Full wwPDB X-ray Structure Validation Report (i)

Oct 25, 2023 – 05:40 PM EDT

PDB ID	:	3B1O
Title	:	Structure of Burkholderia thailandensis nucleoside kinase (BthNK) in ligand-free form
Authors	:	Yasutake, Y.; Ota, H.; Hino, E.; Sakasegawa, S.; Tamura, T.
Deposited on	:	2011-07-05
Resolution	:	2.10 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

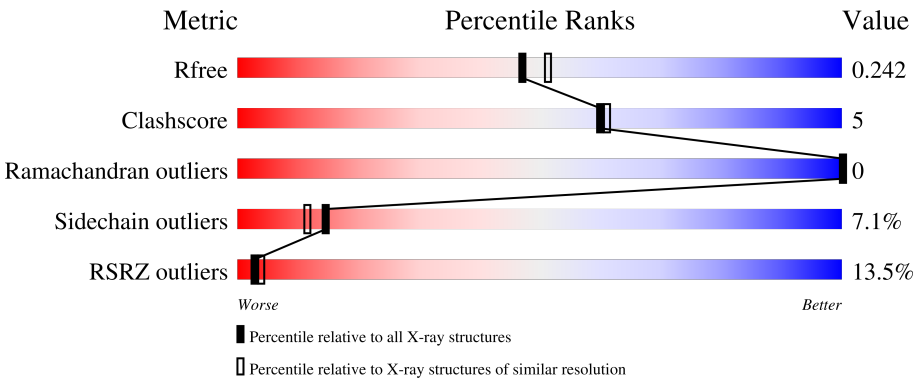
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

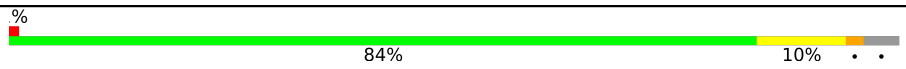
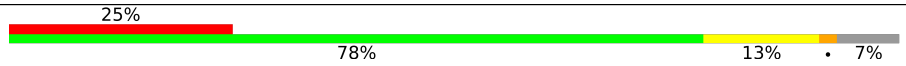
The reported resolution of this entry is 2.10 Å.

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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 of 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 <=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	326	
1	B	326	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4900 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 Ribokinase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2391	1502	425	450	14	0	0	0
1	B	303	2315	1453	411	437	14	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	313	GLY	-	expression tag	UNP Q2SZE4
A	314	SER	-	expression tag	UNP Q2SZE4
A	315	LYS	-	expression tag	UNP Q2SZE4
A	316	LEU	-	expression tag	UNP Q2SZE4
A	317	ARG	-	expression tag	UNP Q2SZE4
A	318	SER	-	expression tag	UNP Q2SZE4
A	319	LEU	-	expression tag	UNP Q2SZE4
A	320	GLU	-	expression tag	UNP Q2SZE4
A	321	HIS	-	expression tag	UNP Q2SZE4
A	322	HIS	-	expression tag	UNP Q2SZE4
A	323	HIS	-	expression tag	UNP Q2SZE4
A	324	HIS	-	expression tag	UNP Q2SZE4
A	325	HIS	-	expression tag	UNP Q2SZE4
A	326	HIS	-	expression tag	UNP Q2SZE4
B	313	GLY	-	expression tag	UNP Q2SZE4
B	314	SER	-	expression tag	UNP Q2SZE4
B	315	LYS	-	expression tag	UNP Q2SZE4
B	316	LEU	-	expression tag	UNP Q2SZE4
B	317	ARG	-	expression tag	UNP Q2SZE4
B	318	SER	-	expression tag	UNP Q2SZE4
B	319	LEU	-	expression tag	UNP Q2SZE4
B	320	GLU	-	expression tag	UNP Q2SZE4
B	321	HIS	-	expression tag	UNP Q2SZE4
B	322	HIS	-	expression tag	UNP Q2SZE4
B	323	HIS	-	expression tag	UNP Q2SZE4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	324	HIS	-	expression tag	UNP Q2SZE4
B	325	HIS	-	expression tag	UNP Q2SZE4
B	326	HIS	-	expression tag	UNP Q2SZE4

- Molecule 2 is water.

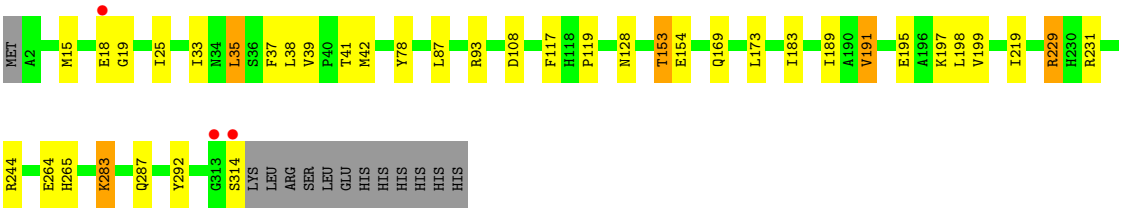
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	145	145	145	0	0
			Total	O		
2	B	49	49	49	0	0

3 Residue-property plots (i)

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.

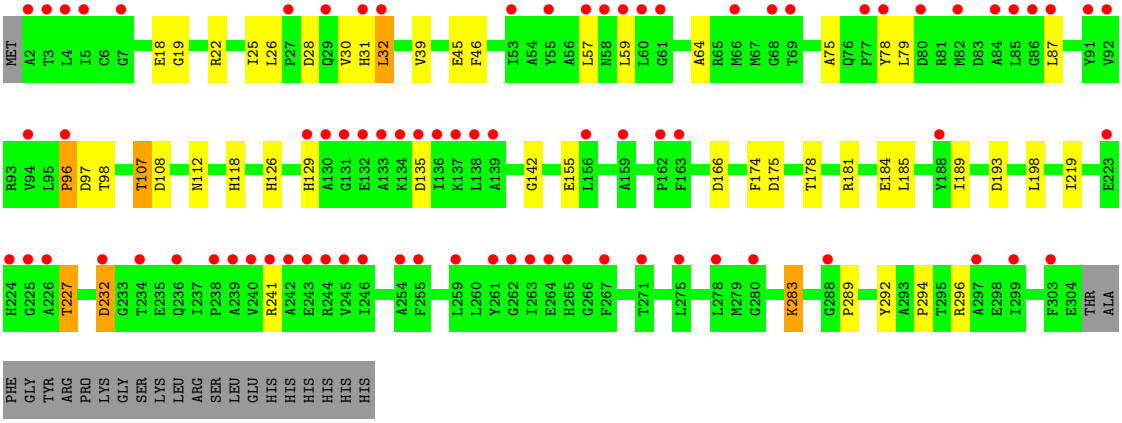
• Molecule 1: Ribokinase, putative

Chain A:



• Molecule 1: Ribokinase, putative

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	85.36Å 85.36Å 160.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.68 – 2.10 38.17 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.8 (42.68-2.10) 95.8 (38.17-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	10.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.236 , 0.277 0.239 , 0.242	Depositor DCC
R_{free} test set	1683 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	25.4	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 43.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4900	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.50	0/2441	0.65	0/3308
1	B	0.44	0/2362	0.58	0/3202
All	All	0.47	0/4803	0.61	0/6510

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	A	2391	0	2335	21	0
1	B	2315	0	2261	26	0
2	A	145	0	0	2	0
2	B	49	0	0	2	0
All	All	4900	0	4596	43	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 5.

All (43) 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:25:ILE:HG22	1:B:25:ILE:HD11	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ARG:HH11	1:A:229:ARG:HB3	1.60	0.65
1:A:153:THR:HG21	2:A:361:HOH:O	1.96	0.65
1:B:107:THR:HG23	2:B:338:HOH:O	2.00	0.62
1:B:26:LEU:HD12	1:B:32:LEU:HB3	1.82	0.61
1:B:219:ILE:HB	1:B:227:THR:HG22	1.81	0.61
1:B:175:ASP:OD2	1:B:178:THR:HG23	2.02	0.60
1:A:283:LYS:C	1:A:283:LYS:HE3	2.24	0.58
1:B:59:LEU:HD13	1:B:294:PRO:HD2	1.85	0.56
1:A:18:GLU:HG2	1:A:18:GLU:O	2.06	0.55
1:B:129:HIS:HB3	1:B:155:GLU:OE1	2.10	0.52
1:A:183:ILE:HG23	1:A:189:ILE:HD11	1.91	0.52
1:B:283:LYS:HG3	1:B:292:TYR:CE1	2.45	0.51
1:A:42:MET:HE3	1:B:118:HIS:CD2	2.45	0.51
1:B:22:ARG:O	1:B:25:ILE:HD12	2.10	0.51
1:B:232:ASP:OD2	1:B:232:ASP:N	2.46	0.49
1:A:15:MET:HG2	1:A:42:MET:HG2	1.95	0.48
1:A:93:ARG:HD2	1:A:128:ASN:ND2	2.27	0.48
1:B:28:ASP:OD2	1:B:32:LEU:HD12	2.13	0.48
1:A:128:ASN:ND2	2:A:382:HOH:O	2.46	0.48
1:B:96:PRO:O	1:B:98:THR:HG23	2.14	0.48
1:A:15:MET:HB3	1:A:39:VAL:HG11	1.97	0.46
1:A:153:THR:HG22	1:A:154:GLU:N	2.30	0.46
1:B:46:PHE:O	1:B:289:PRO:HG2	2.15	0.45
1:A:19:GLY:O	1:A:108:ASP:HB2	2.17	0.45
1:A:35:LEU:HD22	1:A:37:PHE:HD1	1.81	0.45
1:A:191:VAL:O	1:A:219:ILE:HA	2.17	0.45
1:B:19:GLY:O	1:B:108:ASP:HB2	2.17	0.44
1:A:264:GLU:HG3	1:A:265:HIS:CD2	2.53	0.44
1:A:42:MET:HG3	1:B:118:HIS:CG	2.54	0.42
1:B:181:ARG:CZ	1:B:185:LEU:HD21	2.48	0.42
1:A:169:GLN:HA	1:A:169:GLN:OE1	2.19	0.42
1:A:33:ILE:HB	1:B:112:ASN:HB3	2.02	0.42
1:B:142:GLY:HA2	1:B:166:ASP:O	2.19	0.42
1:B:39:VAL:HG23	1:B:39:VAL:O	2.20	0.41
1:B:75:ALA:O	1:B:79:LEU:HG	2.20	0.41
1:A:117:PHE:O	1:A:119:PRO:HD3	2.21	0.41
1:B:30:VAL:O	1:B:31:HIS:C	2.59	0.41
1:B:57:LEU:HD23	1:B:64:ALA:HB2	2.03	0.41
1:A:195:GLU:O	1:A:199:VAL:HG23	2.21	0.40
1:B:45:GLU:HG2	1:B:289:PRO:HD2	2.04	0.40
1:B:126:HIS:HD2	2:B:333:HOH:O	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:PHE:HD1	1:B:178:THR:HG1	1.67	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	311/326 (95%)	307 (99%)	4 (1%)	0	100	100
1	B	301/326 (92%)	293 (97%)	8 (3%)	0	100	100
All	All	612/652 (94%)	600 (98%)	12 (2%)	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	242/255 (95%)	225 (93%)	17 (7%)	15	12
1	B	235/255 (92%)	218 (93%)	17 (7%)	14	11
All	All	477/510 (94%)	443 (93%)	34 (7%)	14	11

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LEU
1	A	38	LEU
1	A	41	THR
1	A	78	TYR
1	A	87	LEU
1	A	153	THR
1	A	173	LEU
1	A	191	VAL
1	A	197	LYS
1	A	198	LEU
1	A	229	ARG
1	A	231	ARG
1	A	244	ARG
1	A	283	LYS
1	A	287	GLN
1	A	292	TYR
1	A	314	SER
1	B	18	GLU
1	B	32	LEU
1	B	78	TYR
1	B	87	LEU
1	B	96	PRO
1	B	97	ASP
1	B	107	THR
1	B	135	ASP
1	B	184	GLU
1	B	189	ILE
1	B	193	ASP
1	B	198	LEU
1	B	227	THR
1	B	232	ASP
1	B	241	ARG
1	B	283	LYS
1	B	296	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	HIS
1	A	128	ASN
1	A	236	GLN
1	B	126	HIS
1	B	129	HIS

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Mol	Chain	Res	Type
1	B	224	HIS

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 monosaccharides 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, 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	A	313/326 (96%)	0.10	3 (0%)	82	85	15, 24, 39, 49	0
1	B	303/326 (92%)	1.23	80 (26%)	0	0	26, 47, 70, 157	0
All	All	616/652 (94%)	0.66	83 (13%)	3	4	15, 34, 65, 157	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	138	LEU	7.9
1	B	130	ALA	7.1
1	B	57	LEU	6.1
1	B	263	ILE	5.2
1	B	2	ALA	4.9
1	B	32	LEU	4.8
1	B	246	ILE	4.6
1	B	188	TYR	4.4
1	B	259	LEU	4.4
1	B	3	THR	4.2
1	B	77	PRO	4.2
1	B	94	VAL	4.1
1	B	134	LYS	3.9
1	B	133	ALA	3.8
1	B	159	ALA	3.8
1	B	84	ALA	3.8
1	B	245	VAL	3.8
1	B	131	GLY	3.7
1	A	313	GLY	3.6
1	A	18	GLU	3.5
1	B	225	GLY	3.5
1	B	264	GLU	3.4
1	B	27	PRO	3.4
1	B	265	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	314	SER	3.3
1	B	267	PHE	3.3
1	B	241	ARG	3.3
1	B	92	VAL	3.3
1	B	255	PHE	3.3
1	B	68	GLY	3.2
1	B	226	ALA	3.0
1	B	4	LEU	3.0
1	B	5	ILE	3.0
1	B	135	ASP	3.0
1	B	280	GLY	3.0
1	B	53	ILE	2.9
1	B	163	PHE	2.9
1	B	132	GLU	2.9
1	B	137	LYS	2.9
1	B	234	THR	2.9
1	B	60	LEU	2.9
1	B	139	ALA	2.8
1	B	232	ASP	2.8
1	B	7	GLY	2.7
1	B	66	MET	2.7
1	B	136	ILE	2.7
1	B	85	LEU	2.7
1	B	278	LEU	2.7
1	B	129	HIS	2.7
1	B	303	PHE	2.7
1	B	29	GLN	2.6
1	B	61	GLY	2.6
1	B	86	GLY	2.5
1	B	238	PRO	2.5
1	B	271	THR	2.5
1	B	239	ALA	2.5
1	B	275	LEU	2.5
1	B	243	GLU	2.4
1	B	236	GLN	2.4
1	B	59	LEU	2.4
1	B	87	LEU	2.4
1	B	55	TYR	2.4
1	B	261	TYR	2.4
1	B	156	LEU	2.3
1	B	80	ASP	2.3
1	B	162	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	240	VAL	2.3
1	B	69	THR	2.3
1	B	297	ALA	2.3
1	B	224	HIS	2.2
1	B	244	ARG	2.2
1	B	242	ALA	2.2
1	B	78	TYR	2.2
1	B	288	GLY	2.2
1	B	254	ALA	2.1
1	B	91	TYR	2.1
1	B	82	MET	2.1
1	B	96	PRO	2.1
1	B	58	ASN	2.1
1	B	262	GLY	2.1
1	B	223	GLU	2.1
1	B	299	ILE	2.0
1	B	31	HIS	2.0

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 monosaccharides 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.