:A:193:ILE:HG21	2.48	0.48
1:A:202:VAL:HG22	1:A:224:ILE:HD13	1.95	0.48
1:A:299:SER:OG	1:A:309:SER:HB3	2.13	0.48
1:A:169:THR:HG23	1:A:182:ALA:HB3	1.96	0.48
1:A:75:ILE:O	1:A:152:ARG:NH2	2.47	0.47
1:A:33:GLN:NE2	1:A:62:VAL:HG23	2.30	0.47
1:A:17:LYS:O	1:A:21:GLN:HG3	2.15	0.47
1:A:12:GLU:HG2	1:A:357:TYR:OH	2.14	0.47
1:A:108:ARG:HD2	1:A:113:GLU:O	2.14	0.46
1:A:290:LEU:HD23	1:A:325:LEU:CD2	2.45	0.46
1:A:112:LEU:HB3	1:A:336:ARG:NH2	2.31	0.45
1:A:7:SER:HB2	1:A:137:PRO:HB2	1.99	0.45
1:A:276:TYR:OH	1:A:359:HIS:HD2	1.98	0.45
1:A:17:LYS:HD2	1:A:355:ALA:O	2.17	0.45
1:A:157:LEU:HA	1:A:157:LEU:HD23	1.73	0.44
1:A:171:GLN:O	1:A:178:VAL:HG22	2.17	0.44
1:A:325:LEU:HA	1:A:325:LEU:HD23	1.80	0.43
1:A:128:ASN:HA	1:A:133:LEU:HD13	2.00	0.43
1:A:147:ARG:HD3	1:A:210:ILE:HD11	2.00	0.43
1:A:266:ASP:O	1:A:269:LYS:HG2	2.19	0.43
1:A:335:LEU:HA	1:A:340:LEU:CD1	2.48	0.43
1:A:13:GLY:HA2	1:A:18:ILE:HG12	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:300:TYR:CE1	1:A:307:PRO:HG3	2.54	0.43
1:A:291:ALA:HA	1:A:317:THR:O	2.19	0.42
1:A:157:LEU:HD22	1:A:159:TRP:CZ2	2.54	0.42
1:A:184:VAL:HA	1:A:223:PHE:O	2.20	0.42
1:A:2:LYS:HA	1:A:172:TYR:O	2.20	0.42
1:A:167:GLN:HB3	1:A:184:VAL:HG13	2.03	0.41
1:A:139:THR:O	1:A:143:ARG:HG3	2.20	0.41
1:A:189:HIS:HD2	1:A:193:ILE:HG23	1.86	0.41
1:A:290:LEU:HD23	1:A:325:LEU:HD21	2.02	0.40
1:A:296:ILE:HD13	1:A:296:ILE:HG21	1.83	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	373/383 (97%)	339 (91%)	32 (9%)	2 (0%)	38 84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	THR
1	A	363	GLU

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	306/311 (98%)	251 (82%)	55 (18%)	2 13

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	31	LEU
1	A	38	ARG
1	A	47	THR
1	A	51	LEU
1	A	52	VAL
1	A	56	ILE
1	A	57	THR
1	A	59	SER
1	A	62	VAL
1	A	81	ASP
1	A	101	ASP
1	A	112	LEU
1	A	119	GLN
1	A	121	LEU
1	A	122	MET
1	A	131	ASP
1	A	144	LEU
1	A	145	VAL
1	A	148	GLN
1	A	154	ASN
1	A	158	PRO
1	A	160	LEU
1	A	169	THR
1	A	184	VAL
1	A	185	LEU
1	A	187	THR
1	A	192	GLU
1	A	196	LYS
1	A	197	SER
1	A	200	GLU
1	A	202	VAL
1	A	230	PHE
1	A	242	THR
1	A	245	LYS
1	A	246	ILE
1	A	248	VAL
1	A	266	ASP
1	A	308	THR
1	A	309	SER
1	A	311	MET
1	A	323	GLU

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Mol	Chain	Res	Type
1	A	326	THR
1	A	327	LEU
1	A	328	LEU
1	A	330	ARG
1	A	331	GLU
1	A	340	LEU
1	A	350	ILE
1	A	354	THR
1	A	366	PRO
1	A	370	THR
1	A	372	LYS
1	A	382	LEU
1	A	383	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	70	ASN
1	A	154	ASN
1	A	189	HIS
1	A	257	HIS
1	A	297	GLN
1	A	348	HIS
1	A	359	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 4 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	$\# Z > 2$
2	PO4	A	384	3	4,4,4	1.34	0	6,6,6	0.37	0
2	PO4	A	385	3	4,4,4	1.11	0	6,6,6	0.31	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
2	PO4	A	384	3	-	0/0/0/0	0/0/0/0
2	PO4	A	385	3	-	0/0/0/0	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.

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.