Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 09:33 PM GMT

PDB ID	:	1PKM
Title	:	THE REFINED THREE-DIMENSIONAL STRUCTURE OF CAT MUSCLE (M1) PYRUVATE KINASE, AT A RESOLUTION OF 2.6 ANGSTROMS
Authors	:	Allen, S.C.; Muirhead, H.
Deposited on	:	1995-07-13
Resolution	:	2.60 Å(reported)

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

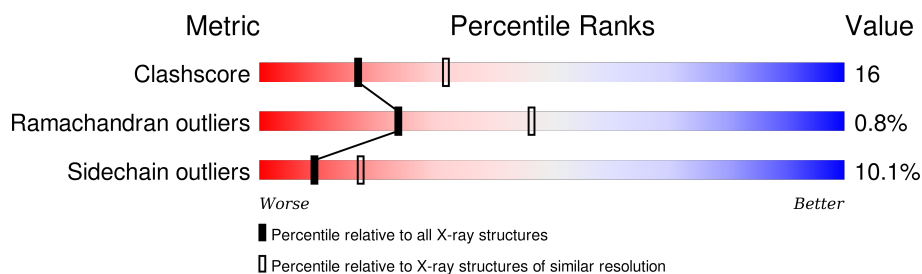|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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		16
Ramachandran outliers		0.8%
Sidechain outliers		10.1%

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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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 <=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	530	61% 32% 5% ·

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3976 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 M1 PYRUVATE KINASE.

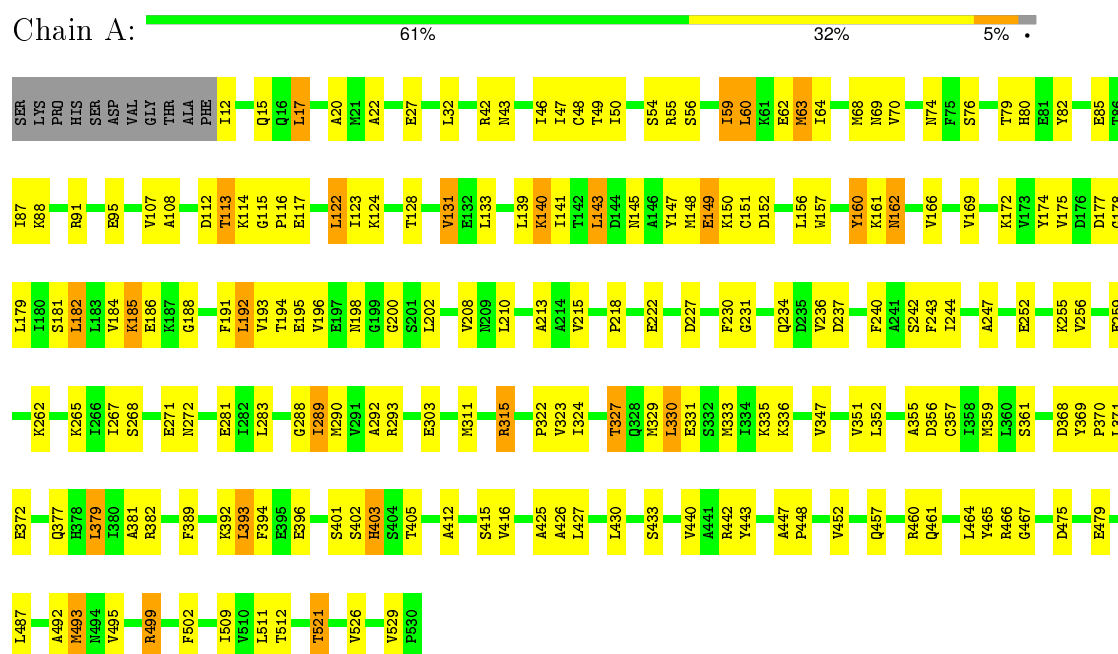| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	519	3976	2494	710	744	28	0	0	0

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: M1 PYRUVATE KINASE

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	88.40Å 115.30Å 131.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.60)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT, X-PLOR	Depositor
R, R_{free}	0.175 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3976	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.56	0/4039	0.80	2/5448 (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})
1	A	192	LEU	CA-CB-CG	6.73	130.78	115.30
1	A	393	LEU	CA-CB-CG	5.23	127.33	115.30

There are no chirality outliers.

There are no planarity outliers.

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	A	3976	0	4051	132	0
All	All	3976	0	4051	132	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 16.

All (132) 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:247:ALA:HB2	1:A:281:GLU:HG2	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:LEU:HB3	1:A:521:THR:CG2	2.01	0.90
1:A:511:LEU:HB3	1:A:521:THR:HG21	1.60	0.82
1:A:392:LYS:O	1:A:396:GLU:HG3	1.79	0.81
1:A:70:VAL:HG22	1:A:108:ALA:HB3	1.65	0.79
1:A:62:GLU:HB3	1:A:371:LEU:HD21	1.66	0.78
1:A:186:GLU:HB3	1:A:193:VAL:HB	1.66	0.78
1:A:174:TYR:HB3	1:A:178:GLY:HA2	1.66	0.76
1:A:76:SER:HA	1:A:114:LYS:HG3	1.69	0.75
1:A:493:MET:HE2	1:A:529:VAL:HG22	1.69	0.74
1:A:79:THR:HG23	1:A:82:TYR:H	1.56	0.70
1:A:22:ALA:HB1	1:A:27:GLU:HB3	1.74	0.69
1:A:335:LYS:HE2	1:A:336:LYS:HE2	1.73	0.69
1:A:166:VAL:HG12	1:A:213:ALA:HB1	1.76	0.66
1:A:240:PHE:HE1	1:A:267:ILE:HD12	1.59	0.66
1:A:511:LEU:HB3	1:A:521:THR:HG23	1.76	0.66
1:A:169:VAL:HA	1:A:184:VAL:HG12	1.78	0.66
1:A:46:ILE:H	1:A:69:ASN:HD22	1.44	0.65
1:A:55:ARG:NH2	1:A:85:GLU:HB3	2.12	0.65
1:A:271:GLU:HB3	1:A:292:ALA:HB3	1.80	0.63
1:A:42:ARG:HH12	1:A:69:ASN:HD21	1.45	0.63
1:A:457:GLN:HG2	1:A:460:ARG:NH1	2.13	0.63
1:A:145:ASN:HB3	1:A:157:TRP:HE1	1.64	0.62
1:A:293:ARG:NH2	1:A:329:MET:HG2	2.13	0.62
1:A:145:ASN:HB2	1:A:148:MET:HB2	1.82	0.62
1:A:452:VAL:CG2	1:A:492:ALA:HB2	2.29	0.61
1:A:240:PHE:CE1	1:A:267:ILE:HD12	2.34	0.61
1:A:210:LEU:HB3	1:A:213:ALA:HB3	1.83	0.61
1:A:166:VAL:CG1	1:A:213:ALA:HB1	2.31	0.61
1:A:509:ILE:HD13	1:A:526:VAL:HG22	1.82	0.61
1:A:188:GLY:HA3	1:A:191:PHE:CE1	2.35	0.61
1:A:521:THR:HG22	1:A:521:THR:O	2.00	0.60
1:A:145:ASN:HB3	1:A:157:TRP:NE1	2.18	0.59
1:A:425:ALA:HB1	1:A:502:PHE:HB3	1.84	0.59
1:A:324:ILE:HG12	1:A:357:CYS:HB2	1.85	0.58
1:A:247:ALA:CB	1:A:281:GLU:HG2	2.28	0.58
1:A:415:SER:OG	1:A:511:LEU:HD21	2.03	0.57
1:A:289:ILE:HG22	1:A:323:VAL:HG23	1.84	0.57
1:A:351:VAL:HG13	1:A:466:ARG:NH2	2.19	0.57
1:A:174:TYR:O	1:A:208:VAL:HA	2.04	0.57
1:A:123:ILE:HG21	1:A:131:VAL:HG21	1.86	0.57
1:A:160:TYR:OH	1:A:166:VAL:HG21	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:VAL:HG21	1:A:492:ALA:HB2	1.87	0.56
1:A:112:ASP:HA	1:A:240:PHE:HB2	1.88	0.55
1:A:237:ASP:OD1	1:A:460:ARG:HD2	2.07	0.54
1:A:322:PRO:HA	1:A:356:ASP:OD2	2.07	0.54
1:A:124:LYS:HB3	1:A:150:LYS:HD2	1.88	0.54
1:A:54:SER:HA	1:A:59:ILE:HG21	1.88	0.54
1:A:290:MET:HE2	1:A:292:ALA:HB2	1.90	0.54
1:A:50:ILE:HD11	1:A:68:MET:CE	2.38	0.53
1:A:182:LEU:HD12	1:A:196:VAL:HA	1.90	0.53
1:A:333:MET:HA	1:A:336:LYS:O	2.08	0.53
1:A:48:CYS:SG	1:A:68:MET:HG3	2.49	0.53
1:A:311:MET:HG2	1:A:315:ARG:HH11	1.73	0.53
1:A:355:ALA:O	1:A:466:ARG:NH1	2.42	0.53
1:A:139:LEU:HD11	1:A:156:LEU:HB2	1.90	0.52
1:A:181:SER:H	1:A:198:ASN:HB2	1.74	0.52
1:A:140:LYS:HD3	1:A:140:LYS:N	2.23	0.52
1:A:493:MET:CE	1:A:529:VAL:HG22	2.38	0.52
1:A:50:ILE:HD11	1:A:68:MET:HE3	1.92	0.52
1:A:116:PRO:HD2	1:A:243:PHE:HB2	1.91	0.52
1:A:123:ILE:HD13	1:A:131:VAL:HG21	1.93	0.51
1:A:85:GLU:HG2	1:A:88:LYS:HE3	1.94	0.50
1:A:210:LEU:HB3	1:A:213:ALA:CB	2.41	0.50
1:A:55:ARG:HD2	1:A:82:TYR:CZ	2.47	0.50
1:A:55:ARG:HH22	1:A:85:GLU:HB3	1.77	0.49
1:A:330:LEU:HD22	1:A:377:GLN:HG3	1.94	0.49
1:A:188:GLY:HA3	1:A:191:PHE:CZ	2.48	0.49
1:A:17:LEU:O	1:A:20:ALA:HB3	2.13	0.49
1:A:426:ALA:HB2	1:A:448:PRO:HG2	1.94	0.49
1:A:412:ALA:O	1:A:416:VAL:HG23	2.13	0.49
1:A:322:PRO:HG3	1:A:465:TYR:CE2	2.48	0.49
1:A:54:SER:O	1:A:60:LEU:HD13	2.12	0.48
1:A:495:VAL:HG13	1:A:499:ARG:HH11	1.78	0.48
1:A:405:THR:HG22	1:A:405:THR:O	2.13	0.48
1:A:185:LYS:HG3	1:A:195:GLU:HB2	1.95	0.48
1:A:55:ARG:HD2	1:A:82:TYR:OH	2.13	0.48
1:A:426:ALA:HA	1:A:447:ALA:HB1	1.96	0.48
1:A:47:ILE:HB	1:A:359:MET:HG3	1.95	0.47
1:A:116:PRO:HD2	1:A:243:PHE:CD1	2.50	0.47
1:A:62:GLU:CB	1:A:371:LEU:HD21	2.41	0.47
1:A:46:ILE:H	1:A:69:ASN:ND2	2.11	0.47
1:A:368:ASP:C	1:A:370:PRO:HD3	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:LEU:HD22	1:A:512:THR:HG22	1.97	0.47
1:A:351:VAL:HG21	1:A:381:ALA:HA	1.96	0.47
1:A:495:VAL:HG13	1:A:499:ARG:NH1	2.30	0.47
1:A:162:ASN:O	1:A:166:VAL:HG23	2.15	0.47
1:A:43:ASN:HB3	1:A:467:GLY:HA2	1.96	0.47
1:A:329:MET:HE1	1:A:347:VAL:HG22	1.97	0.46
1:A:172:LYS:HA	1:A:182:LEU:O	2.15	0.46
1:A:133:LEU:HB2	1:A:200:GLY:O	2.15	0.46
1:A:17:LEU:HA	1:A:17:LEU:HD12	1.80	0.46
1:A:369:TYR:HB3	1:A:372:GLU:HB2	1.97	0.46
1:A:42:ARG:HB2	1:A:382:ARG:HG3	1.97	0.46
1:A:74:ASN:HA	1:A:112:ASP:HB3	1.98	0.46
1:A:259:GLU:O	1:A:262:LYS:HB2	2.16	0.46
1:A:116:PRO:HG3	1:A:218:PRO:O	2.16	0.45
1:A:175:VAL:CG1	1:A:202:LEU:HD11	2.47	0.45
1:A:80:HIS:HE1	1:A:227:ASP:OD1	2.00	0.45
1:A:56:SER:HB3	1:A:59:ILE:HG22	1.98	0.44
1:A:113:THR:HG22	1:A:242:SER:H	1.82	0.44
1:A:60:LEU:HD12	1:A:60:LEU:HA	1.90	0.44
1:A:141:ILE:O	1:A:191:PHE:HA	2.17	0.44
1:A:122:LEU:O	1:A:151:CYS:HB2	2.17	0.44
1:A:401:SER:O	1:A:403:HIS:N	2.50	0.44
1:A:160:TYR:OH	1:A:215:VAL:HA	2.18	0.44
1:A:288:GLY:O	1:A:289:ILE:HD12	2.17	0.44
1:A:230:PHE:CE1	1:A:234:GLN:HG3	2.52	0.44
1:A:87:ILE:O	1:A:91:ARG:HG3	2.18	0.44
1:A:63:MET:HG2	1:A:371:LEU:HD11	1.99	0.43
1:A:143:LEU:HG	1:A:161:LYS:HD3	2.00	0.43
1:A:252:GLU:O	1:A:256:VAL:HG23	2.19	0.43
1:A:124:LYS:HB2	1:A:149:GLU:HG2	2.00	0.42
1:A:427:LEU:HD22	1:A:440:VAL:HG11	2.00	0.42
1:A:379:LEU:HD12	1:A:379:LEU:HA	1.69	0.42
1:A:231:GLY:O	1:A:236:VAL:HG22	2.19	0.42
1:A:32:LEU:HD23	1:A:32:LEU:HA	1.81	0.42
1:A:244:ILE:HG13	1:A:268:SER:HB3	2.01	0.41
1:A:148:MET:HA	1:A:157:TRP:CG	2.55	0.41
1:A:329:MET:CE	1:A:347:VAL:HG22	2.50	0.41
1:A:426:ALA:CB	1:A:448:PRO:HG2	2.50	0.41
1:A:49:THR:HB	1:A:361:SER:HA	2.02	0.41
1:A:457:GLN:O	1:A:461:GLN:HG3	2.20	0.41
1:A:64:ILE:HG12	1:A:107:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:ASP:HB2	1:A:487:LEU:HD21	2.01	0.40
1:A:49:THR:CB	1:A:361:SER:HA	2.52	0.40
1:A:115:GLY:O	1:A:117:GLU:N	2.54	0.40
1:A:15:GLN:O	1:A:15:GLN:HG2	2.21	0.40
1:A:59:ILE:HD13	1:A:63:MET:CG	2.52	0.40
1:A:59:ILE:HD13	1:A:63:MET:HG3	2.02	0.40
1:A:141:ILE:HD12	1:A:194:THR:HG21	2.04	0.40
1:A:394:PHE:HE1	1:A:443:TYR:HB3	1.85	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	517/530 (98%)	480 (93%)	33 (6%)	4 (1%)	24	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	402	SER
1	A	160	TYR
1	A	327	THR
1	A	131	VAL

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	426/435 (98%)	383 (90%)	43 (10%)	9 17

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	17	LEU
1	A	59	ILE
1	A	60	LEU
1	A	63	MET
1	A	95	GLU
1	A	113	THR
1	A	122	LEU
1	A	128	THR
1	A	140	LYS
1	A	143	LEU
1	A	147	TYR
1	A	149	GLU
1	A	152	ASP
1	A	162	ASN
1	A	177	ASP
1	A	179	LEU
1	A	182	LEU
1	A	185	LYS
1	A	192	LEU
1	A	222	GLU
1	A	255	LYS
1	A	265	LYS
1	A	272	ASN
1	A	283	LEU
1	A	289	ILE
1	A	303	GLU
1	A	315	ARG
1	A	327	THR
1	A	330	LEU
1	A	331	GLU
1	A	352	LEU
1	A	379	LEU
1	A	389	PHE
1	A	393	LEU
1	A	403	HIS
1	A	433	SER
1	A	442	ARG

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Mol	Chain	Res	Type
1	A	464	LEU
1	A	479	GLU
1	A	493	MET
1	A	499	ARG
1	A	521	THR

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	15	GLN
1	A	43	ASN
1	A	69	ASN
1	A	80	HIS
1	A	154	ASN
1	A	309	GLN
1	A	328	GLN
1	A	494	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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 (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.