



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:23 am BST

PDB ID : 4RNS
Title : PcpR inducer binding domain (apo-form)
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Deposited on : 2014-10-25
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

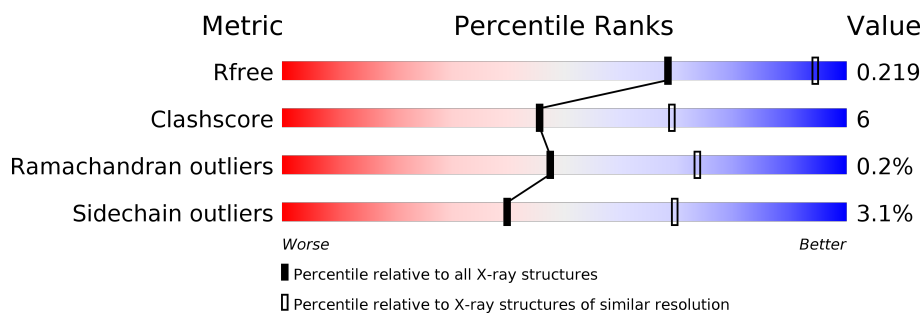
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.70 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))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

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 ≥ 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	223	
1	B	223	
1	C	223	
1	D	223	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7013 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 PCP degradation transcriptional activation protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1720	1101	306	309	4			
1	B	213	Total	C	N	O	S	0	0	0
			1709	1095	302	308	4			
1	C	217	Total	C	N	O	S	0	0	0
			1736	1112	307	313	4			
1	D	217	Total	C	N	O	S	0	0	0
			1736	1112	307	313	4			

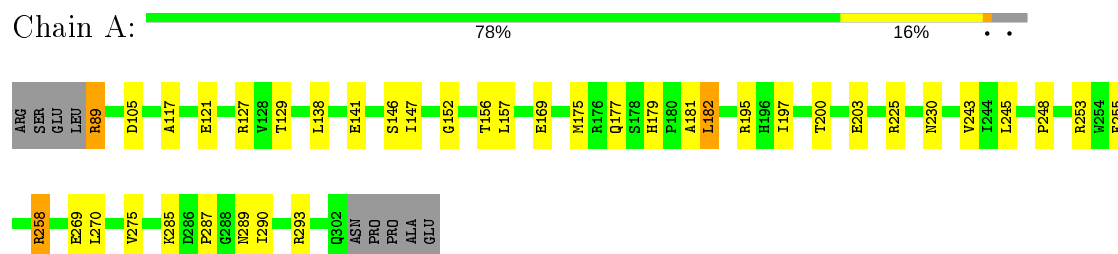
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	32	Total	O	0	0
			32	32		
2	B	18	Total	O	0	0
			18	18		
2	C	33	Total	O	0	0
			33	33		
2	D	29	Total	O	0	0
			29	29		

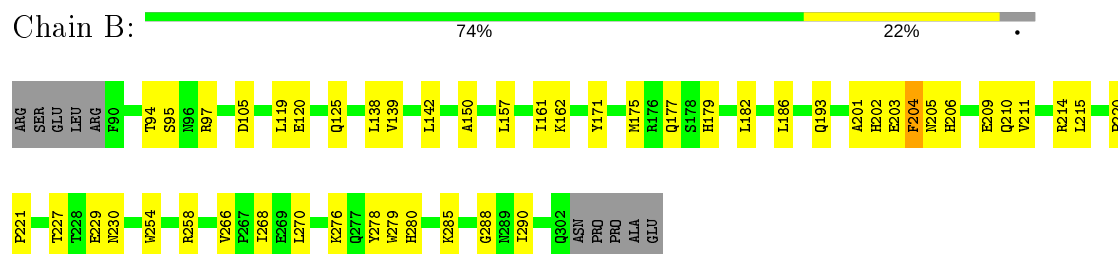
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

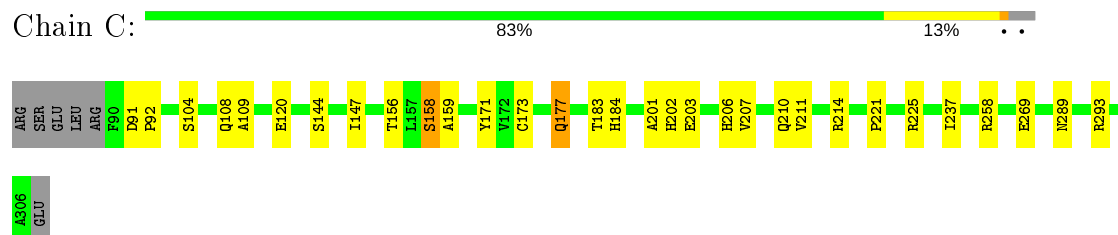
- Molecule 1: PCP degradation transcriptional activation protein



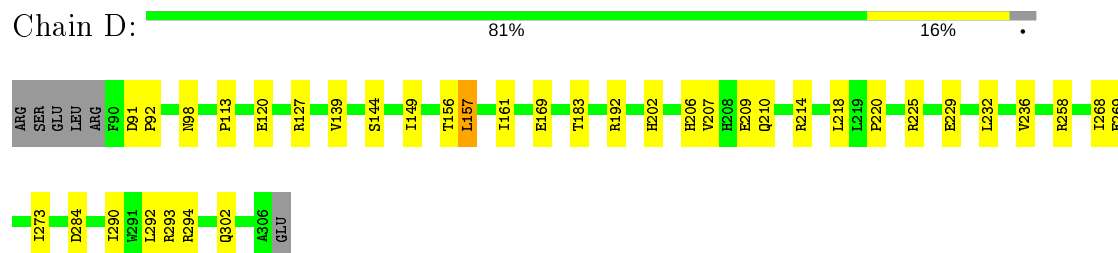
- Molecule 1: PCP degradation transcriptional activation protein



- Molecule 1: PCP degradation transcriptional activation protein



- Molecule 1: PCP degradation transcriptional activation protein



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	169.45Å 169.45Å 109.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.36 – 2.70 49.51 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.36-2.70) 83.3 (49.51-2.22)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	-1.06 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.161 , 0.216 0.168 , 0.219	Depositor DCC
R_{free} test set	2005 reflections (3.49%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7013	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.49	0/1763	0.56	0/2397
1	B	0.49	0/1752	0.55	0/2383
1	C	0.50	1/1781 (0.1%)	0.55	0/2425
1	D	0.48	0/1781	0.55	0/2425
All	All	0.49	1/7077 (0.0%)	0.56	0/9630

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	173	CYS	CB-SG	-5.15	1.73	1.81

There are no bond angle outliers.

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	1720	0	1711	30	0
1	B	1709	0	1698	29	0
1	C	1736	0	1723	18	0
1	D	1736	0	1723	23	0
2	A	32	0	0	3	0
2	B	18	0	0	0	0
2	C	33	0	0	0	0
2	D	29	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7013	0	6855	88	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 6.

All (88) 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:225:ARG:NH2	1:B:120:GLU:OE2	2.11	0.83
1:C:120:GLU:OE2	1:D:225:ARG:NH2	2.19	0.76
1:A:179:HIS:HD2	1:A:181:ALA:H	1.33	0.74
1:D:202:HIS:HA	1:D:209:GLU:HG2	1.70	0.72
1:A:89:ARG:HB2	1:A:287:PRO:HG2	1.77	0.66
1:D:206:HIS:O	1:D:209:GLU:HG3	1.98	0.64
1:A:117:ALA:O	1:A:121:GLU:HG2	2.00	0.62
1:C:214:ARG:NH2	1:C:269:GLU:O	2.32	0.62
1:A:270:LEU:O	2:A:413:HOH:O	2.16	0.60
1:D:149:ILE:HD12	1:D:292:LEU:HD23	1.85	0.58
1:B:266:VAL:HG11	1:B:270:LEU:HD12	1.86	0.58
1:D:139:VAL:HG13	1:D:161:ILE:HD11	1.87	0.56
1:A:225:ARG:HD3	2:A:422:HOH:O	2.06	0.54
1:C:158:SER:OG	1:C:159:ALA:N	2.39	0.54
1:B:138:LEU:HD23	1:B:157:LEU:HD11	1.89	0.54
1:B:175:MET:HE2	1:B:179:HIS:HB3	1.89	0.54
1:A:253:ARG:O	1:A:253:ARG:HD3	2.08	0.54
1:A:179:HIS:CD2	1:A:181:ALA:H	2.20	0.53
1:B:139:VAL:HG13	1:B:161:ILE:HD11	1.90	0.53
1:D:192:ARG:NH1	1:D:220:PRO:HD3	2.24	0.52
1:A:197:ILE:HG23	1:A:245:LEU:HD13	1.92	0.51
1:A:225:ARG:NH1	2:A:422:HOH:O	2.31	0.51
1:A:175:MET:HE1	1:A:181:ALA:HB3	1.93	0.50
1:C:104:SER:O	1:C:108:GLN:HG3	2.11	0.50
1:B:210:GLN:O	1:B:214:ARG:HG2	2.12	0.50
1:C:221:PRO:O	1:D:127:ARG:NH2	2.43	0.50
1:B:138:LEU:HB3	1:B:157:LEU:HD21	1.93	0.49
1:A:138:LEU:HD23	1:A:157:LEU:HD11	1.94	0.49
1:B:162:LYS:HB2	1:B:279:TRP:CE2	2.48	0.49
1:A:225:ARG:HD2	1:B:119:LEU:HD13	1.95	0.49
1:B:201:ALA:HB1	1:B:206:HIS:HB3	1.95	0.48
1:B:142:LEU:HB3	1:B:280:HIS:HB2	1.94	0.48
1:C:109:ALA:HB1	1:D:236:VAL:HG21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:HIS:HA	1:B:209:GLU:HG2	1.95	0.48
1:C:225:ARG:HH21	1:D:120:GLU:HG2	1.79	0.48
1:C:177:GLN:N	1:C:177:GLN:OE1	2.47	0.48
1:C:289:ASN:OD1	1:C:293:ARG:NH1	2.46	0.48
1:A:258:ARG:NH2	1:B:254:TRP:CH2	2.82	0.48
1:A:89:ARG:HG2	1:A:89:ARG:HH11	1.78	0.47
1:B:276:LYS:HB2	1:B:278:TYR:CE1	2.48	0.47
1:B:285:LYS:HA	1:B:290:ILE:HD11	1.96	0.47
1:A:177:GLN:HA	1:A:182:LEU:HD13	1.97	0.47
1:A:289:ASN:O	1:A:293:ARG:HG3	2.14	0.47
1:B:171:TYR:CZ	1:B:211:VAL:HG21	2.49	0.46
1:B:105:ASP:OD2	1:B:230:ASN:HB3	2.15	0.46
1:A:105:ASP:OD2	1:A:230:ASN:HB3	2.15	0.46
1:D:290:ILE:O	1:D:294:ARG:HG2	2.14	0.46
1:C:201:ALA:HB1	1:C:206:HIS:HB3	1.96	0.46
1:C:207:VAL:O	1:C:210:GLN:HG2	2.16	0.46
1:C:237:ILE:HG12	1:D:113:PRO:HG3	1.98	0.46
1:B:95:SER:O	1:B:125:GLN:HB3	2.16	0.45
1:A:152:GLY:HA2	1:A:275:VAL:HG13	1.99	0.45
1:D:207:VAL:HG13	1:D:273:ILE:HD13	1.99	0.45
1:C:225:ARG:NH2	1:D:120:GLU:OE2	2.50	0.44
1:A:141:GLU:OE1	1:A:146:SER:OG	2.33	0.44
1:D:202:HIS:CA	1:D:209:GLU:HG2	2.42	0.44
1:D:214:ARG:NH1	1:D:269:GLU:O	2.51	0.44
1:C:183:THR:OG1	1:C:184:HIS:N	2.50	0.44
1:A:195:ARG:HB3	1:A:243:VAL:HG12	2.00	0.43
1:C:171:TYR:CE1	1:C:211:VAL:HG21	2.52	0.43
1:A:285:LYS:HA	1:A:290:ILE:HD11	2.00	0.43
1:C:289:ASN:O	1:C:293:ARG:HG3	2.18	0.43
1:B:220:PRO:HA	1:B:221:PRO:HD3	1.85	0.43
1:D:210:GLN:O	1:D:214:ARG:HG2	2.19	0.43
1:D:91:ASP:HA	1:D:92:PRO:HD3	1.89	0.43
1:D:284:ASP:HA	1:D:293:ARG:HH12	1.83	0.42
1:A:255:PHE:O	1:A:258:ARG:HG3	2.19	0.42
1:B:177:GLN:O	1:B:182:LEU:HD22	2.19	0.42
1:A:147:ILE:HA	1:A:147:ILE:HD13	1.93	0.42
1:B:276:LYS:HD2	1:B:278:TYR:OH	2.20	0.42
1:A:89:ARG:CG	1:A:89:ARG:HH11	2.33	0.42
1:D:98:ASN:ND2	2:D:409:HOH:O	2.49	0.42
1:B:215:LEU:HD23	1:B:268:ILE:HD12	2.01	0.41
1:D:218:LEU:HD22	1:D:268:ILE:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:TYR:CE1	1:B:211:VAL:HG21	2.54	0.41
1:A:127:ARG:NH2	1:B:221:PRO:O	2.52	0.41
1:B:97:ARG:NH1	1:B:288:GLY:HA3	2.35	0.41
1:B:204:PHE:HZ	1:B:229:GLU:OE1	2.03	0.41
1:A:269:GLU:OE1	1:D:183:THR:OG1	2.37	0.41
1:A:177:GLN:O	1:A:182:LEU:HD22	2.21	0.41
1:D:232:LEU:O	1:D:236:VAL:HG13	2.20	0.41
1:A:169:GLU:HG2	1:A:248:PRO:HB3	2.02	0.40
1:B:186:LEU:HD12	1:B:186:LEU:HA	1.88	0.40
1:A:129:THR:OG1	1:B:227:THR:HB	2.22	0.40
1:D:157:LEU:HG	1:D:161:ILE:HG13	2.03	0.40
1:B:150:ALA:HB3	1:B:278:TYR:HB2	2.02	0.40
1:C:202:HIS:CD2	1:C:203:GLU:HG3	2.56	0.40
1:C:91:ASP:HA	1:C:92:PRO:HD3	1.96	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	212/223 (95%)	202 (95%)	10 (5%)	0	100	100
1	B	211/223 (95%)	197 (93%)	13 (6%)	1 (0%)	29	54
1	C	215/223 (96%)	206 (96%)	8 (4%)	1 (0%)	29	54
1	D	215/223 (96%)	207 (96%)	8 (4%)	0	100	100
All	All	853/892 (96%)	812 (95%)	39 (5%)	2 (0%)	47	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	158	SER

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Mol	Chain	Res	Type
1	B	205	ASN

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	185/193 (96%)	179 (97%)	6 (3%)	39	68
1	B	184/193 (95%)	179 (97%)	5 (3%)	44	74
1	C	187/193 (97%)	182 (97%)	5 (3%)	44	74
1	D	187/193 (97%)	180 (96%)	7 (4%)	34	63
All	All	743/772 (96%)	720 (97%)	23 (3%)	40	69

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	ARG
1	A	156	THR
1	A	182	LEU
1	A	200	THR
1	A	203	GLU
1	A	258	ARG
1	B	94	THR
1	B	193	GLN
1	B	203	GLU
1	B	204	PHE
1	B	258	ARG
1	C	144	SER
1	C	147	ILE
1	C	156	THR
1	C	177	GLN
1	C	258	ARG
1	D	144	SER
1	D	156	THR
1	D	157	LEU
1	D	169	GLU

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Mol	Chain	Res	Type
1	D	229	GLU
1	D	258	ARG
1	D	302	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	HIS
1	D	210	GLN
1	D	303	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.