



# wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 06:49 PM GMT

PDB ID : 1PV2  
Title : Native Form 2 E.coli Chaperone Hsp31  
Authors : Quigley, P.M.; Korotkov, K.; Baneyx, F.; Hol, W.G.J.  
Deposited on : 2003-06-26  
Resolution : 2.71 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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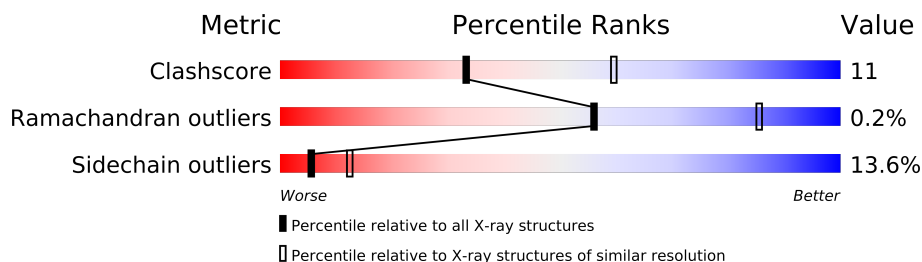
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.71 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	2183 (2.74-2.70)
Ramachandran outliers	78287	2147 (2.74-2.70)
Sidechain outliers	78261	2148 (2.74-2.70)

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  $\geq 3$ , 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	283	
1	B	283	
1	C	283	
1	D	283	
1	E	283	
1	F	283	
1	G	283	
1	H	283	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16233 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 Chaperone protein hchA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1864	1203	309	344	8			
1	B	257	Total	C	N	O	S	0	0	0
			2008	1297	337	365	9			
1	C	249	Total	C	N	O	S	0	0	0
			1940	1252	323	356	9			
1	D	264	Total	C	N	O	S	0	0	0
			2048	1319	342	378	9			
1	E	270	Total	C	N	O	S	0	0	0
			2091	1341	352	389	9			
1	F	261	Total	C	N	O	S	0	0	0
			2031	1310	339	373	9			
1	G	260	Total	C	N	O	S	0	0	0
			2023	1305	338	371	9			
1	H	277	Total	C	N	O	S	0	0	0
			2156	1386	359	402	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING MET	UNP P31658
B	1	MET	-	INITIATING MET	UNP P31658
C	1	MET	-	INITIATING MET	UNP P31658
D	1	MET	-	INITIATING MET	UNP P31658
E	1	MET	-	INITIATING MET	UNP P31658
F	1	MET	-	INITIATING MET	UNP P31658
G	1	MET	-	INITIATING MET	UNP P31658
H	1	MET	-	INITIATING MET	UNP P31658

- Molecule 2 is water.

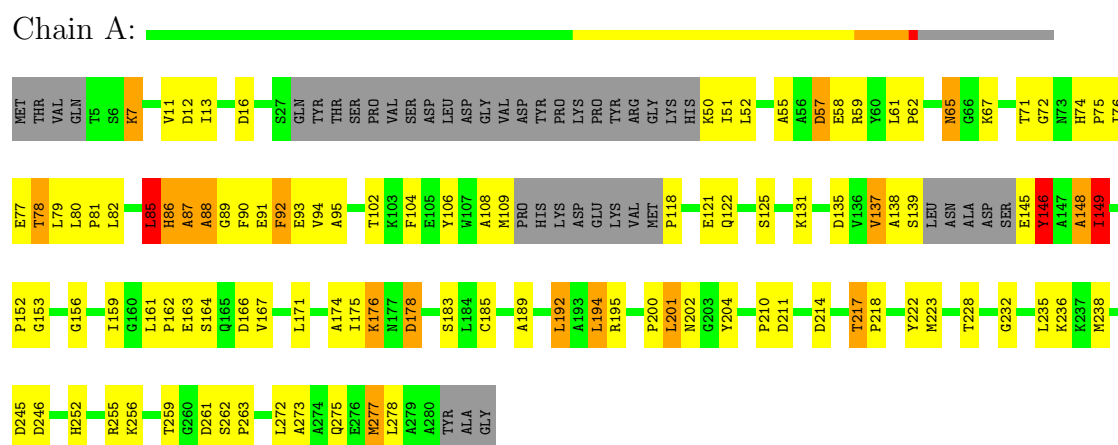
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total 7	O 7	0	0
2	B	7	Total 7	O 7	0	0
2	C	13	Total 13	O 13	0	0
2	D	7	Total 7	O 7	0	0
2	E	6	Total 6	O 6	0	0
2	F	8	Total 8	O 8	0	0
2	G	11	Total 11	O 11	0	0
2	H	13	Total 13	O 13	0	0

### 3 Residue-property plots

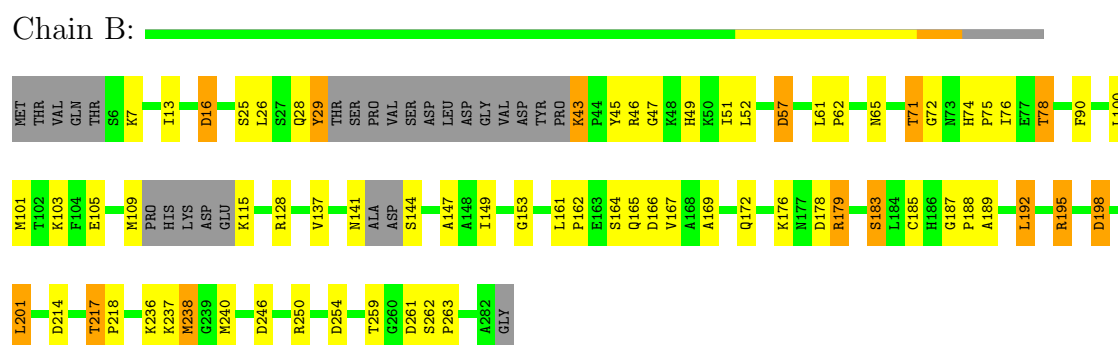
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

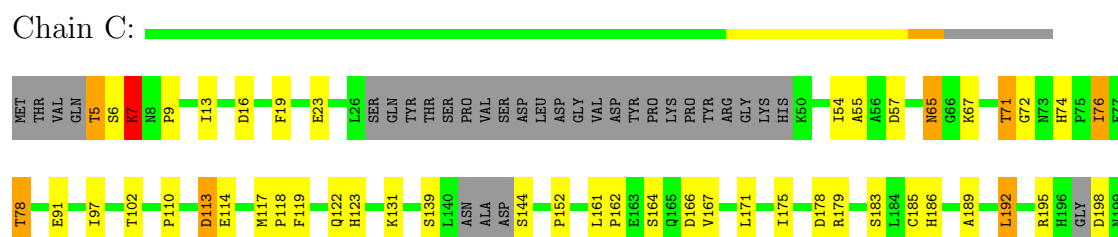
#### • Molecule 1: Chaperone protein hchA

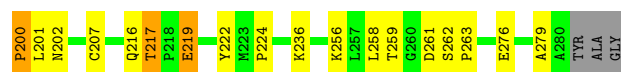


#### • Molecule 1: Chaperone protein hchA



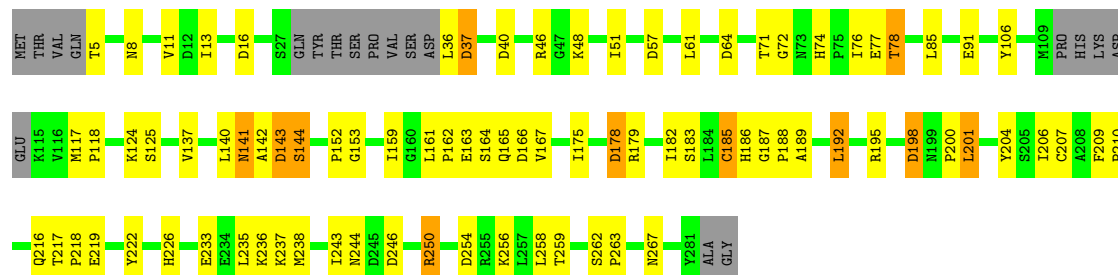
#### • Molecule 1: Chaperone protein hchA





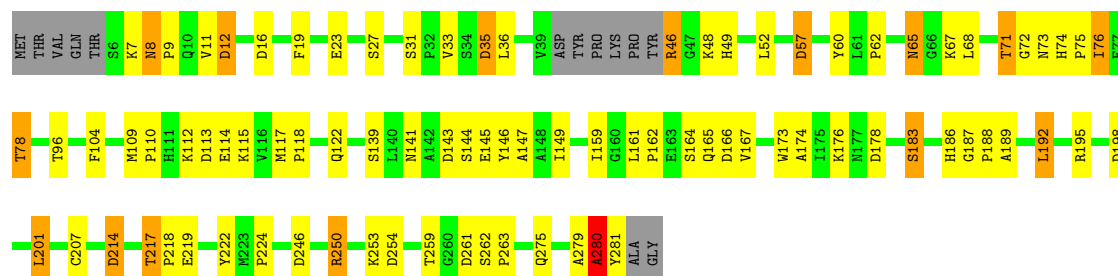
• Molecule 1: Chaperone protein hchA

Chain D:



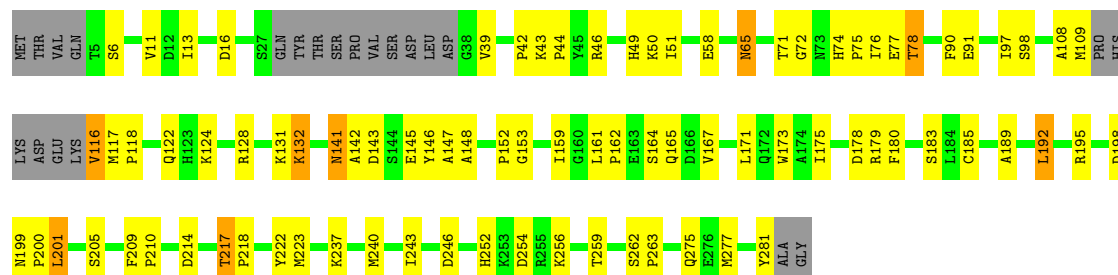
• Molecule 1: Chaperone protein hchA

Chain E:



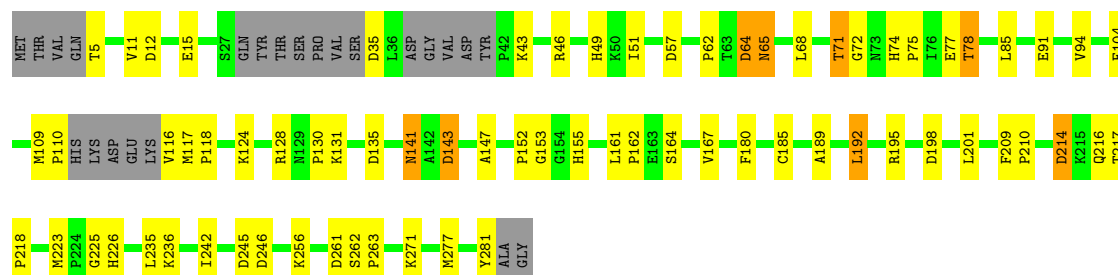
• Molecule 1: Chaperone protein hchA

Chain F:



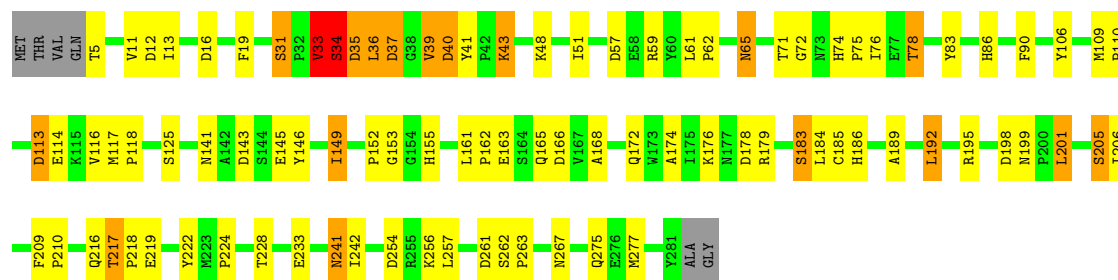
• Molecule 1: Chaperone protein hchA

Chain G:



● Molecule 1: Chaperone protein hchA

Chain H: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.49Å 99.02Å 116.80Å 102.95° 101.52° 94.19°	Depositor
Resolution (Å)	48.80 – 2.71	Depositor
% Data completeness (in resolution range)	94.0 (48.80-2.71)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.221 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16233	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	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	0.42	0/1912	0.98	24/2591 (0.9%)
1	B	0.26	0/2062	0.60	8/2792 (0.3%)
1	C	0.39	2/1991 (0.1%)	0.61	6/2698 (0.2%)
1	D	0.26	0/2104	0.62	10/2853 (0.4%)
1	E	0.32	0/2147	0.68	16/2912 (0.5%)
1	F	0.26	0/2087	0.61	6/2831 (0.2%)
1	G	0.26	0/2078	0.61	11/2817 (0.4%)
1	H	0.30	1/2218 (0.0%)	0.65	12/3014 (0.4%)
All	All	0.31	3/16599 (0.0%)	0.68	93/22508 (0.4%)

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	4
1	C	0	1
1	E	0	2
1	H	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	7	LYS	C-N	-10.12	1.10	1.34
1	C	200	PRO	C-N	8.60	1.53	1.34
1	H	34	SER	C-N	-6.46	1.19	1.34

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	146	TYR	CB-CG-CD2	18.61	132.17	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	ALA	C-N-CA	12.80	153.70	121.70
1	A	146	TYR	CB-CG-CD1	-12.66	113.40	121.00
1	A	87	ALA	N-CA-CB	8.19	121.56	110.10
1	A	146	TYR	CZ-CE2-CD2	-7.67	112.89	119.80

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	146	TYR	Sidechain
1	A	148	ALA	Mainchain,Peptide
1	A	85	LEU	Peptide
1	C	7	LYS	Mainchain
1	E	280	ALA	Mainchain

## 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	1864	0	1818	76	0
1	B	2008	0	1965	45	0
1	C	1940	0	1898	37	0
1	D	2048	0	1987	41	0
1	E	2091	0	2034	37	0
1	F	2031	0	1979	44	0
1	G	2023	0	1976	32	0
1	H	2156	0	2087	48	0
2	A	7	0	0	1	0
2	B	7	0	0	0	0
2	C	13	0	0	1	0
2	D	7	0	0	0	0
2	E	6	0	0	0	0
2	F	8	0	0	0	0
2	G	11	0	0	0	0
2	H	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16233	0	15744	354	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 11.

The worst 5 of 354 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:74:HIS:O	1:A:78:THR:HG22	1.59	1.00
1:A:50:LYS:N	1:A:51:ILE:HA	1.72	0.99
1:A:85:LEU:O	1:A:90:PHE:HB2	1.74	0.86
1:B:49:HIS:HB3	1:B:147:ALA:HB2	1.59	0.85
1:A:75:PRO:HG2	1:A:109:MET:HB3	1.59	0.85

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	233/283 (82%)	204 (88%)	27 (12%)	2 (1%)	25	54
1	B	249/283 (88%)	232 (93%)	17 (7%)	0	100	100
1	C	241/283 (85%)	226 (94%)	14 (6%)	1 (0%)	43	76
1	D	258/283 (91%)	248 (96%)	10 (4%)	0	100	100
1	E	266/283 (94%)	251 (94%)	14 (5%)	1 (0%)	43	76
1	F	255/283 (90%)	242 (95%)	13 (5%)	0	100	100
1	G	252/283 (89%)	242 (96%)	10 (4%)	0	100	100
1	H	275/283 (97%)	256 (93%)	18 (6%)	1 (0%)	43	76
All	All	2029/2264 (90%)	1901 (94%)	123 (6%)	5 (0%)	56	85

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	36	LEU
1	A	86	HIS
1	A	87	ALA
1	E	280	ALA
1	C	279	ALA

### 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	192/230 (84%)	166 (86%)	26 (14%)	6	13
1	B	207/230 (90%)	178 (86%)	29 (14%)	5	11
1	C	202/230 (88%)	177 (88%)	25 (12%)	7	16
1	D	211/230 (92%)	185 (88%)	26 (12%)	7	16
1	E	218/230 (95%)	182 (84%)	36 (16%)	3	8
1	F	210/230 (91%)	179 (85%)	31 (15%)	4	11
1	G	210/230 (91%)	191 (91%)	19 (9%)	14	30
1	H	225/230 (98%)	190 (84%)	35 (16%)	4	9
All	All	1675/1840 (91%)	1448 (86%)	227 (14%)	5	12

5 of 227 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	236	LYS
1	E	141	ASN
1	H	145	GLU
1	D	250	ARG
1	E	46	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	267	ASN
1	E	196	HIS
1	H	196	HIS

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Mol	Chain	Res	Type
1	E	65	ASN
1	E	141	ASN

### 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 ⓘ

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 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.