



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 25, 2024 – 10:18 pm BST

PDB ID : 5L6T  
Title : CRYSTAL STRUCTURE OF HUMAN CARBONIC ANHYDRASE II IN  
COMPLEX WITH A QUINOLINE OLIGOAMIDE FOLDAMER  
Authors : Vallade, M.; Langlois d'Estaintot, B.; Granier, T.; Huc, I.  
Deposited on : 2016-05-31  
Resolution : 2.65 Å(reported)

This is a wwPDB X-ray Structure 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

<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>.

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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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

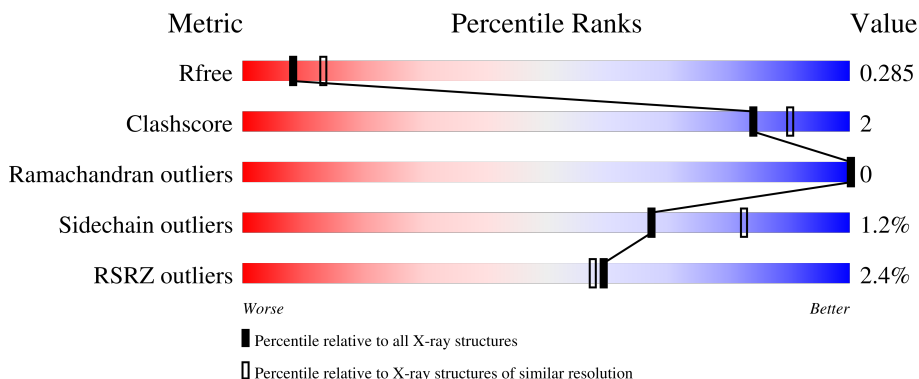
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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))
$R_{free}$	164625	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

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  $\geq 3$ , 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	A	260	
1	B	260	
2	C	6	
2	D	6	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4427 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 Carbonic anhydrase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	1	0
			2051	1316	354	379	2			
1	B	251	Total	C	N	O	S	0	0	0
			1962	1259	338	363	2			

- Molecule 2 is a protein called Aromatic foldamer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	S	0	0	0
			99	70	12	16	1			
2	D	6	Total	C	N	O	S	0	0	0
			99	70	12	16	1			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	10	Total	Zn	0	0
			10	10		
3	B	5	Total	Zn	0	0
			5	5		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

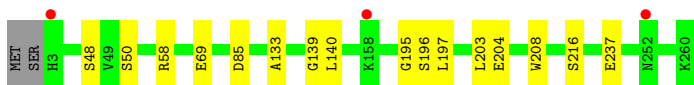
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	103	Total	O	0	0
			103	103		
5	B	66	Total	O	0	0
			66	66		
5	C	3	Total	O	0	0
			3	3		
5	D	5	Total	O	0	0
			5	5		

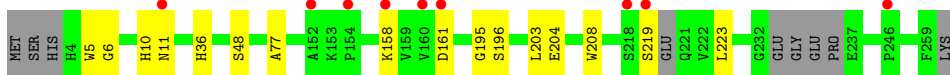
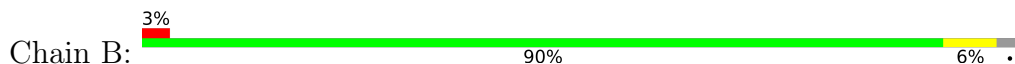
### 3 Residue-property plots

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 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.

- Molecule 1: Carbonic anhydrase 2



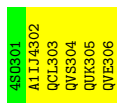
- Molecule 1: Carbonic anhydrase 2



- Molecule 2: Aromatic foldamer



- Molecule 2: Aromatic foldamer



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.49Å 83.81Å 79.85Å 90.00° 99.98° 90.00°	Depositor
Resolution (Å)	78.64 – 2.65 78.64 – 2.65	Depositor EDS
% Data completeness (in resolution range)	88.9 (78.64-2.65) 88.9 (78.64-2.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.220 , 0.278 0.226 , 0.285	Depositor DCC
$R_{free}$ test set	750 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4427	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: QUK, A1IJ4, ZN, QVE, 4SO, QVS, GOL, QCL

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	0.59	0/2116	0.75	0/2872
1	B	0.56	0/2020	0.77	1/2750 (0.0%)
All	All	0.58	0/4136	0.76	1/5622 (0.0%)

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	D	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	77	ALA	N-CA-CB	6.72	119.51	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	303	QCL	Peptide

### 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	2051	0	1989	8	1
1	B	1962	0	1865	10	0
2	C	99	0	6	0	0
2	D	99	0	5	0	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
4	A	12	0	16	0	0
4	B	12	0	16	0	0
5	A	103	0	0	0	0
5	B	66	0	0	1	0
5	C	3	0	0	0	0
5	D	5	0	0	0	0
All	All	4427	0	3897	18	1

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 2.

The worst 5 of 18 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:195:GLY:HA3	1:A:208:TRP:HD1	1.56	0.70
1:B:158:LYS:O	1:B:161:ASP:HB3	1.94	0.67
1:A:195:GLY:HA3	1:A:208:TRP:CD1	2.36	0.59
1:B:195:GLY:HA3	1:B:208:TRP:HD1	1.68	0.59
1:A:196:SER:HB2	1:A:203:LEU:O	2.04	0.57

All (1) 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)
1:A:50:SER:OG	1:A:237:GLU:O[2_746]	2.15	0.05

## 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	257/260 (99%)	243 (95%)	14 (5%)	0	100	100
1	B	245/260 (94%)	229 (94%)	16 (6%)	0	100	100
All	All	502/520 (96%)	472 (94%)	30 (6%)	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	A	220/225 (98%)	217 (99%)	3 (1%)	62	79
1	B	207/225 (92%)	205 (99%)	2 (1%)	73	85
All	All	427/450 (95%)	422 (99%)	5 (1%)	67	82

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	SER
1	A	85	ASP
1	A	216	SER
1	B	10	HIS
1	B	48	SER

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

Mol	Chain	Res	Type
1	B	229	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are 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	QVS	C	304	2	15,15,16	2.10	1 (6%)	19,21,23	3.25	6 (31%)
2	QUK	C	305	2	19,19,20	4.06	2 (10%)	22,25,27	2.86	6 (27%)
2	A1IJ4	D	302	2	16,16,17	1.01	1 (6%)	17,18,20	0.80	0
2	QVE	C	306	2,3	20,20,20	2.95	1 (5%)	27,28,28	1.71	5 (18%)
2	QVE	D	306	2,3	20,20,20	3.19	2 (10%)	27,28,28	1.89	8 (29%)
2	QVS	D	304	2	15,15,16	1.94	3 (20%)	19,21,23	3.28	6 (31%)
2	QUK	D	305	2	19,19,20	3.82	2 (10%)	22,25,27	3.18	8 (36%)
2	A1IJ4	C	302	2	16,16,17	0.89	1 (6%)	17,18,20	0.99	1 (5%)

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	QVS	C	304	2	-	0/2/2/4	0/2/2/2
2	QUK	C	305	2	-	5/7/7/9	0/2/2/2
2	A1IJ4	D	302	2	-	4/10/10/11	0/1/1/1
2	QVE	C	306	2,3	-	4/9/9/9	0/2/2/2
2	QVE	D	306	2,3	-	4/9/9/9	0/2/2/2
2	QVS	D	304	2	-	2/2/2/4	0/2/2/2
2	QUK	D	305	2	-	1/7/7/9	0/2/2/2
2	A1IJ4	C	302	2	-	4/10/10/11	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	305	QUK	C10-C	-17.14	1.30	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	305	QUK	C10-C	-15.95	1.31	1.48
2	D	306	QVE	CA-C	-13.69	1.31	1.50
2	C	306	QVE	CA-C	-12.37	1.33	1.50
2	C	304	QVS	CA-C	-6.41	1.41	1.48

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	305	QUK	C10-N11-C7	11.20	126.61	118.11
2	C	304	QVS	CA-N11-C7	10.91	126.39	118.11
2	D	304	QVS	CA-N11-C7	9.68	125.45	118.11
2	C	305	QUK	C10-N11-C7	9.21	125.09	118.11
2	D	304	QVS	C9-CA-C	6.75	127.06	121.23

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	304	QVS	O-C-CA-C9
2	D	304	QVS	O-C-CA-N11
2	C	305	QUK	O-C-C10-N11
2	C	305	QUK	O-C-C10-C9
2	D	302	A1IJ4	N31-C118-C119-C120

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 15 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z  > 2$
4	GOL	A	312	-	5,5,5	0.36	0	5,5,5	0.56	0
4	GOL	A	303	-	5,5,5	0.26	0	5,5,5	0.23	0
4	GOL	B	303	-	5,5,5	0.39	0	5,5,5	0.80	0
4	GOL	B	307	-	5,5,5	0.37	0	5,5,5	0.43	0

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
4	GOL	A	312	-	-	1/4/4/4	-
4	GOL	A	303	-	-	2/4/4/4	-
4	GOL	B	303	-	-	2/4/4/4	-
4	GOL	B	307	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	GOL	O1-C1-C2-C3
4	A	312	GOL	O1-C1-C2-C3
4	B	303	GOL	O1-C1-C2-C3
4	B	307	GOL	O1-C1-C2-C3
4	B	307	GOL	C1-C2-C3-O3

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	258/260 (99%)	0.21	3 (1%) 76 73	22, 38, 52, 57	1 (0%)
1	B	251/260 (96%)	0.64	9 (3%) 46 44	25, 46, 67, 76	0
2	C	0/6	-	-	-	-
2	D	0/6	-	-	-	-
All	All	509/532 (95%)	0.42	12 (2%) 59 58	22, 41, 63, 76	1 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	246	PRO	3.1
1	B	218	SER	2.7
1	B	161	ASP	2.7
1	A	158	LYS	2.5
1	B	152	ALA	2.4

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
2	QUK	C	305	18/19	0.88	0.14	39,43,52,53	0
2	QUK	D	305	18/19	0.88	0.13	32,36,45,47	0
2	A1IJ4	C	302	16/17	0.91	0.13	30,33,35,35	0
2	A1IJ4	D	302	16/17	0.91	0.12	26,31,42,42	0
2	QVE	C	306	19/19	0.91	0.12	36,38,45,46	0
2	QVS	D	304	14/15	0.92	0.12	26,28,32,34	0
2	QVS	C	304	14/15	0.92	0.14	36,37,41,43	0
2	QVE	D	306	19/19	0.92	0.10	29,30,35,36	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	ZN	B	306	1/1	0.79	0.17	54,54,54,54	1
4	GOL	A	303	6/6	0.85	0.19	35,36,37,38	0
4	GOL	B	307	6/6	0.85	0.14	36,37,38,39	0
3	ZN	B	304	1/1	0.86	0.15	66,66,66,66	1
4	GOL	A	312	6/6	0.86	0.15	26,27,28,29	0
3	ZN	A	311	1/1	0.86	0.12	74,74,74,74	1
4	GOL	B	303	6/6	0.89	0.15	30,33,34,34	0
3	ZN	A	304	1/1	0.89	0.10	68,68,68,68	0
3	ZN	B	305	1/1	0.91	0.20	49,49,49,49	1
3	ZN	A	308	1/1	0.96	0.05	61,61,61,61	0
3	ZN	A	307	1/1	0.97	0.04	63,63,63,63	0
3	ZN	A	305	1/1	0.97	0.04	59,59,59,59	0
3	ZN	A	306	1/1	0.98	0.05	53,53,53,53	0
3	ZN	B	301	1/1	0.98	0.04	24,24,24,24	0
3	ZN	A	309	1/1	0.98	0.09	52,52,52,52	0
3	ZN	B	302	1/1	0.99	0.05	30,30,30,30	0
3	ZN	A	310	1/1	0.99	0.05	37,37,37,37	1
3	ZN	A	302	1/1	1.00	0.05	26,26,26,26	0
3	ZN	A	301	1/1	1.00	0.01	21,21,21,21	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.