



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 25, 2024 – 03:45 PM EST

PDB ID : 1Y13
Title : Structural Analysis of Plasmodium falciparum 6-pyruvoyl tetrahydropterin synthase (PTPS)
Authors : Bosch, J.; Hol, W.G.J.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)
Deposited on : 2004-11-17
Resolution : 2.20 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

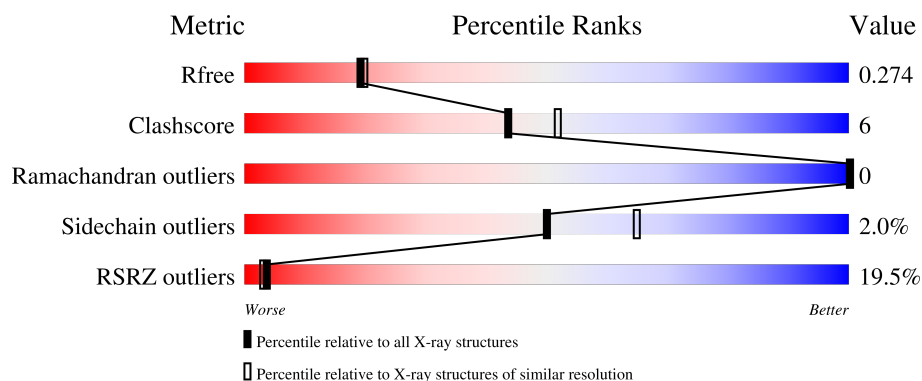
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	181	<div> <div>19%</div> <div>77%</div> <div>13%</div> <div>• 10%</div> </div>
1	B	181	<div> <div>8%</div> <div>80%</div> <div>10%</div> <div>10%</div> </div>
1	C	181	<div> <div>25%</div> <div>76%</div> <div>13%</div> <div>•• 10%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4150 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 6-pyruvoyl tetrahydropterin synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	Se	0	0	0
			1319	848	222	244	4	1			
1	B	163	Total	C	N	O	S	Se	0	0	0
			1324	850	223	246	4	1			
1	C	163	Total	C	N	O	S	Se	0	0	0
			1329	851	224	249	4	1			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	GB 23612358
A	-6	ALA	-	cloning artifact	GB 23612358
A	-5	HIS	-	expression tag	GB 23612358
A	-4	HIS	-	expression tag	GB 23612358
A	-3	HIS	-	expression tag	GB 23612358
A	-2	HIS	-	expression tag	GB 23612358
A	-1	HIS	-	expression tag	GB 23612358
A	0	HIS	-	expression tag	GB 23612358
A	142	MSE	MET	modified residue	GB 23612358
B	-7	MET	-	initiating methionine	GB 23612358
B	-6	ALA	-	cloning artifact	GB 23612358
B	-5	HIS	-	expression tag	GB 23612358
B	-4	HIS	-	expression tag	GB 23612358
B	-3	HIS	-	expression tag	GB 23612358
B	-2	HIS	-	expression tag	GB 23612358
B	-1	HIS	-	expression tag	GB 23612358
B	0	HIS	-	expression tag	GB 23612358
B	142	MSE	MET	modified residue	GB 23612358
C	-7	MET	-	initiating methionine	GB 23612358
C	-6	ALA	-	cloning artifact	GB 23612358
C	-5	HIS	-	expression tag	GB 23612358
C	-4	HIS	-	expression tag	GB 23612358
C	-3	HIS	-	expression tag	GB 23612358

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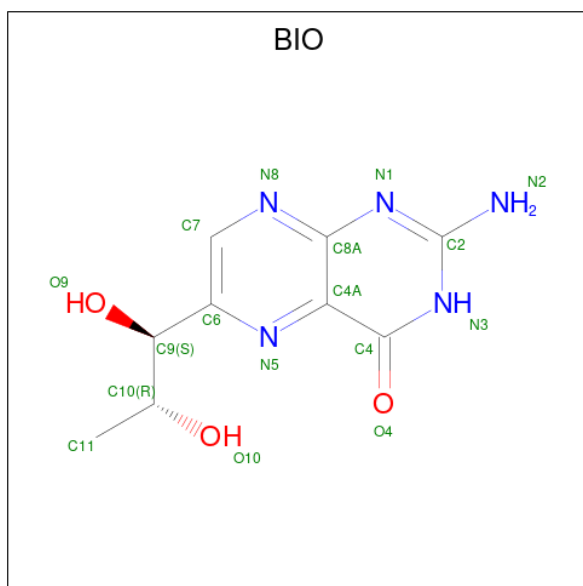
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	GB 23612358
C	-1	HIS	-	expression tag	GB 23612358
C	0	HIS	-	expression tag	GB 23612358
C	142	MSE	MET	modified residue	GB 23612358

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

- Molecule 3 is BIOPTERIN (three-letter code: BIO) (formula: C₉H₁₁N₅O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 15 8 5 2	0	0
3	B	1	Total C N O 17 9 5 3	0	0
3	C	1	Total C N O 17 9 5 3	0	0

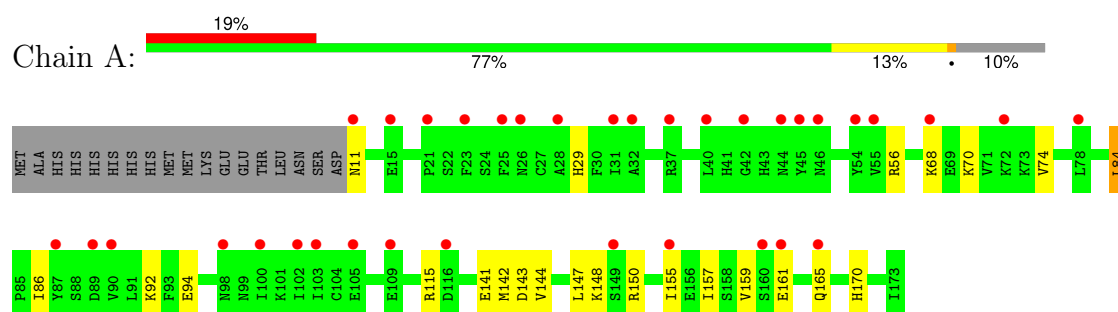
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total 57	O 57	0	0
4	B	50	Total 50	O 50	0	0
4	C	19	Total 19	O 19	0	0

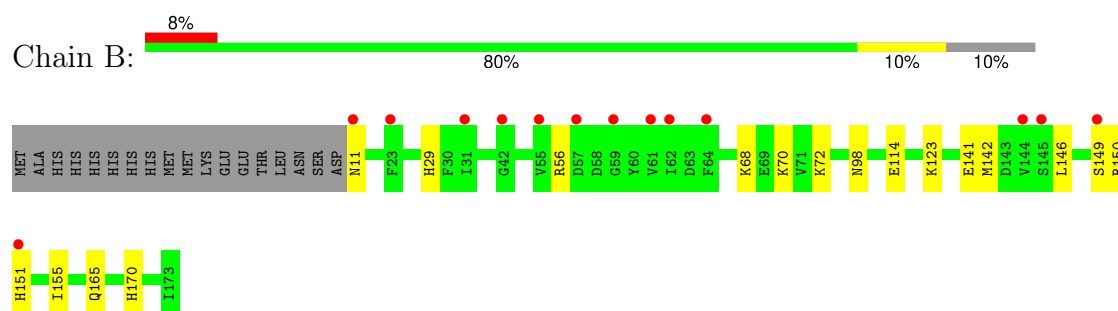
3 Residue-property plots [i](#)

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. 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. 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.

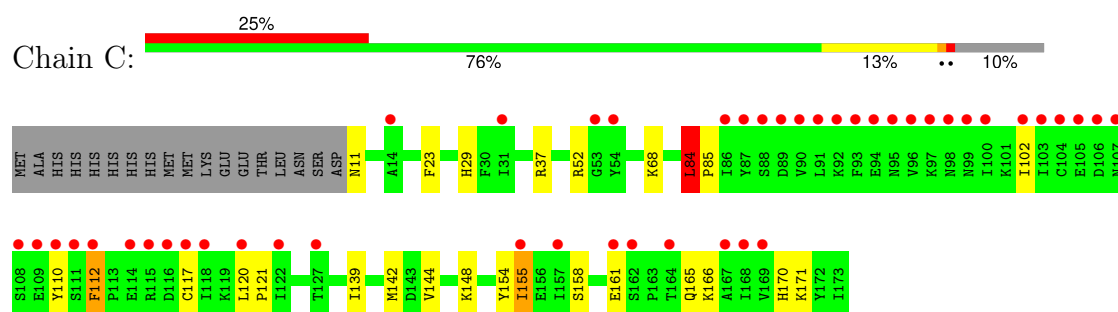
- Molecule 1: 6-pyruvoyl tetrahydropterin synthase



- Molecule 1: 6-pyruvoyl tetrahydropterin synthase



- Molecule 1: 6-pyruvoyl tetrahydropterin synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	103.32Å 103.32Å 131.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.20) 99.6 (20.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.21Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.195 , 0.235 0.235 , 0.274	Depositor DCC
R_{free} test set	1847 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	52.8	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4150	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: ZN, BIO

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	0.60	0/1347	0.71	1/1817 (0.1%)
1	B	0.60	0/1353	0.69	0/1823
1	C	0.47	0/1358	0.60	1/1831 (0.1%)
All	All	0.56	0/4058	0.67	2/5471 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	LEU	CA-CB-CG	7.38	132.28	115.30
1	C	84	LEU	CA-CB-CG	6.14	129.43	115.30

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	1319	0	1296	20	0
1	B	1324	0	1307	15	0
1	C	1329	0	1314	22	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	15	0	8	1	0
3	B	17	0	10	0	0
3	C	17	0	11	0	0
4	A	57	0	0	2	0
4	B	50	0	0	0	0
4	C	19	0	0	1	0
All	All	4150	0	3946	48	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 6.

The worst 5 of 48 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:142:MSE:HE1	1:B:155:ILE:CD1	1.99	0.92
1:A:68:LYS:HE3	1:B:165:GLN:OE1	1.74	0.87
3:A:175:BIO:N3	3:A:175:BIO:C4A	2.43	0.80
1:B:142:MSE:HE1	1:B:155:ILE:HD12	1.64	0.80
1:A:68:LYS:CE	1:B:165:GLN:OE1	2.30	0.79

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	161/181 (89%)	155 (96%)	6 (4%)	0	100	100
1	B	161/181 (89%)	155 (96%)	6 (4%)	0	100	100
1	C	161/181 (89%)	154 (96%)	7 (4%)	0	100	100
All	All	483/543 (89%)	464 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	149/170 (88%)	147 (99%)	2 (1%)	65	78
1	B	152/170 (89%)	149 (98%)	3 (2%)	50	65
1	C	153/170 (90%)	149 (97%)	4 (3%)	41	54
All	All	454/510 (89%)	445 (98%)	9 (2%)	50	65

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	112	PHE
1	C	155	ILE
1	B	72	LYS
1	B	149	SER
1	C	29	HIS

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

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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
3	BIO	A	175	2	11,15,18	2.47	5 (45%)	7,20,26	3.63	3 (42%)
3	BIO	C	175	2	17,18,18	2.65	6 (35%)	14,26,26	3.70	8 (57%)
3	BIO	B	175	2	17,18,18	2.28	4 (23%)	14,26,26	3.92	10 (71%)

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
3	BIO	A	175	2	-	4/8/8/8	0/1/1/2
3	BIO	C	175	2	-	1/8/8/8	0/2/2/2
3	BIO	B	175	2	-	2/8/8/8	0/2/2/2

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	175	BIO	C6-N5	6.81	1.38	1.32
3	B	175	BIO	C6-N5	6.46	1.38	1.32
3	A	175	BIO	C4A-C8A	5.52	1.48	1.41
3	C	175	BIO	C4A-C4	5.23	1.50	1.41
3	C	175	BIO	C4A-C8A	4.38	1.48	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	175	BIO	C8A-C4A-C4	-8.44	114.73	119.96
3	A	175	BIO	C4A-N5-C6	8.07	123.84	117.98
3	C	175	BIO	C8A-C4A-C4	-7.68	115.20	119.96
3	B	175	BIO	N8-C8A-N1	5.36	121.61	115.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	175	BIO	C2-N1-C8A	5.31	121.21	115.48

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	175	BIO	O10-C10-C9-C6
3	A	175	BIO	C11-C10-C9-C6
3	A	175	BIO	C11-C10-C9-O9
3	B	175	BIO	C11-C10-C9-O9
3	B	175	BIO	C7-C6-C9-O9

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	175	BIO	1	0

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](#)

Warning: The R factor obtained from EDS is 0.2769, which does not match the depositor's R factor of 0.19536. Please interpret the results in this section carefully.

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	162/181 (89%)	1.40	35 (21%) 3 2	51, 59, 65, 67	0
1	B	162/181 (89%)	0.94	14 (8%) 18 15	51, 59, 65, 67	0
1	C	162/181 (89%)	1.61	46 (28%) 1 1	51, 59, 65, 66	0
All	All	486/543 (89%)	1.32	95 (19%) 4 3	51, 59, 65, 67	0

The worst 5 of 95 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	110	TYR	5.7
1	C	112	PHE	5.1
1	C	111	SER	4.6
1	C	96	VAL	4.6
1	C	100	ILE	4.6

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](#)

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, 95th 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 ²)	Q<0.9
3	BIO	A	175	15/17	0.66	0.18	55,57,76,78	0
3	BIO	B	175	17/17	0.81	0.15	52,56,77,77	0
3	BIO	C	175	17/17	0.81	0.13	55,57,75,77	0
2	ZN	C	174	1/1	0.95	0.12	65,65,65,65	0
2	ZN	B	174	1/1	0.98	0.05	64,64,64,64	0
2	ZN	A	174	1/1	0.99	0.03	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.