



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:18 AM UTC

PDB ID : 2ER6 / pdb_00002er6
Title : The structure of a synthetic pepsin inhibitor complexed with endothiapepsin.
Authors : Cooper, J.B.; Foundling, S.I.; Szelke, M.; Blundell, T.L.
Deposited on : 1990-10-13
Resolution : 2.00 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

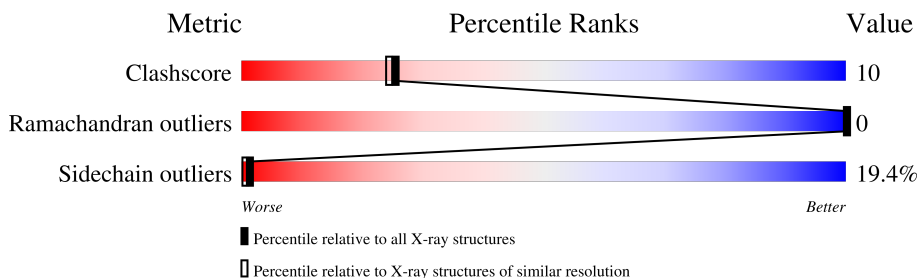
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	330	 65% 28% 7%
2	I	6	 50% 17% 17% 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2775 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 ENDOTHIAPEPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	330	Total	C	N	O	S	0	0	0
			2389	1514	366	507	2			

- Molecule 2 is a protein called H-256 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	6	Total	C	N	O	0	0	0
			65	43	10	12			

- Molecule 3 is water.

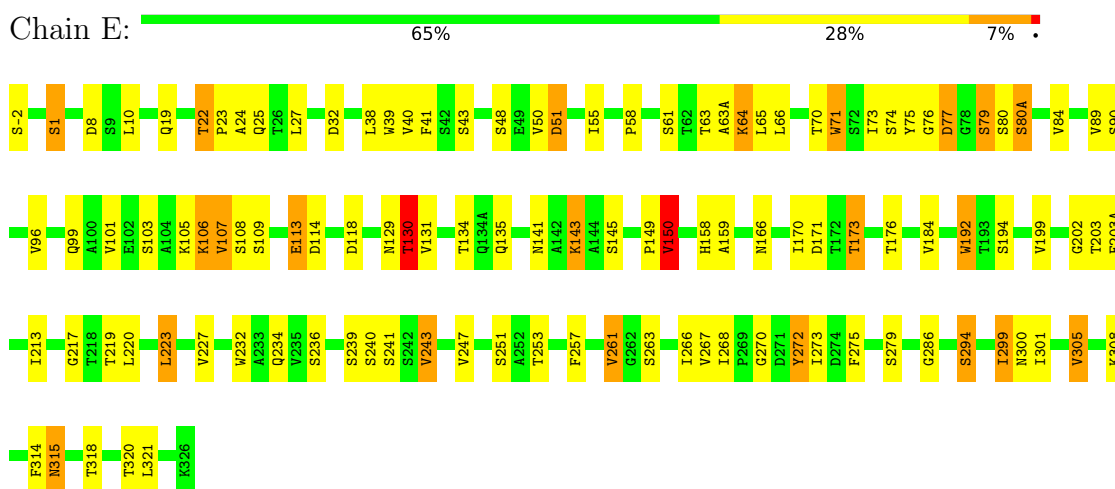
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	311	Total	O	0	0
			311	311		
3	I	10	Total	O	0	0
			10	10		

3 Residue-property plots

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: ENDOTHIAPEPSIN



• Molecule 2: H-256 peptide



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.40Å 73.80Å 45.60Å 90.00° 109.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.200 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2775	wwPDB-VP
Average B, all atoms (Å ²)	0.0	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: PUK

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	E	1.12	12/2445 (0.5%)	1.50	39/3345 (1.2%)
2	I	1.18	0/43	1.52	2/53 (3.8%)
All	All	1.12	12/2488 (0.5%)	1.50	41/3398 (1.2%)

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	I	0	2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	320	THR	C-N	9.51	1.46	1.33
1	E	158	HIS	CE1-NE2	7.18	1.39	1.32
1	E	158	HIS	ND1-CE1	6.62	1.39	1.32
1	E	19	GLN	CD-OE1	5.36	1.33	1.23
1	E	99	GLN	CD-OE1	5.33	1.33	1.23
1	E	192	TRP	NE1-CE2	-5.29	1.31	1.37
1	E	25	GLN	CD-OE1	5.26	1.33	1.23
1	E	232	TRP	NE1-CE2	-5.16	1.31	1.37
1	E	39	TRP	NE1-CE2	-5.15	1.31	1.37
1	E	71	TRP	NE1-CE2	-5.11	1.31	1.37
1	E	234	GLN	CD-OE1	5.08	1.33	1.23
1	E	223	LEU	N-CA	5.04	1.50	1.45

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	261	VAL	CA-CB-CG2	9.80	127.06	110.40
1	E	107	VAL	CA-CB-CG2	8.86	125.47	110.40
1	E	320	THR	O-C-N	7.16	131.84	123.17
1	E	243	VAL	CA-CB-CG2	7.15	122.55	110.40
1	E	257	PHE	CA-CB-CG	-6.83	106.97	113.80
1	E	143	LYS	O-C-N	6.73	131.54	122.59
1	E	158	HIS	CA-CB-CG	-6.72	107.08	113.80
1	E	315	ASN	O-C-N	6.52	131.57	122.77
1	E	315	ASN	CA-C-N	-6.43	108.81	121.41
1	E	315	ASN	C-N-CA	-6.43	108.81	121.41
1	E	84	VAL	CA-CB-CG2	6.42	121.31	110.40
1	E	76	GLY	CA-C-N	6.32	129.04	120.38
1	E	76	GLY	C-N-CA	6.32	129.04	120.38
2	I	2	THR	CB-CA-C	6.18	122.30	109.38
1	E	202	GLY	CA-C-N	6.10	129.50	120.95
1	E	202	GLY	C-N-CA	6.10	129.50	120.95
1	E	267	VAL	CA-CB-CG2	6.04	120.67	110.40
1	E	199	VAL	CA-CB-CG2	5.86	120.36	110.40
1	E	247	VAL	CA-CB-CG2	5.69	120.07	110.40
1	E	130	THR	N-CA-CB	-5.68	102.30	110.65
1	E	51	ASP	CB-CA-C	-5.54	102.60	111.86
1	E	184	VAL	CA-CB-CG2	5.53	119.80	110.40
1	E	40	VAL	CA-CB-CG2	5.45	119.66	110.40
1	E	89	VAL	CA-CB-CG2	5.44	119.65	110.40
1	E	8	ASP	CA-CB-CG	5.37	117.97	112.60
1	E	268	ILE	CA-C-N	-5.37	114.43	119.85
1	E	268	ILE	C-N-CA	-5.37	114.43	119.85
1	E	305	VAL	CA-CB-CG1	5.34	119.48	110.40
1	E	24	ALA	CA-C-N	5.33	129.86	122.77
1	E	24	ALA	C-N-CA	5.33	129.86	122.77
1	E	159	ALA	CA-C-N	-5.33	115.09	120.21
1	E	159	ALA	C-N-CA	-5.33	115.09	120.21
2	I	5	ARG	NE-CZ-NH2	5.30	123.97	119.20
1	E	25	GLN	OE1-CD-NE2	-5.28	117.32	122.60
1	E	150	VAL	CA-CB-CG2	5.27	119.36	110.40
1	E	275	PHE	CA-CB-CG	-5.27	108.53	113.80
1	E	101	VAL	CA-CB-CG2	5.17	119.19	110.40
1	E	149	PRO	N-CA-CB	-5.16	98.96	102.73
1	E	22	THR	CA-C-N	-5.06	114.86	127.00
1	E	22	THR	C-N-CA	-5.06	114.86	127.00
1	E	227	VAL	CA-CB-CG2	5.02	118.94	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	4	PUK	Peptide,Mainchain

5.2 Too-close contacts [i](#)

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	E	2389	0	2280	46	3
2	I	65	0	55	2	0
3	E	311	0	0	6	10
3	I	10	0	0	0	0
All	All	2775	0	2335	46	10

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 10.

All (46) 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:E:113:GLU:HG3	3:E:603:HOH:O	1.69	0.91
1:E:1:SER:HB3	1:E:166:ASN:ND2	1.94	0.83
1:E:299:ILE:HG12	3:E:498:HOH:O	1.84	0.78
1:E:171:ASP:OD2	1:E:173:THR:HB	1.84	0.77
1:E:27:LEU:HD23	1:E:118:ASP:HB3	1.74	0.70
1:E:73:ILE:HD13	1:E:75:TYR:CZ	2.26	0.70
1:E:129:ASN:ND2	1:E:131:VAL:H	1.95	0.65
1:E:150:VAL:HG23	1:E:315:ASN:HA	1.79	0.64
1:E:113:GLU:CG	3:E:603:HOH:O	2.38	0.60
1:E:270:GLY:HA2	1:E:273:ILE:HD12	1.83	0.59
1:E:32:ASP:OD1	1:E:217:GLY:HA3	2.04	0.57
1:E:77:ASP:HB3	1:E:79:SER:H	1.70	0.57
1:E:71:TRP:HB2	1:E:130:THR:HG22	1.86	0.56
1:E:301:ILE:HD11	2:I:4:PUK:C17	2.36	0.55
1:E:1:SER:HB3	1:E:166:ASN:HD22	1.66	0.55
1:E:129:ASN:HD21	1:E:131:VAL:HB	1.71	0.55
1:E:134:THR:HG23	3:E:571:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:171:ASP:C	1:E:173:THR:H	2.17	0.52
1:E:22:THR:HA	1:E:23:PRO:C	2.32	0.51
1:E:73:ILE:HD13	1:E:75:TYR:OH	2.10	0.50
1:E:314:PHE:CD1	1:E:314:PHE:N	2.80	0.50
1:E:219:THR:O	1:E:305:VAL:HG23	2.11	0.50
1:E:273:ILE:HG22	1:E:273:ILE:O	2.12	0.49
1:E:213:ILE:HG23	1:E:299:ILE:HD13	1.95	0.49
1:E:220:LEU:HD22	1:E:286:GLY:HA2	1.94	0.49
1:E:192:TRP:CH2	1:E:194:SER:HB2	2.48	0.48
1:E:71:TRP:HH2	1:E:80(A):SER:HG	1.58	0.47
1:E:213:ILE:HG23	1:E:299:ILE:CD1	2.45	0.47
1:E:272:TYR:CD1	1:E:272:TYR:N	2.83	0.47
1:E:150:VAL:CG2	1:E:315:ASN:HA	2.43	0.47
1:E:301:ILE:CD1	2:I:4:PUK:C17	2.94	0.46
1:E:272:TYR:N	1:E:272:TYR:HD1	2.14	0.45
1:E:294:SER:CB	1:E:300:ASN:ND2	2.80	0.45
1:E:41:PHE:HB3	1:E:55:ILE:HG22	2.00	0.43
1:E:96:VAL:HG11	1:E:141:ASN:HB3	2.01	0.43
1:E:64:LYS:HD3	1:E:64:LYS:HA	1.75	0.42
1:E:134:THR:CG2	3:E:571:HOH:O	2.66	0.42
1:E:1:SER:HB3	1:E:166:ASN:HD21	1.77	0.42
1:E:171:ASP:C	1:E:173:THR:N	2.76	0.41
1:E:43:SER:OG	1:E:58:PRO:HD2	2.21	0.41
1:E:61:SER:HB3	1:E:63(A):ALA:HB2	2.02	0.41
1:E:273:ILE:O	1:E:273:ILE:CG2	2.69	0.41
1:E:294:SER:HB3	1:E:300:ASN:ND2	2.36	0.41
1:E:135:GLN:NE2	3:E:532:HOH:O	2.53	0.41
1:E:71:TRP:HH2	1:E:80(A):SER:OG	2.04	0.41
1:E:38:LEU:C	1:E:38:LEU:HD23	2.46	0.40

All (10) 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)
3:E:415:HOH:O	3:E:523:HOH:O[2_645]	0.15	2.05
3:E:375:HOH:O	3:E:446:HOH:O[1_455]	0.19	2.01
3:E:466:HOH:O	3:E:539:HOH:O[2_655]	0.20	2.00
3:E:336:HOH:O	3:E:486:HOH:O[2_655]	0.67	1.53
3:E:368:HOH:O	3:E:491:HOH:O[1_655]	0.87	1.33
1:E:251:SER:OG	3:E:358:HOH:O[1_454]	0.89	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:345:HOH:O	3:E:409:HOH:O[2_655]	0.89	1.31
3:E:455:HOH:O	3:E:602:HOH:O[1_556]	1.72	0.48
1:E:251:SER:CB	3:E:358:HOH:O[1_454]	2.04	0.16
1:E:106:LYS:NZ	3:E:491:HOH:O[1_655]	2.09	0.11

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	E	328/330 (99%)	317 (97%)	11 (3%)	0	100	100
2	I	3/6 (50%)	2 (67%)	1 (33%)	0	100	100
All	All	331/336 (98%)	319 (96%)	12 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	E	263/263 (100%)	212 (81%)	51 (19%)	1	1
2	I	5/5 (100%)	4 (80%)	1 (20%)	1	0
All	All	268/268 (100%)	216 (81%)	52 (19%)	1	1

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	-2	SER
1	E	1	SER
1	E	10	LEU
1	E	48	SER
1	E	50	VAL
1	E	51	ASP
1	E	63	THR
1	E	64	LYS
1	E	65	LEU
1	E	66	LEU
1	E	70	THR
1	E	74	SER
1	E	77	ASP
1	E	79	SER
1	E	80	SER
1	E	80(A)	SER
1	E	90	SER
1	E	103	SER
1	E	105	LYS
1	E	106	LYS
1	E	107	VAL
1	E	108	SER
1	E	109	SER
1	E	113	GLU
1	E	114	ASP
1	E	130	THR
1	E	143	LYS
1	E	145	SER
1	E	150	VAL
1	E	170	ILE
1	E	173	THR
1	E	176	THR
1	E	203	THR
1	E	203(A)	PHE
1	E	223	LEU
1	E	236	SER
1	E	239	SER
1	E	240	SER
1	E	241	SER
1	E	243	VAL
1	E	253	THR
1	E	261	VAL
1	E	263	SER

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Mol	Chain	Res	Type
1	E	266	ILE
1	E	272	TYR
1	E	279	SER
1	E	294	SER
1	E	299	ILE
1	E	308	LYS
1	E	318	THR
1	E	321	LEU
2	I	5	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	19	GLN
1	E	99	GLN
1	E	129	ASN
1	E	134(A)	GLN
1	E	135	GLN
1	E	141	ASN
1	E	166	ASN
1	E	187	GLN
1	E	300	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	PUK	I	4	2	21,22,23	0.80	0	23,27,29	1.10	1 (4%)

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	PUK	I	4	2	-	4/14/15/17	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	4	PUK	C2-N2-C10	4.54	122.45	114.00

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	4	PUK	CA-C2-N2-C10
2	I	4	PUK	CA-C3-C4-C6
2	I	4	PUK	CA-C3-C4-C5
2	I	4	PUK	C-C10-N2-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	4	PUK	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 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.