



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 07:40 AM EDT

PDB ID : 4JIS  
Title : Crystal structure of ribitol 5-phosphate cytidylyltransferase (TarI) from *Bacillus subtilis*  
Authors : Yang, C.S.; Chen, S.C.; Chen, Y.R.; Kuan, S.M.; Liu, Y.H.; Chen, Y.  
Deposited on : 2013-03-06  
Resolution : 1.77 Å (reported)

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<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  
Xtriage (Phenix) : 1.20.1  
EDS : 2.36.2  
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) : 2.36.2

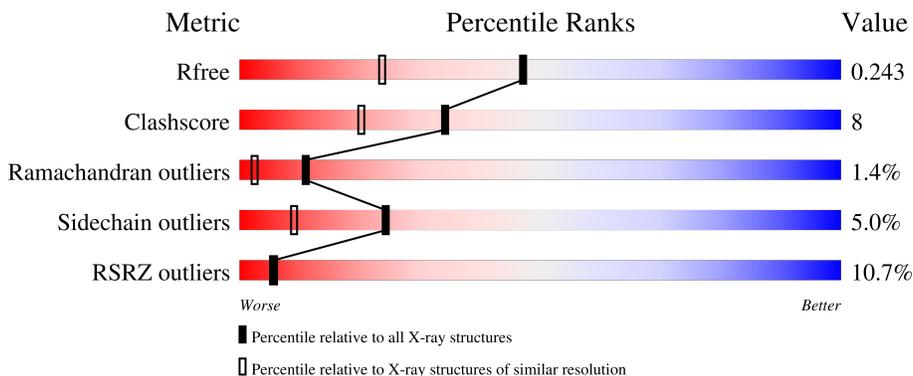
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.77 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	247	 9% 73% 13% •• 11%
1	B	247	 10% 72% 13% • 11%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 3841 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 ribitol-5-phosphate cytidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	221	1766	1130	296	334	6	0	0	0
1	B	219	1750	1119	294	332	5	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP Q8RKI9
A	0	GLY	-	expression tag	UNP Q8RKI9
A	238	LEU	-	expression tag	UNP Q8RKI9
A	239	GLU	-	expression tag	UNP Q8RKI9
A	240	HIS	-	expression tag	UNP Q8RKI9
A	241	HIS	-	expression tag	UNP Q8RKI9
A	242	HIS	-	expression tag	UNP Q8RKI9
A	243	HIS	-	expression tag	UNP Q8RKI9
A	244	HIS	-	expression tag	UNP Q8RKI9
A	245	HIS	-	expression tag	UNP Q8RKI9
B	-1	MET	-	expression tag	UNP Q8RKI9
B	0	GLY	-	expression tag	UNP Q8RKI9
B	238	LEU	-	expression tag	UNP Q8RKI9
B	239	GLU	-	expression tag	UNP Q8RKI9
B	240	HIS	-	expression tag	UNP Q8RKI9
B	241	HIS	-	expression tag	UNP Q8RKI9
B	242	HIS	-	expression tag	UNP Q8RKI9
B	243	HIS	-	expression tag	UNP Q8RKI9
B	244	HIS	-	expression tag	UNP Q8RKI9
B	245	HIS	-	expression tag	UNP Q8RKI9

- Molecule 2 is water.

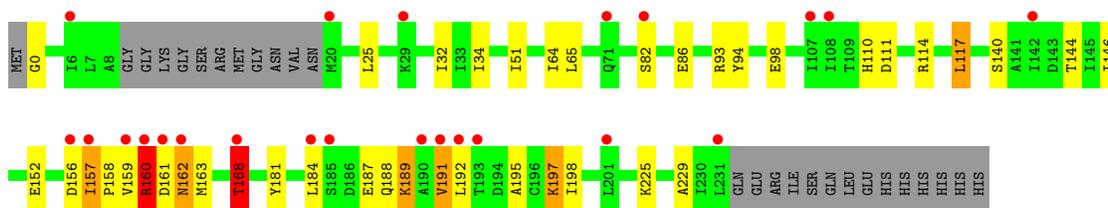
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	A	160	Total 160	O 160	0	0
2	B	165	Total 165	O 165	0	0

### 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.

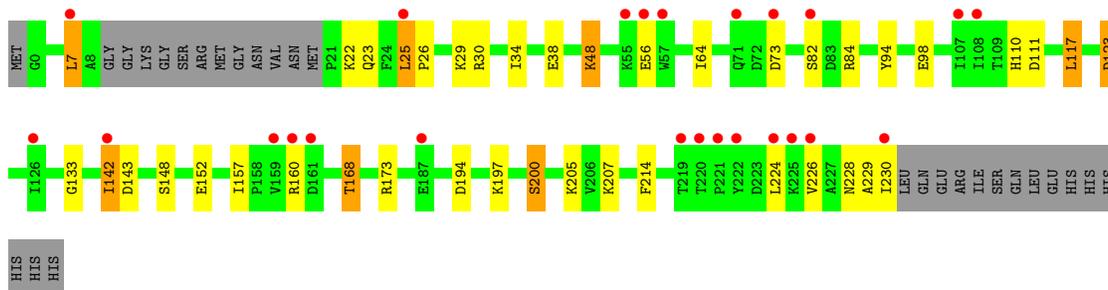
- Molecule 1: ribitol-5-phosphate cytidyltransferase

Chain A: 



- Molecule 1: ribitol-5-phosphate cytidyltransferase

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.75Å 60.98Å 91.81Å 90.00° 113.44° 90.00°	Depositor
Resolution (Å)	24.71 – 1.77 24.71 – 1.77	Depositor EDS
% Data completeness (in resolution range)	97.4 (24.71-1.77) 97.4 (24.71-1.77)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.19 (at 1.77Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.206 , 0.241 0.208 , 0.243	Depositor DCC
$R_{free}$ test set	2534 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.6	Xtrriage
Anisotropy	0.018	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 56.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.015 for $1/2^*h+3/2^*k, 1/2^*h-1/2^*k, -1/2^*h-1/2^*k-l$ 0.011 for $1/2^*h-3/2^*k, -1/2^*h-1/2^*k, -1/2^*h+1/2^*k-l$	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3841	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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](#)

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	0.39	0/1793	0.61	2/2423 (0.1%)
1	B	0.39	0/1777	0.64	0/2401
All	All	0.39	0/3570	0.62	2/4824 (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
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	THR	C-N-CD	-6.68	105.90	120.60
1	A	117	LEU	CA-CB-CG	5.13	127.11	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	168	THR	Peptide,Mainchain
1	B	160	ARG	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	1766	0	1813	34	0
1	B	1750	0	1794	31	0
2	A	160	0	0	5	4
2	B	165	0	0	8	4
All	All	3841	0	3607	60	4

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 (60) 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:205:LYS:NZ	2:B:448:HOH:O	1.97	0.94
1:A:111:ASP:H	1:A:168:THR:HG21	1.39	0.88
1:A:159:VAL:O	2:A:376:HOH:O	1.96	0.84
1:B:111:ASP:H	1:B:168:THR:HG21	1.44	0.82
1:B:152:GLU:OE1	2:B:404:HOH:O	2.04	0.75
1:B:56:GLU:OE1	2:B:462:HOH:O	2.07	0.73
1:B:82:SER:HB2	2:B:394:HOH:O	1.89	0.73
1:A:184:LEU:HD11	1:A:198:ILE:HD12	1.72	0.70
1:B:133:GLY:HA2	1:B:173:ARG:HG3	1.72	0.70
1:B:142:ILE:HD12	1:B:143:ASP:H	1.56	0.69
1:A:51:ILE:HD12	1:A:65:LEU:HD11	1.79	0.64
1:A:160:ARG:O	2:A:335:HOH:O	2.15	0.64
1:A:157:ILE:HG21	1:B:197:LYS:HG2	1.80	0.64
1:B:197:LYS:HA	1:B:200:SER:HB2	1.79	0.63
1:A:86:GLU:OE2	1:A:181:TYR:OH	2.08	0.63
1:B:7:LEU:HD23	1:B:84:ARG:HE	1.65	0.61
1:A:160:ARG:O	1:A:162:ASN:N	2.34	0.61
1:B:205:LYS:NZ	2:B:450:HOH:O	2.35	0.60
1:A:191:VAL:HG13	1:A:192:LEU:HD12	1.85	0.59
1:A:34:ILE:HD11	1:A:64:ILE:HG22	1.85	0.58
1:A:157:ILE:HG13	1:A:160:ARG:HH22	1.69	0.57
1:A:111:ASP:H	1:A:168:THR:CG2	2.16	0.57
1:B:111:ASP:H	1:B:168:THR:CG2	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ILE:HD13	1:A:157:ILE:HB	1.88	0.56
1:A:93:ARG:NH1	2:A:449:HOH:O	2.38	0.55
1:B:29:LYS:NZ	2:B:438:HOH:O	2.01	0.53
1:A:195:ALA:HA	1:A:198:ILE:HG12	1.91	0.53
1:B:30:ARG:HH12	1:B:38:GLU:CD	2.13	0.53
1:B:194:ASP:HB3	1:B:197:LYS:HG3	1.90	0.52
1:A:144:THR:HG23	1:A:160:ARG:HH21	1.74	0.52
1:B:94:TYR:CZ	1:B:98:GLU:HG3	2.45	0.52
1:A:189:LYS:HB2	2:A:371:HOH:O	2.09	0.51
1:B:123:ASP:HB3	2:B:393:HOH:O	2.09	0.51
1:B:48:LYS:NZ	1:B:73:ASP:O	2.33	0.51
1:B:110:HIS:HA	1:B:168:THR:HG23	1.93	0.50
1:A:144:THR:HG23	1:A:160:ARG:NH2	2.27	0.49
1:A:162:ASN:HB2	1:B:148:SER:O	2.12	0.49
1:A:0:GLY:O	2:A:301:HOH:O	2.20	0.48
1:B:110:HIS:CE1	1:B:117:LEU:HG	2.49	0.48
1:A:188:GLN:H	1:A:188:GLN:HG2	1.40	0.47
1:B:34:ILE:HD11	1:B:64:ILE:HG22	1.95	0.47
1:A:152:GLU:OE1	1:B:207:LYS:NZ	2.46	0.47
1:A:191:VAL:HG22	1:A:192:LEU:H	1.80	0.46
1:B:22:LYS:N	1:B:22:LYS:HD2	2.31	0.45
1:B:228:ASN:ND2	2:B:454:HOH:O	2.00	0.45
1:A:94:TYR:CZ	1:A:98:GLU:HG3	2.51	0.45
1:A:197:LYS:HA	1:B:157:ILE:HD12	1.98	0.45
1:B:214:PHE:HB2	1:B:230:ILE:HD13	1.98	0.45
1:B:197:LYS:HE2	1:B:197:LYS:HB3	1.70	0.45
1:A:229:ALA:HB2	1:B:229:ALA:HB2	1.99	0.44
1:B:25:LEU:HA	1:B:26:PRO:HD3	1.80	0.44
1:A:110:HIS:HA	1:A:168:THR:HG23	1.99	0.43
1:B:110:HIS:ND1	1:B:168:THR:CG2	2.82	0.43
1:A:114:ARG:HD2	1:A:168:THR:HG22	1.99	0.43
1:A:25:LEU:O	1:A:32:ILE:HG13	2.19	0.43
1:A:94:TYR:CE2	1:A:98:GLU:HG3	2.55	0.42
1:A:110:HIS:ND1	1:A:168:THR:CG2	2.83	0.42
1:A:158:PRO:HD2	1:A:160:ARG:HH12	1.84	0.42
1:A:160:ARG:HA	1:A:163:MET:HG3	2.00	0.42
1:A:110:HIS:ND1	1:A:168:THR:HG23	2.35	0.42

All (4) 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)
2:A:400:HOH:O	2:B:393:HOH:O[3_455]	1.56	0.64
2:A:428:HOH:O	2:B:435:HOH:O[3_455]	1.81	0.39
2:A:397:HOH:O	2:B:331:HOH:O[3_455]	2.01	0.19
2:A:431:HOH:O	2:B:437:HOH:O[3_455]	2.08	0.12

### 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	217/247 (88%)	205 (94%)	6 (3%)	6 (3%)	5	0
1	B	215/247 (87%)	208 (97%)	7 (3%)	0	100	100
All	All	432/494 (87%)	413 (96%)	13 (3%)	6 (1%)	11	2

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	ASP
1	A	162	ASN
1	A	189	LYS
1	A	191	VAL
1	A	187	GLU
1	A	160	ARG

#### 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	200/222 (90%)	191 (96%)	9 (4%)	27	11
1	B	198/222 (89%)	187 (94%)	11 (6%)	21	7
All	All	398/444 (90%)	378 (95%)	20 (5%)	24	9

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

Mol	Chain	Res	Type
1	A	82	SER
1	A	117	LEU
1	A	140	SER
1	A	156	ASP
1	A	157	ILE
1	A	160	ARG
1	A	168	THR
1	A	197	LYS
1	A	225	LYS
1	B	7	LEU
1	B	23	GLN
1	B	25	LEU
1	B	48	LYS
1	B	117	LEU
1	B	123	ASP
1	B	142	ILE
1	B	168	THR
1	B	200	SER
1	B	224	LEU
1	B	226	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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

### 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	221/247 (89%)	0.75	23 (10%) <b>6</b>   <b>6</b>	22, 38, 61, 75	0
1	B	219/247 (88%)	0.60	24 (10%) <b>5</b>   <b>5</b>	21, 37, 56, 70	0
All	All	440/494 (89%)	0.67	47 (10%) <b>6</b>   <b>5</b>	21, 37, 57, 75	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	226	VAL	8.7
1	A	190	ALA	8.5
1	A	191	VAL	6.7
1	A	161	ASP	6.4
1	A	162	ASN	4.9
1	A	160	ARG	4.7
1	B	159	VAL	4.5
1	A	192	LEU	4.5
1	A	159	VAL	4.4
1	B	161	ASP	4.3
1	A	184	LEU	3.9
1	B	160	ARG	3.8
1	A	20	MET	3.6
1	A	157	ILE	3.6
1	A	71	GLN	3.4
1	B	25	LEU	3.4
1	A	193	THR	3.3
1	B	108	ILE	3.2
1	B	142	ILE	3.2
1	B	230	ILE	3.2
1	B	82	SER	3.2
1	A	29	LYS	3.2
1	B	187	GLU	3.1
1	B	71	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	225	LYS	3.0
1	B	56	GLU	3.0
1	B	222	TYR	2.9
1	A	108	ILE	2.7
1	A	201	LEU	2.6
1	A	231	LEU	2.6
1	B	224	LEU	2.4
1	A	142	ILE	2.4
1	B	126	ILE	2.4
1	B	219	THR	2.4
1	A	185	SER	2.4
1	B	7	LEU	2.3
1	B	57	TRP	2.3
1	B	55	LYS	2.3
1	B	221	PRO	2.3
1	B	73	ASP	2.3
1	A	82	SER	2.2
1	A	168	THR	2.2
1	A	107	ILE	2.2
1	A	6	ILE	2.2
1	B	220	THR	2.2
1	B	107	ILE	2.1
1	A	156	ASP	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.