



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:24 AM GMT

PDB ID : 2FEE  
Title : Structure of the Cl<sup>-</sup>/H<sup>+</sup> exchanger CLC-ec1 from E.Coli in NaBr  
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Miller, C.  
Deposited on : 2005-12-15  
Resolution : 3.20 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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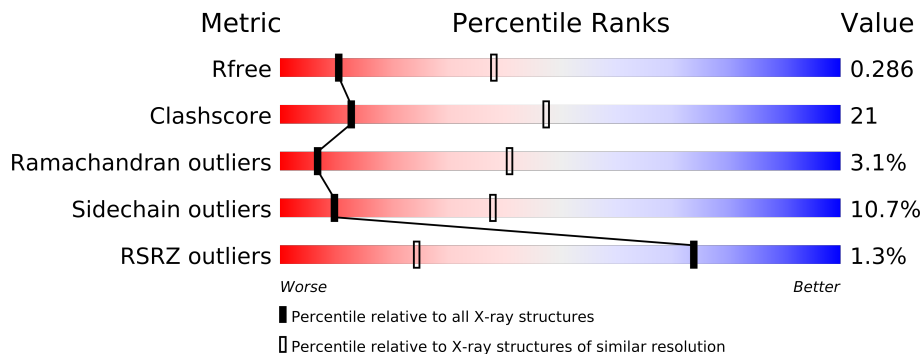
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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 3.20 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))
$R_{free}$	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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.

Mol	Chain	Length	Quality of chain
1	A	465	
1	B	465	
2	I	222	
2	J	222	
3	L	211	
3	O	211	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13223 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 H(+)/Cl(-) exchange transporter clcA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3333	2190	560	563	20			
1	B	441	Total	C	N	O	S	0	0	0
			3304	2174	553	557	20			

- Molecule 2 is a protein called Fab fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			
2	I	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			

- Molecule 3 is a protein called Fab fragment, light chain.

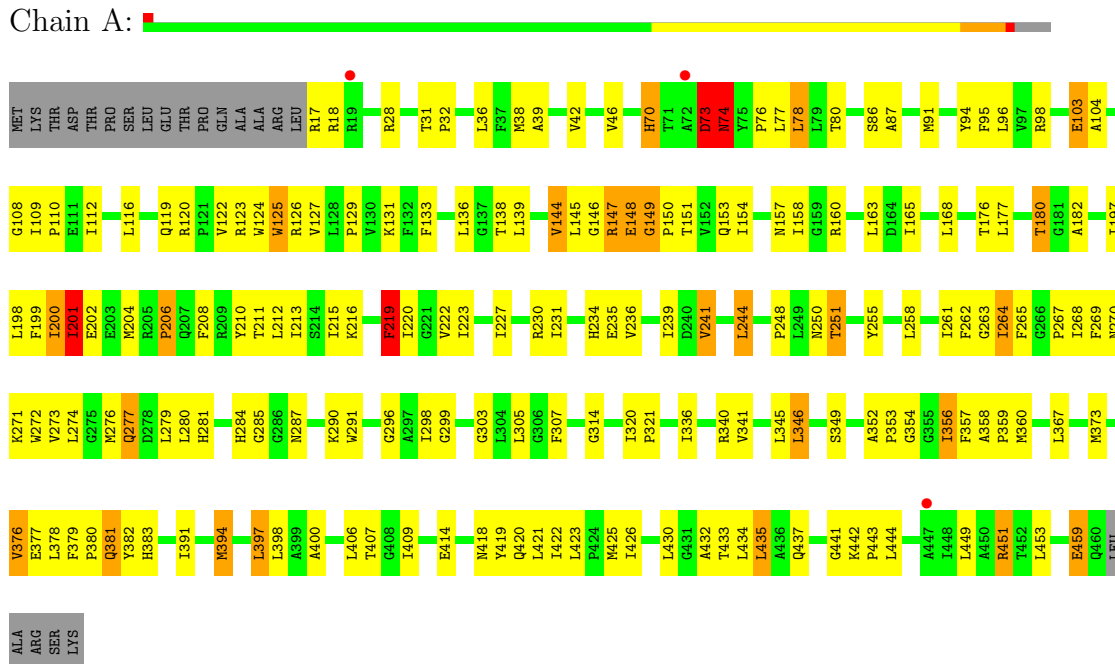
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	O	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			
3	L	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			

### 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 ( $\text{RSRZ} > 2$ ). 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.

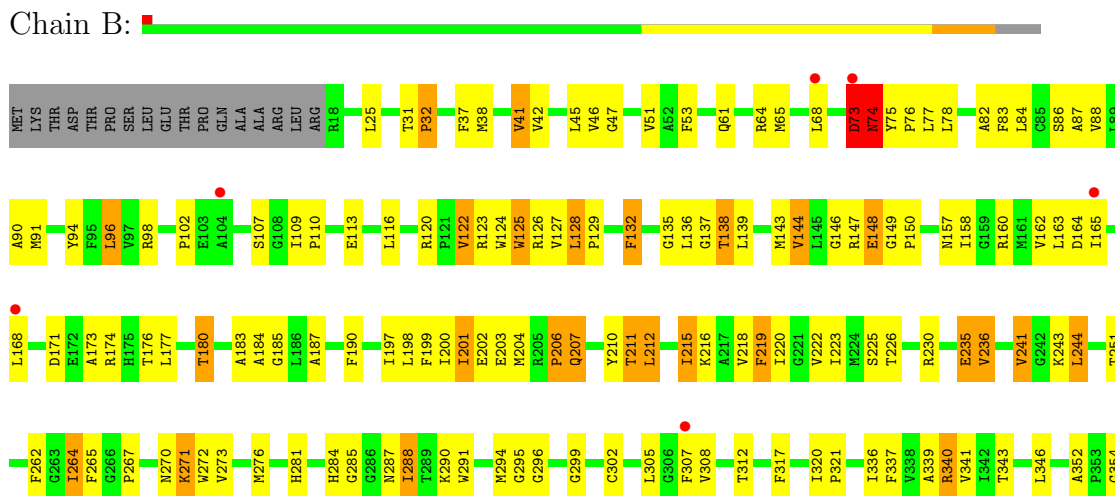
- Molecule 1: H(+)/Cl(-) exchange transporter clcA

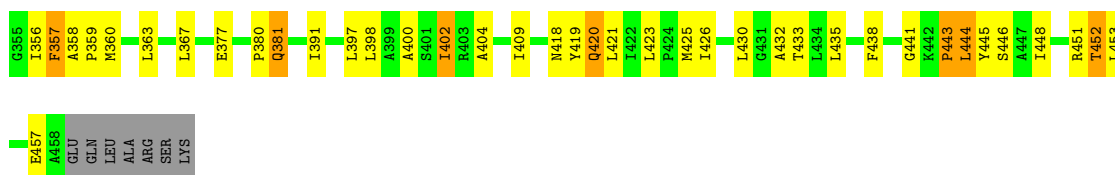
Chain A:



- Molecule 1: H(+)/Cl(-) exchange transporter clcA

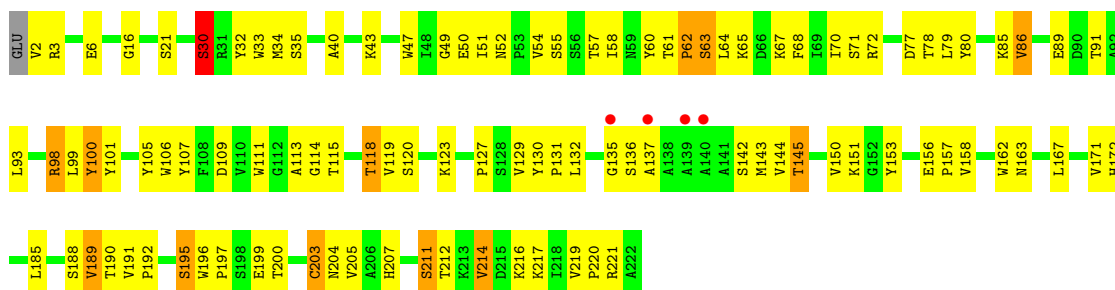
Chain B:





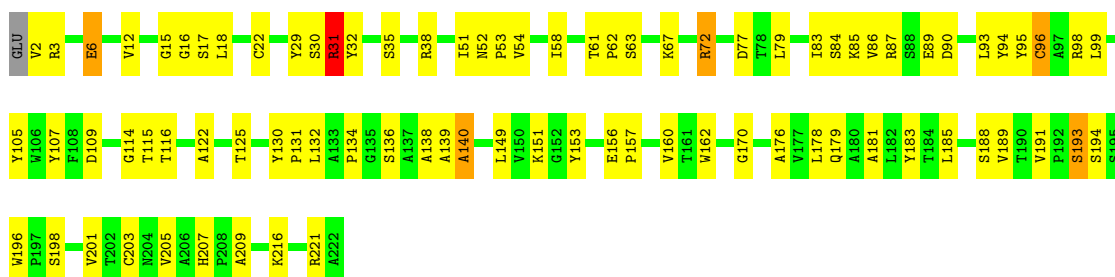
- Molecule 2: Fab fragment, heavy chain

Chain J:



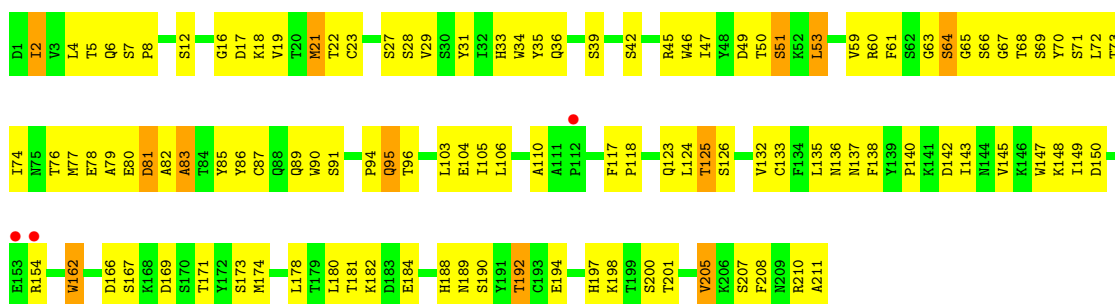
- Molecule 2: Fab fragment, heavy chain

Chain I:



- Molecule 3: Fab fragment, light chain

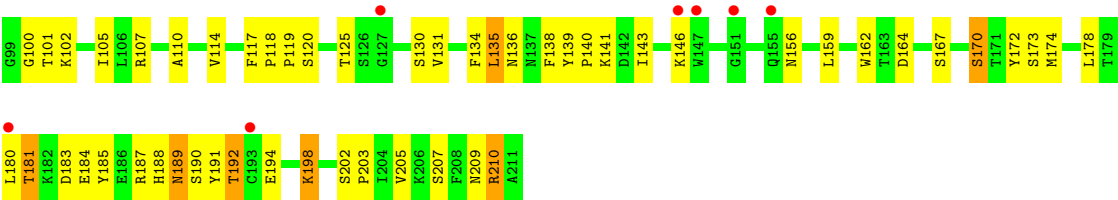
Chain O:



- Molecule 3: Fab fragment, light chain

Chain L:





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	230.82Å 97.68Å 170.20Å 90.00° 131.11° 90.00°	Depositor
Resolution (Å)	128.04 – 3.20 44.36 – 3.20	Depositor EDS
% Data completeness (in resolution range)	97.8 (128.04-3.20) 97.8 (44.36-3.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.251 , 0.293 0.250 , 0.286	Depositor DCC
$R_{free}$ test set	2341 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	109.4	Xtriage
Anisotropy	0.386	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 100.0	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 46298 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	13223	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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	0.57	0/3405	0.67	1/4621 (0.0%)
1	B	0.69	2/3376 (0.1%)	0.70	3/4583 (0.1%)
2	I	0.60	0/1721	0.72	0/2355
2	J	0.70	1/1721 (0.1%)	0.75	0/2355
3	L	0.60	0/1660	0.72	0/2257
3	O	0.56	0/1660	0.73	1/2257 (0.0%)
All	All	0.62	3/13543 (0.0%)	0.71	5/18428 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	271	LYS	CD-CE	13.54	1.85	1.51
2	J	195	SER	CB-OG	12.51	1.58	1.42
1	B	271	LYS	CE-NZ	9.61	1.73	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	LEU	CA-CB-CG	6.14	129.42	115.30
1	A	398	LEU	CA-CB-CG	5.31	127.50	115.30
1	B	177	LEU	CA-CB-CG	5.12	127.07	115.30
3	O	53	LEU	CA-CB-CG	5.10	127.04	115.30
1	B	45	LEU	CA-CB-CG	5.08	126.97	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	3333	0	3484	160	0
1	B	3304	0	3457	158	0
2	I	1672	0	1654	49	0
2	J	1672	0	1654	68	0
3	L	1621	0	1546	72	0
3	O	1621	0	1546	91	0
All	All	13223	0	13341	556	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 21.

The worst 5 of 556 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:271:LYS:CD	1:B:271:LYS:CE	1.85	1.54
1:B:271:LYS:NZ	1:B:271:LYS:CE	1.73	1.46
2:J:60:TYR:HE2	2:J:70:ILE:HG13	1.04	1.14
2:J:135:GLY:HA2	2:J:221:ARG:HD3	1.31	1.11
3:L:194:GLU:HG2	3:L:205:VAL:HG12	1.37	1.06

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	442/465 (95%)	377 (85%)	52 (12%)	13 (3%)	7	43
1	B	439/465 (94%)	369 (84%)	54 (12%)	16 (4%)	5	36
2	I	219/222 (99%)	190 (87%)	21 (10%)	8 (4%)	5	34
2	J	219/222 (99%)	186 (85%)	26 (12%)	7 (3%)	6	39
3	L	209/211 (99%)	183 (88%)	24 (12%)	2 (1%)	22	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	O	209/211 (99%)	180 (86%)	21 (10%)	8 (4%)	5	34
All	All	1737/1796 (97%)	1485 (86%)	198 (11%)	54 (3%)	7	41

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	125	TRP
2	J	65	LYS
3	O	51	SER
3	O	125	THR
3	O	200	SER

### 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	335/353 (95%)	298 (89%)	37 (11%)	9	36
1	B	332/353 (94%)	293 (88%)	39 (12%)	8	34
2	I	181/182 (100%)	166 (92%)	15 (8%)	16	55
2	J	181/182 (100%)	156 (86%)	25 (14%)	5	24
3	L	185/185 (100%)	170 (92%)	15 (8%)	17	56
3	O	185/185 (100%)	166 (90%)	19 (10%)	10	40
All	All	1399/1440 (97%)	1249 (89%)	150 (11%)	10	38

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	402	ILE
2	J	77	ASP
3	L	92	SER
1	B	423	LEU
2	J	2	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	277	GLN
1	B	381	GLN
3	L	6	GLN
1	B	287	ASN
1	B	327	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 ⓘ

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	444/465 (95%)	0.14	3 (0%) 84 38	94, 117, 145, 163	0
1	B	441/465 (94%)	0.20	6 (1%) 72 22	94, 116, 145, 162	0
2	I	221/222 (99%)	0.17	0 100 100	92, 118, 143, 162	0
2	J	221/222 (99%)	0.24	4 (1%) 65 18	90, 117, 142, 162	0
3	L	211/211 (100%)	0.34	7 (3%) 44 9	82, 112, 145, 154	0
3	O	211/211 (100%)	0.26	3 (1%) 72 22	96, 126, 145, 153	0
All	All	1749/1796 (97%)	0.21	23 (1%) 74 24	82, 118, 145, 163	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	135	GLY	3.9
1	B	73	ASP	3.1
2	J	139	ALA	2.8
3	L	146	LYS	2.8
1	B	165	ILE	2.7

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.