



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 09:23 am GMT

PDB ID : 3E6D  
Title : Crystal Structure of CprK C200S  
Authors : Levy, C.  
Deposited on : 2008-08-15  
Resolution : 2.00 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](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.

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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
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

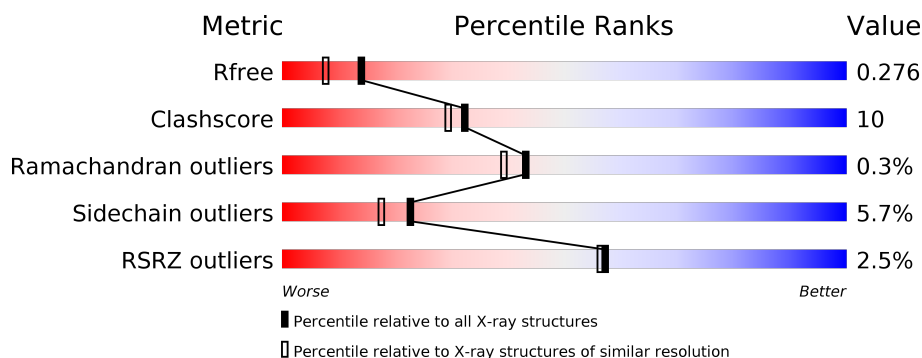
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	111664	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (2.00-2.00)

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. 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	250	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>17%</div> <div>•</div> <div>19%</div> </div> </div>
1	B	250	<div> <div>%</div> <div> <div></div> <div>64%</div> <div>15%</div> <div>•</div> <div>19%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3420 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 Cyclic nucleotide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1605	1037	266	294	8			
1	B	203	Total	C	N	O	S	0	0	0
			1634	1055	271	300	8			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	200	SER	CYS	ENGINEERED	UNP Q18R04
A	233	SER	-	EXPRESSION TAG	UNP Q18R04
A	234	ASP	-	EXPRESSION TAG	UNP Q18R04
A	235	PRO	-	EXPRESSION TAG	UNP Q18R04
A	236	ASN	-	EXPRESSION TAG	UNP Q18R04
A	237	SER	-	EXPRESSION TAG	UNP Q18R04
A	238	SER	-	EXPRESSION TAG	UNP Q18R04
A	239	SER	-	EXPRESSION TAG	UNP Q18R04
A	240	VAL	-	EXPRESSION TAG	UNP Q18R04
A	241	ASP	-	EXPRESSION TAG	UNP Q18R04
A	242	LYS	-	EXPRESSION TAG	UNP Q18R04
A	243	LEU	-	EXPRESSION TAG	UNP Q18R04
A	244	ALA	-	EXPRESSION TAG	UNP Q18R04
A	245	ALA	-	EXPRESSION TAG	UNP Q18R04
A	246	ALA	-	EXPRESSION TAG	UNP Q18R04
A	247	LEU	-	EXPRESSION TAG	UNP Q18R04
A	248	ASP	-	EXPRESSION TAG	UNP Q18R04
A	249	HIS	-	EXPRESSION TAG	UNP Q18R04
A	250	HIS	-	EXPRESSION TAG	UNP Q18R04
B	200	SER	CYS	ENGINEERED	UNP Q18R04
B	233	SER	-	EXPRESSION TAG	UNP Q18R04
B	234	ASP	-	EXPRESSION TAG	UNP Q18R04
B	235	PRO	-	EXPRESSION TAG	UNP Q18R04
B	236	ASN	-	EXPRESSION TAG	UNP Q18R04
B	237	SER	-	EXPRESSION TAG	UNP Q18R04

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Chain	Residue	Modelled	Actual	Comment	Reference
B	238	SER	-	EXPRESSION TAG	UNP Q18R04
B	239	SER	-	EXPRESSION TAG	UNP Q18R04
B	240	VAL	-	EXPRESSION TAG	UNP Q18R04
B	241	ASP	-	EXPRESSION TAG	UNP Q18R04
B	242	LYS	-	EXPRESSION TAG	UNP Q18R04
B	243	LEU	-	EXPRESSION TAG	UNP Q18R04
B	244	ALA	-	EXPRESSION TAG	UNP Q18R04
B	245	ALA	-	EXPRESSION TAG	UNP Q18R04
B	246	ALA	-	EXPRESSION TAG	UNP Q18R04
B	247	LEU	-	EXPRESSION TAG	UNP Q18R04
B	248	ASP	-	EXPRESSION TAG	UNP Q18R04
B	249	HIS	-	EXPRESSION TAG	UNP Q18R04
B	250	HIS	-	EXPRESSION TAG	UNP Q18R04

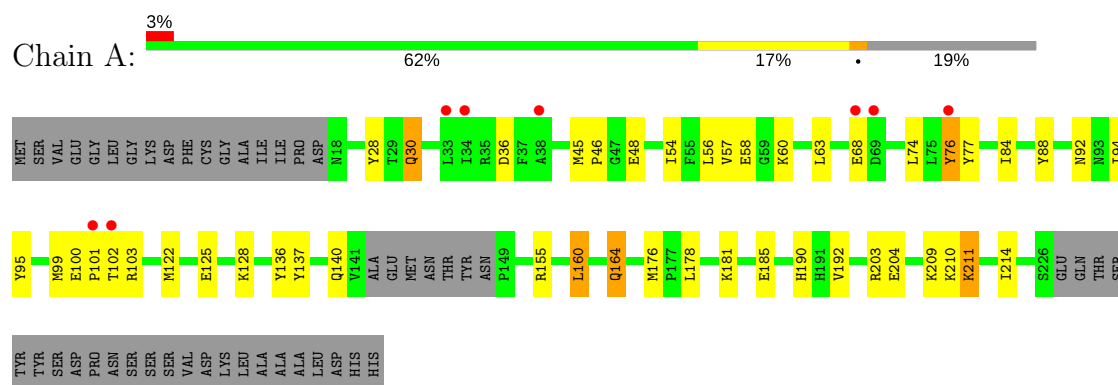
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	87	Total O 87 87	0	0
2	B	94	Total O 94 94	0	0

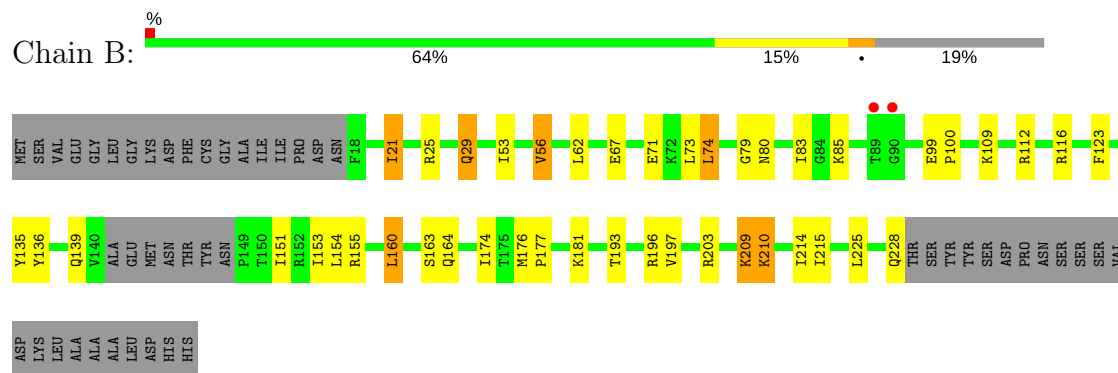
### 3 Residue-property plots [i](#)

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 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: Cyclic nucleotide-binding protein



#### • Molecule 1: Cyclic nucleotide-binding protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.95Å 86.82Å 124.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.60 – 2.00 35.60 – 2.00	Depositor EDS
% Data completeness (in resolution range)	85.7 (35.60-2.00) 85.7 (35.60-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.15 (at 2.00Å)	Xtriage
Refinement program	PHENIX ?	Depositor
R, $R_{free}$	0.231 , 0.280 0.225 , 0.276	Depositor DCC
$R_{free}$ test set	1429 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.8	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 54.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3420	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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

### 5.1 Standard geometry

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	0.26	0/1635	0.44	0/2205
1	B	0.27	0/1664	0.46	0/2239
All	All	0.26	0/3299	0.45	0/4444

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

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	1605	0	1615	34	0
1	B	1634	0	1667	33	0
2	A	87	0	0	0	0
2	B	94	0	0	3	0
All	All	3420	0	3282	62	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 10.

All (62) 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:190:HIS:HD2	1:A:192:VAL:H	1.28	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:PRO:HG3	1:A:95:TYR:HB2	1.66	0.77
1:B:197:VAL:HG22	2:B:545:HOH:O	1.83	0.77
1:B:29:GLN:HE21	1:B:29:GLN:H	1.34	0.73
1:A:137:TYR:HB3	1:B:136:TYR:HB3	1.69	0.73
1:A:190:HIS:CD2	1:A:192:VAL:H	2.08	0.71
1:B:29:GLN:NE2	1:B:29:GLN:H	1.89	0.70
1:B:193:THR:O	1:B:197:VAL:HG23	1.91	0.70
1:A:45:MET:O	1:A:48:GLU:HB3	1.99	0.63
1:B:112:ARG:O	1:B:116:ARG:HG3	2.00	0.62
1:B:153:ILE:HD12	1:B:197:VAL:HG21	1.84	0.59
1:A:203:ARG:HD2	1:A:204:GLU:OE2	2.03	0.59
1:A:190:HIS:HD2	1:A:192:VAL:N	2.01	0.58
1:A:185:GLU:HB3	1:B:155:ARG:HD3	1.86	0.57
1:A:210:LYS:O	1:A:211:LYS:HE2	2.04	0.57
1:A:176:MET:HB2	1:B:163:SER:OG	2.05	0.55
1:A:28:TYR:HA	1:A:30:GLN:HE22	1.73	0.54
1:B:209:LYS:HG2	1:B:214:ILE:HG12	1.91	0.53
1:A:164:GLN:HG3	1:B:164:GLN:OE1	2.09	0.53
1:A:63:LEU:HD22	1:A:76:TYR:CE2	2.44	0.52
1:A:136:TYR:O	1:A:140:GLN:HG2	2.11	0.51
1:A:160:LEU:O	1:A:164:GLN:HB2	2.10	0.51
1:A:74:LEU:HD11	1:A:77:TYR:CE1	2.45	0.51
1:A:68:GLU:N	1:A:68:GLU:OE1	2.36	0.51
1:B:210:LYS:HE3	1:B:215:ILE:CD1	2.40	0.51
1:B:25:ARG:NH2	1:B:56:VAL:O	2.43	0.49
1:B:67:GLU:HG3	1:B:67:GLU:O	2.12	0.49
1:B:210:LYS:HE3	1:B:215:ILE:HD11	1.93	0.49
1:A:181:LYS:HD3	1:A:185:GLU:OE2	2.14	0.48
1:B:196:ARG:NH2	2:B:545:HOH:O	2.45	0.48
1:B:29:GLN:HE21	1:B:29:GLN:N	2.08	0.46
1:A:28:TYR:HA	1:A:30:GLN:NE2	2.31	0.46
1:A:60:LYS:HD3	1:A:99:MET:HE3	1.96	0.46
1:A:100:GLU:HB2	1:A:101:PRO:HD2	1.97	0.45
1:A:88:TYR:OH	1:B:123:PHE:HB3	2.16	0.45
1:B:154:LEU:HD13	1:B:225:LEU:HB3	1.97	0.45
1:A:209:LYS:HG3	1:A:214:ILE:HG12	1.97	0.45
1:A:211:LYS:HB2	1:A:211:LYS:HE2	1.39	0.45
1:B:21:ILE:HG13	1:B:21:ILE:O	2.17	0.45
1:A:58:GLU:O	1:A:103:ARG:N	2.46	0.44
1:B:135:TYR:O	1:B:139:GLN:HG2	2.18	0.44
1:B:53:ILE:HB	1:B:83:ILE:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:GLY:O	1:B:80:ASN:HB2	2.18	0.43
1:B:73:LEU:HD23	1:B:74:LEU:N	2.33	0.43
1:B:151:ILE:HD11	2:B:676:HOH:O	2.17	0.43
1:B:209:LYS:HE3	1:B:210:LYS:O	2.19	0.43
1:B:181:LYS:NZ	1:B:181:LYS:HB3	2.35	0.42
1:B:160:LEU:HB3	1:B:174:ILE:HD13	2.00	0.42
1:B:109:LYS:HD2	1:B:109:LYS:HA	1.83	0.42
1:B:151:ILE:HD12	1:B:228:GLN:HB2	2.02	0.42
1:A:100:GLU:HB2	1:A:101:PRO:CD	2.49	0.42
1:A:58:GLU:HB2	1:A:103:ARG:HB3	2.00	0.42
1:A:122:MET:CE	1:A:125:GLU:HG3	2.49	0.42
1:A:58:GLU:O	1:A:102:THR:HA	2.20	0.41
1:A:136:TYR:CZ	1:A:140:GLN:NE2	2.89	0.41
1:A:46:PRO:HD3	1:A:95:TYR:HD2	1.85	0.41
1:B:62:LEU:O	1:B:74:LEU:HB2	2.21	0.41
1:A:92:ASN:O	1:A:94:ILE:HG12	2.21	0.40
1:A:46:PRO:HD3	1:A:95:TYR:CD2	2.56	0.40
1:B:176:MET:HA	1:B:177:PRO:HD3	1.92	0.40
1:B:99:GLU:O	1:B:100:PRO:C	2.60	0.40
1:A:54:ILE:HB	1:A:84:ILE:HG13	2.02	0.40

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	198/250 (79%)	189 (96%)	8 (4%)	1 (0%)	31	25
1	B	199/250 (80%)	193 (97%)	6 (3%)	0	100	100
All	All	397/500 (79%)	382 (96%)	14 (4%)	1 (0%)	43	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	LEU

### 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	172/220 (78%)	162 (94%)	10 (6%)	22	17
1	B	179/220 (81%)	169 (94%)	10 (6%)	23	18
All	All	351/440 (80%)	331 (94%)	20 (6%)	23	17

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	36	ASP
1	A	56	LEU
1	A	57	VAL
1	A	76	TYR
1	A	128	LYS
1	A	155	ARG
1	A	160	LEU
1	A	164	GLN
1	A	211	LYS
1	B	21	ILE
1	B	29	GLN
1	B	56	VAL
1	B	71	GLU
1	B	74	LEU
1	B	85	LYS
1	B	160	LEU
1	B	203	ARG
1	B	209	LYS
1	B	210	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	30	GLN
1	A	140	GLN
1	A	180	GLN
1	A	190	HIS
1	A	191	HIS
1	B	26	ASN
1	B	29	GLN
1	B	180	GLN

### 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](#)

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	202/250 (80%)	-0.03	8 (3%) 38 38	20, 38, 56, 66	0
1	B	203/250 (81%)	-0.07	2 (0%) 82 81	19, 32, 57, 74	0
All	All	405/500 (81%)	-0.05	10 (2%) 57 56	19, 35, 56, 74	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	90	GLY	3.4
1	A	38	ALA	3.1
1	A	34	ILE	2.8
1	A	33	LEU	2.5
1	A	101	PRO	2.4
1	A	102	THR	2.3
1	A	69	ASP	2.3
1	A	76	TYR	2.2
1	A	68	GLU	2.1
1	B	89	THR	2.1

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.