



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 08:15 am BST

PDB ID : 5TTE
Title : Crystal Structure of an RBR E3 ubiquitin ligase in complex with an E2-Ub thioester intermediate mimic
Authors : Yuan, L.; Lv, Z.; Olsen, S.K.
Deposited on : 2016-11-03
Resolution : 3.50 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

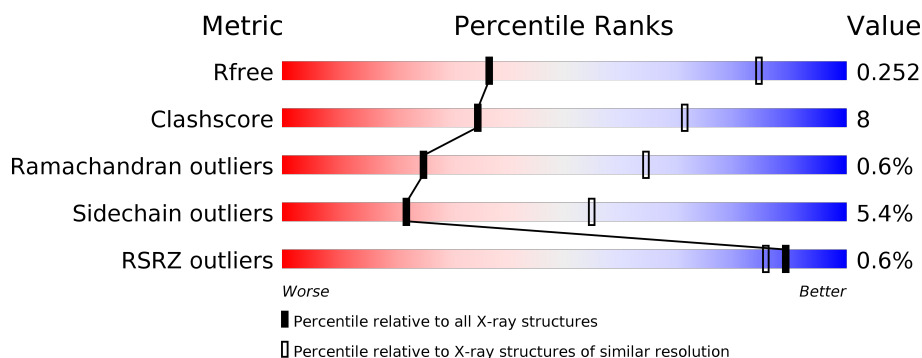
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	B	558	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>19%</div> <div>•</div> <div>21%</div> </div> </div>
2	E	167	<div> <div>%</div> <div> <div></div> <div>73%</div> <div>16%</div> <div>•</div> <div>10%</div> </div> </div>
3	F	86	<div> <div></div> <div>79%</div> <div>13%</div> <div>8%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5551 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 E3 ubiquitin-protein ligase ARIH1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	442	Total	C	N	O	S	0	0	0
			3668	2309	647	668	44			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP Q9Y4X5

- Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	151	Total	C	N	O	S	0	1	0
			1245	798	215	229	3			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	17	SER	CYS	engineered mutation	UNP P68036
E	86	LYS	CYS	engineered mutation	UNP P68036
E	155	LYS	-	expression tag	UNP P68036
E	156	LEU	-	expression tag	UNP P68036
E	157	ALA	-	expression tag	UNP P68036
E	158	ALA	-	expression tag	UNP P68036
E	159	ALA	-	expression tag	UNP P68036
E	160	LEU	-	expression tag	UNP P68036
E	161	GLU	-	expression tag	UNP P68036
E	162	HIS	-	expression tag	UNP P68036
E	163	HIS	-	expression tag	UNP P68036
E	164	HIS	-	expression tag	UNP P68036
E	165	HIS	-	expression tag	UNP P68036
E	166	HIS	-	expression tag	UNP P68036
E	167	HIS	-	expression tag	UNP P68036

- Molecule 3 is a protein called ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	79	Total	C	N	O	S	0	0	0
			632	386	124	121	1			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-9	MET	-	initiating methionine	UNP A0A1D6DHW0
F	-8	HIS	-	expression tag	UNP A0A1D6DHW0
F	-7	HIS	-	expression tag	UNP A0A1D6DHW0
F	-6	HIS	-	expression tag	UNP A0A1D6DHW0
F	-5	HIS	-	expression tag	UNP A0A1D6DHW0
F	-4	HIS	-	expression tag	UNP A0A1D6DHW0
F	-3	HIS	-	expression tag	UNP A0A1D6DHW0
F	-2	GLY	-	expression tag	UNP A0A1D6DHW0
F	-1	SER	-	expression tag	UNP A0A1D6DHW0
F	0	HIS	-	expression tag	UNP A0A1D6DHW0
F	6	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	11	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	27	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	29	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	33	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	48	ARG	LYS	engineered mutation	UNP A0A1D6DHW0
F	63	ARG	LYS	engineered mutation	UNP A0A1D6DHW0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	6	Total	Zn	0	0
			6	6		

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.23 Å 154.23 Å 285.50 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.71 – 3.50 49.71 – 3.50	Depositor EDS
% Data completeness (in resolution range)	95.1 (49.71-3.50) 95.1 (49.71-3.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 3.48 Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.226 , 0.252 0.226 , 0.252	Depositor DCC
R_{free} test set	2000 reflections (8.08%)	wwPDB-VP
Wilson B-factor (Å ²)	98.7	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 65.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5551	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	B	0.25	0/3756	0.40	0/5066
2	E	0.25	0/1279	0.40	0/1727
3	F	0.24	0/638	0.46	0/859
All	All	0.25	0/5673	0.40	0/7652

There are no bond length outliers.

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	B	3668	0	3523	72	0
2	E	1245	0	1259	17	0
3	F	632	0	640	6	0
4	B	6	0	0	0	0
All	All	5551	0	5422	91	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 8.

All (91) 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:B:276:CYS:CB	1:B:297:CYS:SG	2.66	0.83
1:B:445:MET:N	1:B:445:MET:SD	2.58	0.75
1:B:347:CYS:HB3	1:B:367:CYS:SG	2.32	0.70
1:B:299:CYS:O	1:B:301:ARG:N	2.25	0.69
2:E:21:ASN:HD22	2:E:109:ILE:HG21	1.61	0.65
1:B:276:CYS:HB3	1:B:297:CYS:SG	2.34	0.65
1:B:465:LEU:HD21	1:B:506:SER:HB2	1.78	0.65
1:B:116:CYS:SG	1:B:142:LYS:NZ	2.66	0.64
1:B:232:PRO:HA	2:E:96:LYS:HD2	1.80	0.64
1:B:316:LYS:HB2	1:B:319:TRP:HD1	1.65	0.61
1:B:220:ILE:HD13	1:B:258:TYR:HB2	1.82	0.60
1:B:356:GLY:HA3	1:B:431:GLU:HG3	1.83	0.60
1:B:452:TRP:HA	1:B:455:VAL:HG22	1.84	0.59
1:B:388:ASN:OD1	1:B:391:ARG:NH2	2.35	0.59
1:B:483:LYS:O	1:B:485:ASN:ND2	2.33	0.59
1:B:353:LYS:NZ	1:B:358:ASN:OD1	2.29	0.57
2:E:88:PRO:HG3	3:F:76:GLY:HA3	1.87	0.57
2:E:60:GLU:OE1	2:E:60:GLU:N	2.38	0.56
1:B:482:LEU:HD22	1:B:552:TRP:HB2	1.86	0.56
1:B:381:PRO:HB2	1:B:387:TYR:CD2	2.41	0.56
1:B:201:LEU:HD11	1:B:240:VAL:HG22	1.87	0.55
1:B:550:ASP:N	1:B:550:ASP:OD2	2.40	0.55
1:B:381:PRO:HB2	1:B:387:TYR:HD2	1.71	0.55
1:B:127:PRO:HB2	1:B:130:ILE:HD13	1.89	0.54
1:B:217:THR:HG23	1:B:249:ILE:HD12	1.89	0.54
1:B:497:ASP:HB3	1:B:535:ARG:HD2	1.90	0.54
2:E:40:VAL:HG11	2:E:152:PRO:HD2	1.89	0.54
1:B:276:CYS:HB2	1:B:297:CYS:SG	2.42	0.53
2:E:48:LYS:NZ	2:E:141:GLU:OE2	2.39	0.53
1:B:278:ALA:HB3	1:B:281:CYS:HB3	1.91	0.52
1:B:171:ARG:HD3	1:B:171:ARG:N	2.24	0.52
1:B:297:CYS:O	1:B:298:LYS:HB3	2.09	0.52
2:E:39:ILE:HD11	2:E:53:ILE:HD13	1.92	0.52
2:E:65:PRO:HB3	2:E:95:TRP:CD2	2.46	0.51
1:B:126:ASN:ND2	1:B:149:TYR:OH	2.42	0.51
1:B:213:SER:O	1:B:217:THR:OG1	2.20	0.51
1:B:292:ALA:HA	1:B:306:ASN:HB2	1.93	0.50
3:F:-1:SER:N	3:F:16:GLU:OE2	2.36	0.49
1:B:469:ARG:NH2	1:B:503:GLU:OE2	2.44	0.49
1:B:129:THR:HA	1:B:132:ARG:HD3	1.94	0.49
1:B:307:CYS:SG	1:B:308:GLY:N	2.85	0.49
1:B:271:ARG:HH11	1:B:290:PRO:HD2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:358:ASN:ND2	1:B:503:GLU:OE2	2.46	0.48
2:E:76:HIS:NE2	2:E:115:PRO:HB3	2.28	0.48
1:B:312:HIS:HA	1:B:474:TYR:CD2	2.49	0.48
1:B:472:LEU:HD21	1:B:499:GLU:HA	1.94	0.47
1:B:344:CYS:CB	1:B:347:CYS:SG	3.02	0.47
1:B:132:ARG:NE	1:B:227:GLN:OE1	2.45	0.47
1:B:294:PRO:HD3	1:B:311:TRP:CH2	2.50	0.47
1:B:517:SER:OG	1:B:520:ASP:OD2	2.33	0.47
2:E:102:ASP:HA	2:E:105:ILE:HD12	1.96	0.47
2:E:87:LEU:HG	2:E:89:VAL:HG12	1.97	0.47
1:B:389:CYS:O	1:B:420:ARG:NH2	2.37	0.47
1:B:190:TYR:CD2	2:E:6:ARG:HG3	2.50	0.47
1:B:427:SER:HB3	1:B:469:ARG:NH1	2.30	0.47
1:B:217:THR:HG22	1:B:254:VAL:HG11	1.97	0.46
3:F:50:LEU:HD22	3:F:67:LEU:HD11	1.97	0.46
3:F:5:VAL:HG22	3:F:67:LEU:HB3	1.98	0.46
1:B:431:GLU:OE1	1:B:469:ARG:HG3	2.15	0.46
1:B:457:PHE:HE2	1:B:526:GLN:HB2	1.81	0.46
1:B:434:LEU:O	1:B:438:VAL:N	2.45	0.45
1:B:441:LYS:HD3	1:B:441:LYS:HA	1.68	0.45
1:B:535:ARG:HD3	1:B:535:ARG:HA	1.79	0.45
1:B:215:TYR:CZ	1:B:232:PRO:HB3	2.52	0.45
1:B:293:LYS:HE3	1:B:294:PRO:HD2	1.98	0.45
2:E:76:HIS:CE1	2:E:115:PRO:HB3	2.52	0.45
1:B:117:ILE:O	1:B:121:ASN:HB2	2.16	0.44
2:E:124:ASP:N	2:E:124:ASP:OD1	2.50	0.44
2:E:22:PHE:CD2	2:E:105:ILE:HD13	2.52	0.44
1:B:375:CYS:HB3	1:B:389:CYS:HB2	1.99	0.44
3:F:18:GLU:N	3:F:21:ASP:OD2	2.51	0.44
1:B:327:CYS:HA	1:B:332:GLU:HB2	2.00	0.44
1:B:244:THR:HG22	1:B:247:ARG:HH12	1.82	0.44
2:E:116:GLN:HB2	2:E:118:GLU:OE1	2.18	0.43
1:B:312:HIS:H	1:B:312:HIS:CD2	2.36	0.43
1:B:215:TYR:CE1	1:B:232:PRO:HB3	2.54	0.43
1:B:316:LYS:HB2	1:B:319:TRP:CD1	2.51	0.43
1:B:130:ILE:HG13	1:B:163:VAL:CG2	2.48	0.43
1:B:341:THR:HG22	1:B:352:GLU:HB3	2.00	0.42
1:B:468:CYS:O	1:B:472:LEU:HB2	2.19	0.42
1:B:281:CYS:SG	1:B:283:HIS:ND1	2.93	0.42
1:B:478:PHE:O	1:B:482:LEU:HG	2.20	0.42
1:B:379:TRP:HH2	1:B:503:GLU:HG2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:PRO:HD2	1:B:197:TYR:CE1	2.55	0.41
1:B:297:CYS:HB3	1:B:299:CYS:O	2.20	0.41
3:F:23:ILE:HG23	3:F:52:ASP:HA	2.02	0.41
1:B:188:ILE:HG23	2:E:97:PRO:HB2	2.03	0.41
1:B:109:ILE:HG13	1:B:284:VAL:HG21	2.02	0.41
1:B:267:VAL:HG13	1:B:273:LEU:HB3	2.02	0.41
1:B:543:VAL:HA	1:B:552:TRP:CZ2	2.56	0.40
1:B:144:LYS:HD3	1:B:144:LYS:HA	1.84	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	B	436/558 (78%)	393 (90%)	40 (9%)	3 (1%)	22	61
2	E	150/167 (90%)	141 (94%)	9 (6%)	0	100	100
3	F	77/86 (90%)	72 (94%)	4 (5%)	1 (1%)	12	48
All	All	663/811 (82%)	606 (91%)	53 (8%)	4 (1%)	25	64

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	GLY
1	B	484	LYS
1	B	222	GLU
3	F	75	GLY

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	B	408/489 (83%)	381 (93%)	27 (7%)	16	49
2	E	138/148 (93%)	132 (96%)	6 (4%)	29	62
3	F	69/76 (91%)	69 (100%)	0	100	100
All	All	615/713 (86%)	582 (95%)	33 (5%)	22	55

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	112	HIS
1	B	149	TYR
1	B	164	ILE
1	B	169	LYS
1	B	171	ARG
1	B	222	GLU
1	B	223	GLU
1	B	225	MET
1	B	229	ILE
1	B	231	CYS
1	B	236	CYS
1	B	312	HIS
1	B	323	TRP
1	B	336	TRP
1	B	387	TYR
1	B	394	GLU
1	B	441	LYS
1	B	445	MET
1	B	446	GLN
1	B	450	MET
1	B	452	TRP
1	B	457	PHE
1	B	503	GLU
1	B	512	ASP
1	B	550	ASP
1	B	552	TRP

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Mol	Chain	Res	Type
1	B	554	TYR
2	E	19	MET
2	E	22	PHE
2	E	25	ILE
2	E	40	VAL
2	E	82	LYS
2	E	114	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	423	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](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	442/558 (79%)	-0.15	3 (0%) 87 83	68, 110, 201, 281	0
2	E	151/167 (90%)	-0.16	1 (0%) 87 83	75, 112, 183, 208	0
3	F	79/86 (91%)	-0.07	0 100 100	78, 116, 187, 221	0
All	All	672/811 (82%)	-0.15	4 (0%) 89 86	68, 112, 196, 281	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	454	GLU	2.8
1	B	456	GLN	2.6
1	B	457	PHE	2.2
2	E	49	GLY	2.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ZN	B	602	1/1	0.84	0.33	216,216,216,216	0
4	ZN	B	606	1/1	0.97	0.06	143,143,143,143	0
4	ZN	B	601	1/1	0.98	0.12	150,150,150,150	0
4	ZN	B	605	1/1	0.98	0.09	119,119,119,119	0
4	ZN	B	603	1/1	0.99	0.17	123,123,123,123	0
4	ZN	B	604	1/1	0.99	0.20	141,141,141,141	0

6.5 Other polymers [i](#)

There are no such residues in this entry.