



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:54 PM GMT

PDB ID : 1MJ3
Title : Crystal Structure Analysis of rat enoyl-CoA hydratase in complex with hexadienoyl-CoA
Authors : Bell, A.F.; Feng, Y.; Hofstein, H.A.; Parikh, S.; Wu, J.; Rudolph, M.J.; Kisker, C.; Tonge, P.J.
Deposited on : 2002-08-26
Resolution : 2.10 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
<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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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

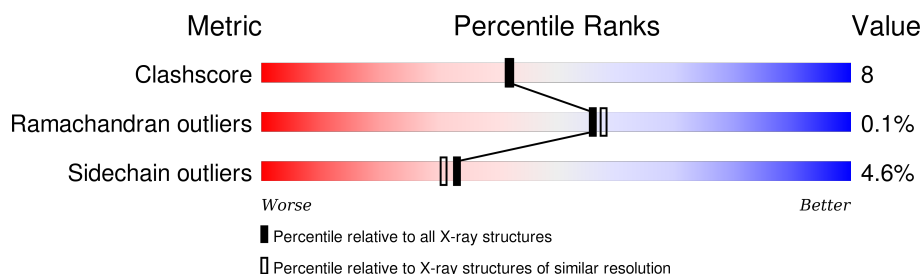
1 Overall quality at a glance

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	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (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 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 $\leq 5\%$. 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 was not executed.

Mol	Chain	Length	Quality of chain
1	A	260	 82% 13% ...
1	B	260	 79% 17% ...
1	C	260	 74% 23% ...
1	D	260	 74% 20% ...
1	E	260	 85% 11% ...
1	F	260	 85% 13% ...

2 Entry composition [i](#)

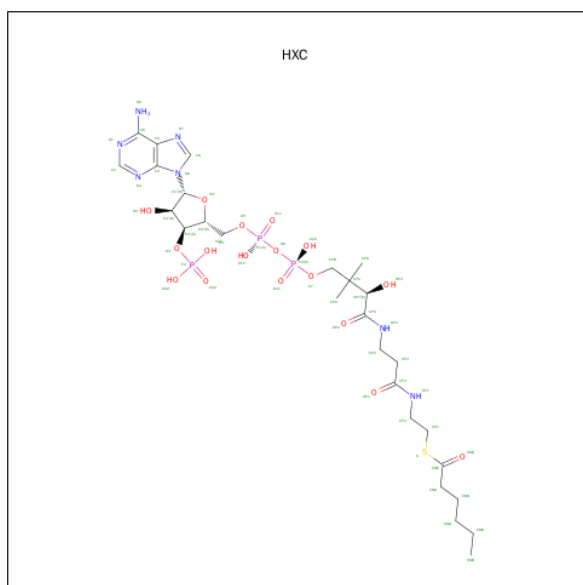
There are 3 unique types of molecules in this entry. The entry contains 12924 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENOYL-COA HYDRATASE, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			
1	B	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			
1	C	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			
1	D	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			
1	E	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			
1	F	258	Total	C	N	O	S	0	0	0
			1955	1230	336	376	13			

- Molecule 2 is HEXANOYL-COENZYME A (three-letter code: HXC) (formula: $C_{27}H_{46}N_7O_{17}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			55	27	7	17	3	1		

- Molecule 3 is water.

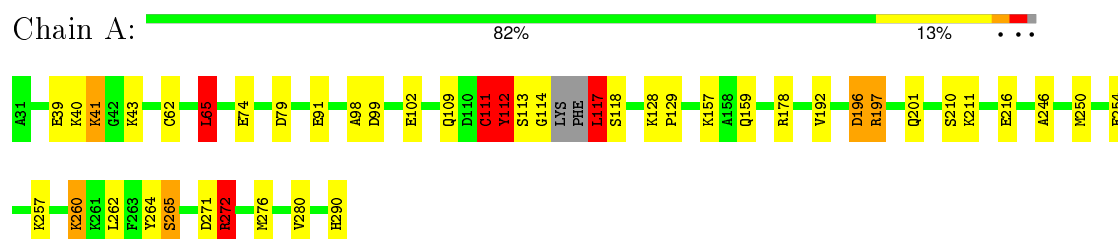
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	162	Total	O	0	0
			162	162		
3	B	167	Total	O	0	0
			167	167		
3	C	126	Total	O	0	0
			126	126		
3	D	145	Total	O	0	0
			145	145		
3	E	153	Total	O	0	0
			153	153		
3	F	166	Total	O	0	0
			166	166		

3 Residue-property plots

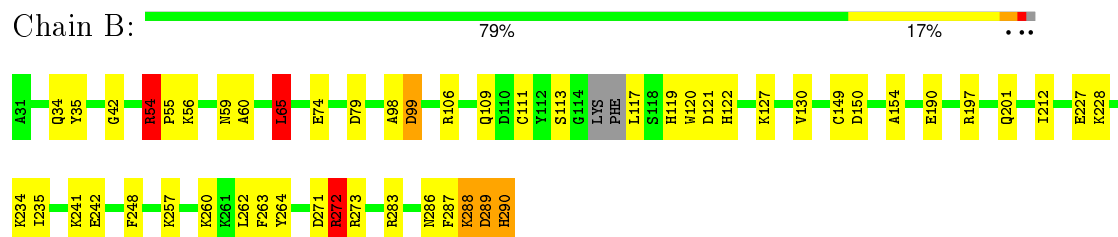
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

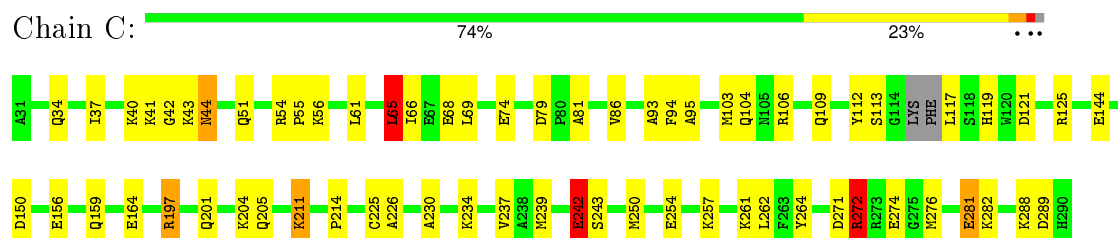
• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL



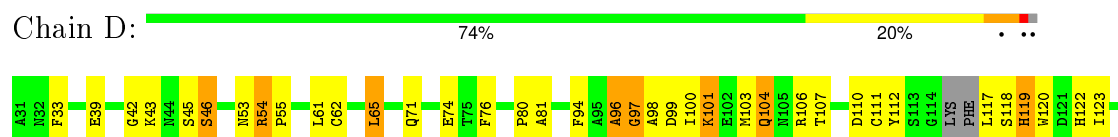
• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL

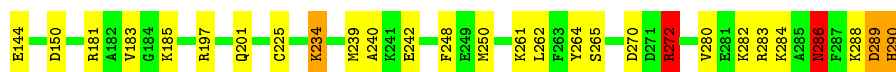


• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL



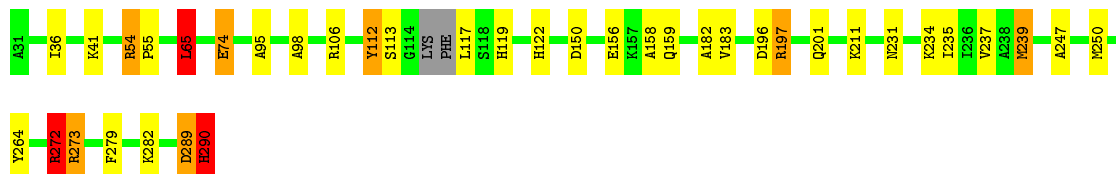
• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL





• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL

Chain E: 85% 11% ...



• Molecule 1: ENOYL-COA HYDRATASE, MITOCHONDRIAL

Chain F: 85% 13% ...



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.88 Å 95.20 Å 249.43 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.10	Depositor
% Data completeness (in resolution range)	90.2 (48.80-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.172 , 0.230	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12924	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: HXC

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	1.44	13/1980 (0.7%)	1.36	13/2659 (0.5%)
1	B	1.52	11/1980 (0.6%)	1.46	17/2659 (0.6%)
1	C	1.49	19/1980 (1.0%)	1.34	16/2659 (0.6%)
1	D	1.54	18/1980 (0.9%)	1.55	25/2659 (0.9%)
1	E	1.47	10/1980 (0.5%)	1.55	18/2659 (0.7%)
1	F	1.43	13/1980 (0.7%)	1.35	16/2659 (0.6%)
All	All	1.48	84/11880 (0.7%)	1.44	105/15954 (0.7%)

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	C	0	1

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	272	ARG	CZ-NH1	14.93	1.52	1.33
1	B	272	ARG	CZ-NH1	14.91	1.52	1.33
1	B	287	PHE	CE1-CZ	12.61	1.61	1.37
1	A	111	CYS	CB-SG	-10.55	1.64	1.82
1	D	272	ARG	CZ-NH1	9.85	1.45	1.33

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	272	ARG	NE-CZ-NH2	-35.46	102.57	120.30
1	B	272	ARG	NE-CZ-NH2	-30.85	104.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	272	ARG	NE-CZ-NH1	25.62	133.11	120.30
1	D	272	ARG	NE-CZ-NH1	24.99	132.79	120.30
1	B	272	ARG	NE-CZ-NH1	24.95	132.77	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	117	LEU	Peptide

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	1955	0	1975	43	0
1	B	1955	0	1975	42	3
1	C	1955	0	1975	32	1
1	D	1955	0	1975	44	3
1	E	1955	0	1975	37	3
1	F	1955	0	1975	31	3
2	A	55	0	40	4	0
2	B	55	0	41	6	0
2	C	55	0	41	3	0
2	E	55	0	40	2	0
2	F	55	0	39	7	0
3	A	162	0	0	16	0
3	B	167	0	0	9	0
3	C	126	0	0	8	0
3	D	145	0	0	20	0
3	E	153	0	0	3	0
3	F	166	0	0	6	0
All	All	12924	0	12051	202	7

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 8.

The worst 5 of 202 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)
2:C:953:HXC:C3'	2:C:953:HXC:C2'	1.93	1.43
1:A:276:MET:CE	1:A:276:MET:SD	2.05	1.42
2:B:952:HXC:C2'	2:B:952:HXC:C3'	1.96	1.34
2:F:955:HXC:C2'	2:F:955:HXC:C3'	2.09	1.24
1:D:62:CYS:N	3:D:386:HOH:O	1.70	1.23

The worst 5 of 7 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)
1:D:42:GLY:O	1:E:282:LYS:NZ[4_466]	1.45	0.75
1:B:227:GLU:OE1	1:F:288:LYS:NZ[3_756]	1.79	0.41
1:D:42:GLY:O	1:E:282:LYS:CE[4_466]	1.86	0.34
1:D:45:SER:N	1:E:282:LYS:NZ[4_466]	1.94	0.26
1:C:44:ASN:OD1	1:C:56:LYS:O[4_576]	2.19	0.01

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	254/260 (98%)	249 (98%)	4 (2%)	1 (0%)	39	37
1	B	254/260 (98%)	247 (97%)	7 (3%)	0	100	100
1	C	254/260 (98%)	246 (97%)	8 (3%)	0	100	100
1	D	254/260 (98%)	244 (96%)	9 (4%)	1 (0%)	39	37
1	E	254/260 (98%)	249 (98%)	5 (2%)	0	100	100
1	F	254/260 (98%)	250 (98%)	4 (2%)	0	100	100
All	All	1524/1560 (98%)	1485 (97%)	37 (2%)	2 (0%)	56	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	TYR
1	D	104	GLN

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	202/205 (98%)	189 (94%)	13 (6%)	22	18
1	B	202/205 (98%)	194 (96%)	8 (4%)	38	38
1	C	202/205 (98%)	190 (94%)	12 (6%)	24	20
1	D	202/205 (98%)	193 (96%)	9 (4%)	34	32
1	E	202/205 (98%)	192 (95%)	10 (5%)	30	27
1	F	202/205 (98%)	198 (98%)	4 (2%)	63	68
All	All	1212/1230 (98%)	1156 (95%)	56 (5%)	33	31

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	106	ARG
1	C	243	SER
1	E	290	HIS
1	C	112	TYR
1	C	156	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	159	GLN
1	D	53	ASN
1	E	53	ASN
1	C	122	HIS
1	E	122	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

5 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	$\# Z > 2$
2	HXC	A	951	-	47,57,57	4.11	20 (42%)	59,83,83	3.17	29 (49%)
2	HXC	B	952	-	47,57,57	4.93	18 (38%)	59,83,83	3.42	28 (47%)
2	HXC	C	953	-	47,57,57	4.78	17 (36%)	59,83,83	3.08	24 (40%)
2	HXC	E	954	-	47,57,57	3.92	19 (40%)	59,83,83	3.41	22 (37%)
2	HXC	F	955	-	47,57,57	5.66	15 (31%)	59,83,83	3.30	28 (47%)

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	HXC	A	951	-	-	0/52/72/72	0/3/3/3
2	HXC	B	952	-	-	0/52/72/72	0/3/3/3
2	HXC	C	953	-	-	0/52/72/72	0/3/3/3
2	HXC	E	954	-	-	0/52/72/72	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HXC	F	955	-	-	0/52/72/72	0/3/3/3

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	955	HXC	CM2-CM1	-20.92	1.27	1.50
2	A	951	HXC	CM2-CM1	-16.87	1.31	1.50
2	E	954	HXC	CM2-CM1	-16.28	1.32	1.50
2	C	953	HXC	CM2-CM1	-15.17	1.33	1.50
2	B	952	HXC	CM2-CM1	-13.64	1.35	1.50

The worst 5 of 131 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	954	HXC	OM2-CM1-S	-10.45	114.54	122.83
2	C	953	HXC	OP1-CP3-CP4	-9.70	105.25	121.98
2	F	955	HXC	O3'-C3'-C2'	-9.35	75.15	111.51
2	F	955	HXC	OP1-CP3-CP4	-9.30	105.93	121.98
2	B	952	HXC	CP5-CP4-CP3	-8.57	98.18	112.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	951	HXC	4	0
2	B	952	HXC	6	0
2	C	953	HXC	3	0
2	E	954	HXC	2	0
2	F	955	HXC	7	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.