Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 12:22 AM GMT

PDB ID	:	1CB7
Title	:	GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM RE-CONSTITUTED WITH METHYL-COBALAMIN
Authors	:	Gruber, K.; Reitzer, R.; Kratky, C.
Deposited on	:	1999-03-02
Resolution	:	2.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
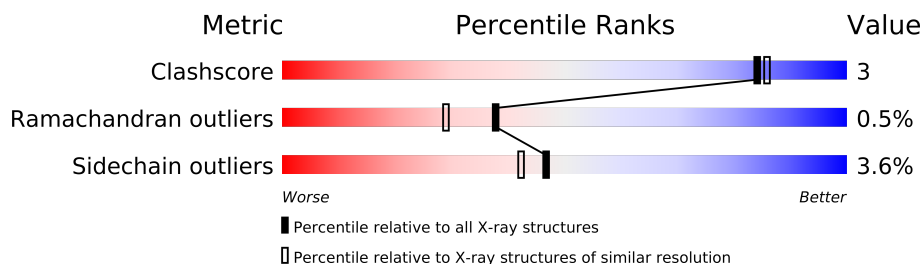
A user guide is available at http://wwpdb.org/ValidationPDFNotes.html

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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 2.00 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	Percentile Ranks	Value
Clashscore		3
Ramachandran outliers		0.5%
Sidechain outliers		3.6%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)

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	137	
1	C	137	
2	B	483	
2	D	483	

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10825 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 PROTEIN (GLUTAMATE MUTASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	0	0
			1041	663	175	198	5			
1	C	137	Total	C	N	O	S	0	0	0
			1041	663	175	198	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	LEU	VAL	CONFLICT	UNP P80078
A	60	VAL	LEU	CONFLICT	UNP P80078
C	45	LEU	VAL	CONFLICT	UNP P80078
C	60	VAL	LEU	CONFLICT	UNP P80078

- Molecule 2 is a protein called PROTEIN (GLUTAMATE MUTASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	483	Total	C	N	O	S	0	0	0
			3762	2383	643	714	22			
2	D	483	Total	C	N	O	S	0	0	0
			3762	2383	643	714	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	130	PHE	TYR	CONFLICT	UNP P80077
D	130	PHE	TYR	CONFLICT	UNP P80077

- Molecule 3 is CO-METHYLCOBALAMIN (three-letter code: COB) (formula: $C_{63}H_{91}CoN_{13}O_{14}P$).
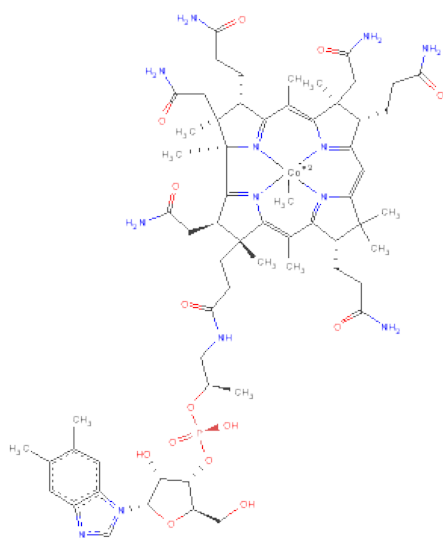
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Co	N	O	P	0	1
			93	64	1	13	14	1		
3	C	1	Total	C	Co	N	O	P	0	1
			93	64	1	13	14	1		

- Molecule 4 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: $C_4H_6O_6$).
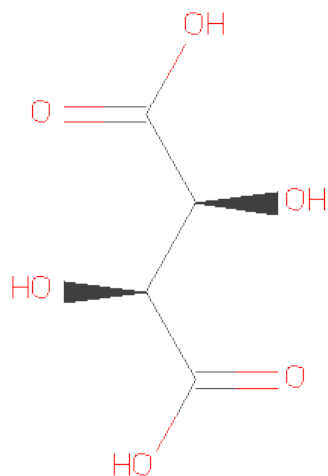
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			10	4	6		
4	D	1	Total	C	O	0	0
			10	4	6		

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	90	Total 90	O 90	0	0
5	B	422	Total 422	O 422	0	0
5	C	81	Total 81	O 81	0	0
5	D	420	Total 420	O 420	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: PROTEIN (GLUTAMATE MUTASE)

Chain A:
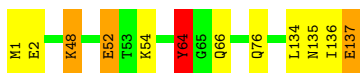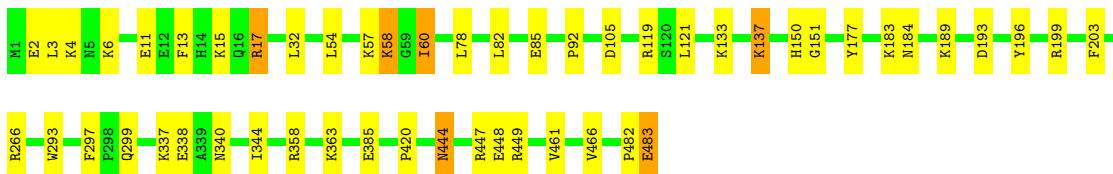
- Molecule 1: PROTEIN (GLUTAMATE MUTASE)

Chain C:

- Molecule 2: PROTEIN (GLUTAMATE MUTASE)

Chain B:

- Molecule 2: PROTEIN (GLUTAMATE MUTASE)

Chain D:

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	64.33Å 113.14Å 108.61Å 90.00° 95.62° 90.00°	Depositor
Resolution (Å)	25.00 – 2.00	Depositor
% Data completeness (in resolution range)	96.1 (25.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.160 , 0.218	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10825	wwPDB-VP
Average B, all atoms (Å^2)	19.0	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: COB, TAR

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	0.32	0/1058	0.93	1/1427 (0.1%)
1	C	0.33	0/1058	0.92	1/1427 (0.1%)
2	B	0.33	0/3833	0.98	9/5171 (0.2%)
2	D	0.33	0/3833	0.98	12/5171 (0.2%)
All	All	0.33	0/9782	0.97	23/13196 (0.2%)

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
2	D	0	1

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	196	TYR	CB-CG-CD1	8.80	126.28	121.00
2	B	422	ARG	NE-CZ-NH2	-8.53	116.04	120.30
2	D	447	ARG	NE-CZ-NH1	8.13	124.36	120.30
2	B	447	ARG	NE-CZ-NH1	6.87	123.74	120.30
2	D	358	ARG	NE-CZ-NH2	-6.84	116.88	120.30
2	D	196	TYR	CB-CG-CD1	6.74	125.04	121.00
1	C	89	TYR	CB-CG-CD1	6.73	125.04	121.00
1	A	64	TYR	CB-CG-CD1	6.68	125.01	121.00
2	B	66	ARG	NE-CZ-NH1	6.42	123.51	120.30
2	D	358	ARG	NE-CZ-NH1	6.14	123.37	120.30
2	B	213	ARG	NE-CZ-NH1	6.14	123.37	120.30
2	D	17	ARG	NE-CZ-NH1	6.01	123.30	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	449	ARG	CD-NE-CZ	5.95	131.93	123.60
2	B	449	ARG	CD-NE-CZ	5.85	131.79	123.60
2	D	105	ASP	CB-CG-OD1	5.82	123.53	118.30
2	D	11	GLU	C-N-CA	5.64	135.79	121.70
2	B	149	ARG	NE-CZ-NH1	5.50	123.05	120.30
2	B	429	ARG	NE-CZ-NH1	5.36	122.98	120.30
2	D	266	ARG	CD-NE-CZ	5.28	131.00	123.60
2	B	196	TYR	CG-CD1-CE1	5.23	125.49	121.30
2	D	199	ARG	NE-CZ-NH1	5.07	122.83	120.30
2	D	177	TYR	CB-CG-CD1	5.05	124.03	121.00
2	D	119	ARG	NE-CZ-NH2	-5.03	117.78	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	92	PRO	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	1041	0	1057	7	0
1	C	1041	0	1057	8	0
2	B	3762	0	3762	20	0
2	D	3762	0	3762	18	0
3	A	93	0	0	0	0
3	C	93	0	0	0	0
4	B	10	0	4	0	0
4	D	10	0	4	0	0
5	A	90	0	0	1	0
5	B	422	0	0	8	0
5	C	81	0	0	3	0
5	D	420	0	0	4	0
All	All	10825	0	9646	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 3.

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

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:133:LYS:O	2:D:137:LYS:HD2	1.87	0.74
2:D:444:ASN:O	2:D:448:GLU:HG3	1.93	0.68
1:C:82:GLY:HA2	1:C:84:GLU:OE2	1.98	0.64
2:D:189:LYS:HE3	2:D:193:ASP:OD2	2.01	0.61
2:B:137:LYS:HD2	5:B:1298:HOH:O	2.00	0.60
2:B:482:PRO:O	2:B:483:GLU:HB3	2.01	0.59
2:D:461:VAL:HG22	5:D:1185:HOH:O	2.02	0.59
2:D:60:ILE:HG22	5:D:1266:HOH:O	2.04	0.57
1:C:1:MET:HG3	1:C:136:ILE:O	2.07	0.55
2:D:337:LYS:HE2	2:D:338:GLU:OE2	2.07	0.53
2:B:7:LYS:HG2	5:B:1299:HOH:O	2.08	0.53
1:C:48:LYS:HD2	5:C:843:HOH:O	2.08	0.52
2:B:2:GLU:OE2	2:B:4:LYS:HE3	2.09	0.52
2:B:369:MET:HE2	5:B:1277:HOH:O	2.08	0.52
2:B:444:ASN:O	2:B:448:GLU:HG3	2.09	0.52
1:A:48:LYS:HE2	1:A:52:GLU:OE2	2.10	0.51
2:B:73:ASP:O	2:B:77:GLU:HG3	2.11	0.50
2:D:85:GLU:HG3	5:D:1177:HOH:O	2.12	0.50
2:D:2:GLU:HG2	2:D:3:LEU:N	2.27	0.49
2:B:133:LYS:HG2	5:B:1180:HOH:O	2.13	0.47
2:D:482:PRO:O	2:D:483:GLU:HB2	2.13	0.47
1:A:1:MET:HG2	1:A:2:GLU:N	2.29	0.47
2:D:420:PRO:O	2:D:466:VAL:HG22	2.15	0.46
1:A:48:LYS:HG3	1:A:52:GLU:OE2	2.16	0.45
2:B:461:VAL:HG22	5:B:1072:HOH:O	2.15	0.45
2:D:444:ASN:ND2	5:D:1264:HOH:O	2.50	0.45
1:C:1:MET:N	5:C:862:HOH:O	2.50	0.45
2:B:377:LYS:NZ	5:B:1295:HOH:O	2.50	0.44
2:D:54:LEU:O	2:D:58:LYS:HG3	2.19	0.43
2:B:66:ARG:O	2:B:67:ALA:HB2	2.18	0.43
2:D:183:LYS:HD3	2:D:184:ASN:OD1	2.18	0.43
2:D:32:LEU:HD13	2:D:203:PHE:CE2	2.53	0.43
2:D:32:LEU:HD13	2:D:203:PHE:CZ	2.54	0.43
2:B:419:MET:SD	2:B:431:LEU:HD23	2.59	0.42
2:B:93:SER:HB2	2:B:167:TRP:CZ3	2.54	0.42
2:B:337:LYS:NZ	5:B:1278:HOH:O	2.50	0.42
2:B:41:LYS:HE2	5:B:1076:HOH:O	2.19	0.42
1:A:134:LEU:O	1:A:136:ILE:HG23	2.19	0.42
2:B:13:PHE:CE2	2:B:17:ARG:HD2	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:137:GLU:OE1	1:C:137:GLU:N	2.51	0.42
1:A:64:TYR:CE1	1:A:66:GLN:HB2	2.55	0.41
2:B:216:PHE:CD1	2:B:218:PRO:HD2	2.55	0.41
2:D:13:PHE:O	2:D:17:ARG:HG3	2.19	0.41
2:B:68:GLY:HA2	2:B:75:HIS:CE1	2.55	0.41
1:A:137:GLU:HG2	1:A:137:GLU:OXT	2.20	0.41
1:C:25:HIS:HD2	5:C:881:HOH:O	2.02	0.41
2:B:299:GLN:CD	2:B:332:ILE:HD11	2.41	0.41
2:D:340:ASN:O	2:D:344:ILE:HG13	2.21	0.41
1:C:60:VAL:O	1:C:90:VAL:HA	2.20	0.40
1:A:137:GLU:HG3	5:A:874:HOH:O	2.21	0.40
2:B:87:GLY:O	2:B:348:LYS:NZ	2.50	0.40
2:D:78:LEU:O	2:D:82:LEU:HG	2.20	0.40
1:C:115:ARG:NH2	1:C:132:LYS:HE3	2.36	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	135/137 (98%)	133 (98%)	2 (2%)	0	100	100
1	C	135/137 (98%)	133 (98%)	2 (2%)	0	100	100
2	B	481/483 (100%)	471 (98%)	7 (2%)	3 (1%)	33	24
2	D	481/483 (100%)	470 (98%)	8 (2%)	3 (1%)	33	24
All	All	1232/1240 (99%)	1207 (98%)	19 (2%)	6 (0%)	38	29

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	150	HIS
2	B	151	GLY
2	B	293	TRP
2	D	150	HIS

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Mol	Chain	Res	Type
2	D	151	GLY
2	D	293	TRP

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	111/111 (100%)	104 (94%)	7 (6%)	25	18
1	C	111/111 (100%)	105 (95%)	6 (5%)	31	24
2	B	396/396 (100%)	387 (98%)	9 (2%)	63	63
2	D	396/396 (100%)	382 (96%)	14 (4%)	48	43
All	All	1014/1014 (100%)	978 (96%)	36 (4%)	47	42

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LYS
1	A	52	GLU
1	A	54	LYS
1	A	64	TYR
1	A	76	GLN
1	A	135	ASN
1	A	137	GLU
2	B	2	GLU
2	B	4	LYS
2	B	6	LYS
2	B	48	PHE
2	B	56	LYS
2	B	60	ILE
2	B	121	LEU
2	B	441	GLU
2	B	483	GLU
1	C	3	LYS
1	C	21	LYS
1	C	48	LYS
1	C	52	GLU

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Mol	Chain	Res	Type
1	C	64	TYR
1	C	76	GLN
2	D	4	LYS
2	D	6	LYS
2	D	15	LYS
2	D	57	LYS
2	D	58	LYS
2	D	60	ILE
2	D	121	LEU
2	D	137	LYS
2	D	297	PHE
2	D	299	GLN
2	D	363	LYS
2	D	385	GLU
2	D	444	ASN
2	D	483	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	135	ASN
2	B	5	ASN
2	B	23	GLN
2	B	207	GLN
2	D	5	ASN
2	D	23	GLN

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 modelled with single atom - 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	#$|Z| > 2$
4	TAR	B	900	-	9,9,9	1.13	0	12,12,12	1.28	1 (8%)
4	TAR	D	900	-	9,9,9	1.08	0	12,12,12	1.05	1 (8%)

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	TAR	B	900	-	-	0/12/12/12	0/0/0/0
4	TAR	D	900	-	-	0/12/12/12	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	900	TAR	O2-C2-C1	2.84	116.83	110.73
4	D	900	TAR	O2-C2-C1	2.42	115.91	110.73

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.