



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:28 AM GMT

PDB ID : 3IJ6
Title : CRYSTAL STRUCTURE OF AN UNCHARACTERIZED METAL-DEPENDENT HYDROLASE FROM *Lactobacillus acidophilus*
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Deposited on : 2009-08-03
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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

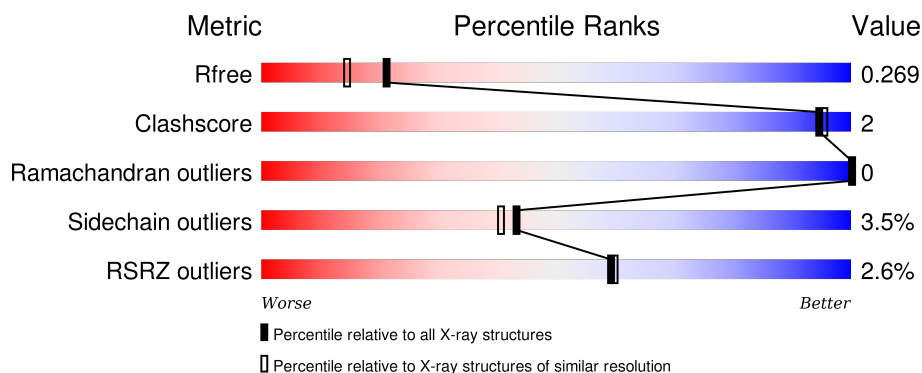
1 Overall quality at a glance

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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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 ≥ 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	312	 92% 5% .
1	B	312	 91% 6% .
1	C	312	 88% 8% . .
1	D	312	 88% 9% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10133 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 UNCHARACTERIZED METAL-DEPENDENT HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	5	0
			2440	1574	400	456	10			
1	B	303	Total	C	N	O	S	0	4	0
			2433	1567	399	457	10			
1	C	302	Total	C	N	O	S	0	7	0
			2441	1578	400	453	10			
1	D	302	Total	C	N	O	S	0	4	0
			2427	1565	399	453	10			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q5FK79
A	1	SER	-	expression tag	UNP Q5FK79
A	2	LEU	-	expression tag	UNP Q5FK79
A	305	GLY	-	expression tag	UNP Q5FK79
A	306	HIS	-	expression tag	UNP Q5FK79
A	307	HIS	-	expression tag	UNP Q5FK79
A	308	HIS	-	expression tag	UNP Q5FK79
A	309	HIS	-	expression tag	UNP Q5FK79
A	310	HIS	-	expression tag	UNP Q5FK79
A	311	HIS	-	expression tag	UNP Q5FK79
B	0	MET	-	expression tag	UNP Q5FK79
B	1	SER	-	expression tag	UNP Q5FK79
B	2	LEU	-	expression tag	UNP Q5FK79
B	305	GLY	-	expression tag	UNP Q5FK79
B	306	HIS	-	expression tag	UNP Q5FK79
B	307	HIS	-	expression tag	UNP Q5FK79
B	308	HIS	-	expression tag	UNP Q5FK79
B	309	HIS	-	expression tag	UNP Q5FK79
B	310	HIS	-	expression tag	UNP Q5FK79
B	311	HIS	-	expression tag	UNP Q5FK79

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	expression tag	UNP Q5FK79
C	1	SER	-	expression tag	UNP Q5FK79
C	2	LEU	-	expression tag	UNP Q5FK79
C	305	GLY	-	expression tag	UNP Q5FK79
C	306	HIS	-	expression tag	UNP Q5FK79
C	307	HIS	-	expression tag	UNP Q5FK79
C	308	HIS	-	expression tag	UNP Q5FK79
C	309	HIS	-	expression tag	UNP Q5FK79
C	310	HIS	-	expression tag	UNP Q5FK79
C	311	HIS	-	expression tag	UNP Q5FK79
D	0	MET	-	expression tag	UNP Q5FK79
D	1	SER	-	expression tag	UNP Q5FK79
D	2	LEU	-	expression tag	UNP Q5FK79
D	305	GLY	-	expression tag	UNP Q5FK79
D	306	HIS	-	expression tag	UNP Q5FK79
D	307	HIS	-	expression tag	UNP Q5FK79
D	308	HIS	-	expression tag	UNP Q5FK79
D	309	HIS	-	expression tag	UNP Q5FK79
D	310	HIS	-	expression tag	UNP Q5FK79
D	311	HIS	-	expression tag	UNP Q5FK79

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

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Na 1 1	0	0
3	A	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Na 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total 113	O 113	0	0
4	B	131	Total 131	O 131	0	0
4	C	72	Total 72	O 72	0	0
4	D	68	Total 68	O 68	0	0

3 Residue-property plots [i](#)

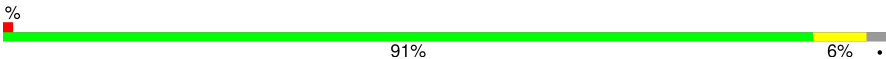
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($RSRZ > 2$). 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: UNCHARACTERIZED METAL-DEPENDENT HYDROLASE

Chain A: 




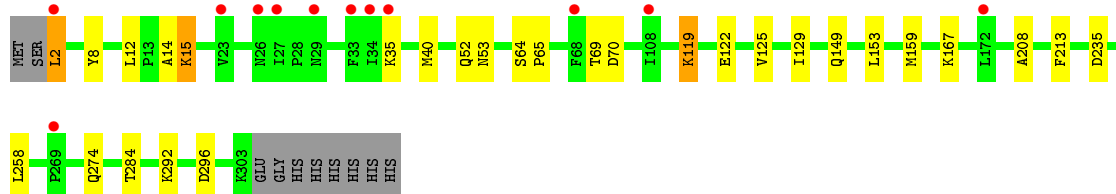
• Molecule 1: UNCHARACTERIZED METAL-DEPENDENT HYDROLASE

Chain B: 




• Molecule 1: UNCHARACTERIZED METAL-DEPENDENT HYDROLASE

Chain C: 



• Molecule 1: UNCHARACTERIZED METAL-DEPENDENT HYDROLASE

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	170.72Å 96.43Å 96.03Å 90.00° 90.40° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 34.02 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.00) 97.4 (34.02-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.3.0034	Depositor
R, R_{free}	0.221 , 0.268 0.221 , 0.269	Depositor DCC
R_{free} test set	3132 reflections (3.09%)	DCC
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.3	EDS
Estimated twinning fraction	0.040 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.044 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.037 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.046 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.230 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	1 of 104976 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10133	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, ZN

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	0.43	0/2514	0.59	0/3411
1	B	0.44	0/2504	0.60	0/3400
1	C	0.40	0/2521	0.57	1/3421 (0.0%)
1	D	0.47	0/2498	0.57	1/3391 (0.0%)
All	All	0.44	0/10037	0.58	2/13623 (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	C	2	LEU	CA-CB-CG	5.32	127.54	115.30
1	D	2	LEU	CA-CB-CG	-5.12	103.53	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	2440	0	2438	9	0
1	B	2433	0	2418	8	0
1	C	2441	0	2454	12	0
1	D	2427	0	2420	14	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	113	0	0	0	0
4	B	131	0	0	0	0
4	C	72	0	0	0	0
4	D	68	0	0	0	0
All	All	10133	0	9730	33	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 2.

All (33) 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:D:292:LYS:HA	1:D:296:ASP:HB2	1.72	0.71
1:C:119[A]:LYS:HE3	1:C:153:LEU:HB3	1.74	0.70
1:D:36:ILE:HG12	1:D:268:MET:HE3	1.78	0.66
1:D:265:PHE:O	1:D:266:ALA:HB3	1.99	0.61
1:D:36:ILE:HG12	1:D:268:MET:CE	2.31	0.60
1:D:187:LEU:HD22	1:D:192:LEU:HD22	1.84	0.59
1:B:59:SER:HB3	1:B:100:VAL:HB	1.84	0.58
1:B:292:LYS:HA	1:B:296:ASP:HB2	1.86	0.57
1:B:37:LYS:HB2	1:B:44:GLU:HG2	1.87	0.57
1:A:292:LYS:HA	1:A:296:ASP:HB2	1.87	0.57
1:C:167:LYS:HG2	1:D:168:PRO:HD2	1.89	0.55
1:A:208:ALA:HA	1:B:213:PHE:HZ	1.72	0.54
1:C:292:LYS:HA	1:C:296:ASP:HB2	1.89	0.54
1:A:213:PHE:HZ	1:B:208:ALA:HA	1.73	0.53
1:A:213:PHE:CE1	1:B:177[B]:GLU:HG2	2.46	0.51
1:A:213:PHE:CZ	1:B:177[B]:GLU:HG2	2.46	0.50
1:A:34:ILE:HA	1:A:40:MET:HE1	1.94	0.50
1:C:208:ALA:HA	1:D:213:PHE:HZ	1.78	0.49
1:C:14:ALA:HB3	1:C:15[A]:LYS:HZ1	1.79	0.48
1:D:12:LEU:HD21	1:D:63:ILE:HD12	1.95	0.48
1:A:177:GLU:HB2	1:B:209:MET:HE1	1.99	0.45
1:C:213:PHE:CE1	1:D:177:GLU:HG2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:PHE:CZ	1:D:177:GLU:HG2	2.53	0.43
1:A:187:LEU:HD22	1:A:192:LEU:HD22	2.01	0.42
1:C:213:PHE:HZ	1:D:208:ALA:HA	1.84	0.42
1:C:149:GLN:HE21	1:C:153:LEU:HD11	1.84	0.42
1:D:300:SER:HA	1:D:303:LYS:HD2	2.01	0.42
1:C:235:ASP:HA	1:C:258:LEU:O	2.19	0.42
1:D:24:GLU:HA	1:D:25:PRO:HD3	1.90	0.42
1:D:69:THR:HB	1:D:73:THR:HB	2.02	0.41
1:C:64:SER:HA	1:C:65:PRO:HD3	1.83	0.41
1:C:129:ILE:O	1:C:159:MET:HA	2.21	0.40
1:A:64:SER:HA	1:A:65:PRO:HD3	1.93	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	306/312 (98%)	298 (97%)	8 (3%)	0	100	100
1	B	305/312 (98%)	297 (97%)	8 (3%)	0	100	100
1	C	307/312 (98%)	296 (96%)	11 (4%)	0	100	100
1	D	304/312 (97%)	293 (96%)	11 (4%)	0	100	100
All	All	1222/1248 (98%)	1184 (97%)	38 (3%)	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	271/274 (99%)	267 (98%)	4 (2%)	72	75
1	B	270/274 (98%)	260 (96%)	10 (4%)	41	38
1	C	272/274 (99%)	255 (94%)	17 (6%)	22	16
1	D	269/274 (98%)	259 (96%)	10 (4%)	41	38
All	All	1082/1096 (99%)	1041 (96%)	41 (4%)	43	36

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	TYR
1	A	12	LEU
1	A	88	LEU
1	A	204	HIS
1	B	3	THR
1	B	8	TYR
1	B	12	LEU
1	B	35	LYS
1	B	43	ASP
1	B	52[A]	GLN
1	B	52[B]	GLN
1	B	134	LEU
1	B	204	HIS
1	B	304	GLU
1	C	2	LEU
1	C	8	TYR
1	C	12	LEU
1	C	15[A]	LYS
1	C	15[B]	LYS
1	C	35	LYS
1	C	40	MET
1	C	52	GLN
1	C	53	ASN
1	C	69	THR
1	C	70	ASP
1	C	119[A]	LYS
1	C	119[B]	LYS
1	C	122	GLU
1	C	125	VAL
1	C	274	GLN

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Mol	Chain	Res	Type
1	C	284	THR
1	D	8	TYR
1	D	34	ILE
1	D	35	LYS
1	D	43	ASP
1	D	73	THR
1	D	88	LEU
1	D	125	VAL
1	D	204	HIS
1	D	287[A]	ASP
1	D	287[B]	ASP

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

Mol	Chain	Res	Type
1	B	29	ASN
1	B	149	GLN
1	C	53	ASN
1	C	149	GLN
1	C	295	HIS
1	D	154	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	303/312 (97%)	0.05	1 (0%) 94 94	18, 35, 68, 91	0
1	B	303/312 (97%)	0.01	2 (0%) 89 89	17, 35, 65, 86	0
1	C	302/312 (96%)	0.25	12 (3%) 42 44	25, 46, 81, 101	0
1	D	302/312 (96%)	0.31	17 (5%) 28 29	26, 48, 81, 106	0
All	All	1210/1248 (96%)	0.15	32 (2%) 59 60	17, 40, 77, 106	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	23	VAL	6.5
1	B	2	LEU	4.5
1	C	26	ASN	4.4
1	D	25	PRO	4.1
1	D	63	ILE	4.0
1	D	35	LYS	4.0
1	D	34	ILE	3.5
1	C	35	LYS	3.5
1	C	68	PHE	3.3
1	C	27	ILE	3.1
1	C	269	PRO	3.0
1	D	18	GLN	2.9
1	C	33	PHE	2.8
1	B	35	LYS	2.7
1	A	34	ILE	2.6
1	C	2	LEU	2.5
1	D	12	LEU	2.5
1	C	29	ASN	2.4
1	D	31	PHE	2.4
1	D	119	LYS	2.4
1	C	23	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	34	ILE	2.3
1	D	50	PRO	2.3
1	C	108	ILE	2.3
1	D	32	PRO	2.3
1	D	64	SER	2.2
1	D	269	PRO	2.2
1	D	270	SER	2.2
1	D	17	TYR	2.1
1	D	21	LEU	2.1
1	D	19	LYS	2.1
1	C	172	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	NA	B	313	1/1	0.89	0.14	-0.53	49,49,49,49	0
2	ZN	A	312	1/1	1.00	0.10	-0.78	34,34,34,34	1
3	NA	C	313	1/1	0.86	0.12	-1.06	61,61,61,61	0
3	NA	A	313	1/1	0.90	0.10	-1.07	58,58,58,58	0
3	NA	D	313	1/1	0.96	0.06	-1.28	43,43,43,43	0
2	ZN	B	312	1/1	0.98	0.08	-2.41	37,37,37,37	1
2	ZN	C	312	1/1	0.94	0.06	-	50,50,50,50	1
2	ZN	D	312	1/1	0.96	0.06	-	51,51,51,51	1

6.5 Other polymers

There are no such residues in this entry.