



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:26 PM UTC

PDB ID : 5UD2 / pdb_00005ud2
Title : Class II fructose-1,6-bisphosphate aldolase H180Q variant of *Helicobacter pylori* with DHAP
Authors : Jacques, B.; Sygusch, J.
Deposited on : 2016-12-23
Resolution : 1.77 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 ⓘ 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

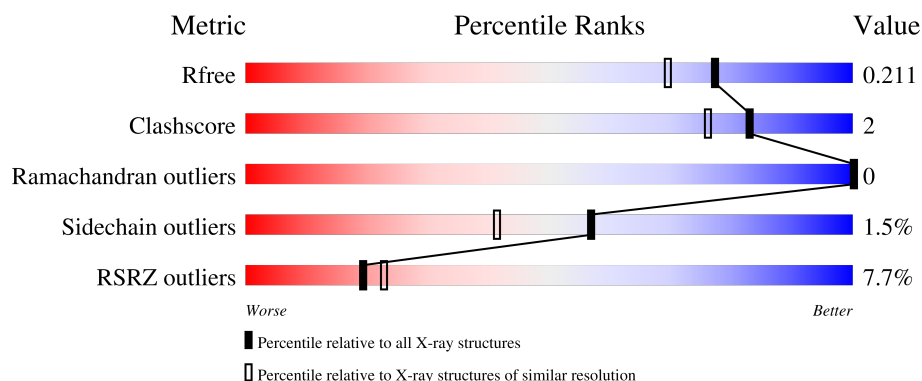
1 Overall quality at a glance

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}	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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 $\leq 5\%$. 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	307	7% 91% 5%
1	B	307	7% 88% 7% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9616 atoms, of which 4596 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 Fructose-bisphosphate aldolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	292	Total	C	H	N	O	S	0	5	0
			4592	1463	2293	396	428	12			
1	B	292	Total	C	H	N	O	S	0	5	0
			4592	1463	2293	396	428	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	ALA	THR	conflict	UNP P56109
A	67	ILE	THR	conflict	UNP P56109
A	180	GLN	HIS	engineered mutation	UNP P56109
B	48	ALA	THR	conflict	UNP P56109
B	67	ILE	THR	conflict	UNP P56109
B	180	GLN	HIS	engineered mutation	UNP P56109

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

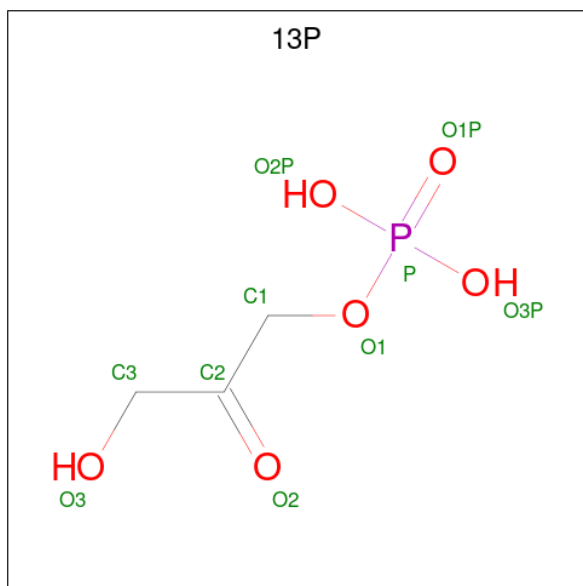
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is 1,3-DIHYDROXYACETONEPHOSPHATE (CCD ID: 13P) (formula:

C₃H₇O₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	O	P	0	0
			15	3	5	6	1		
4	B	1	Total	C	H	O	P	0	0
			15	3	5	6	1		

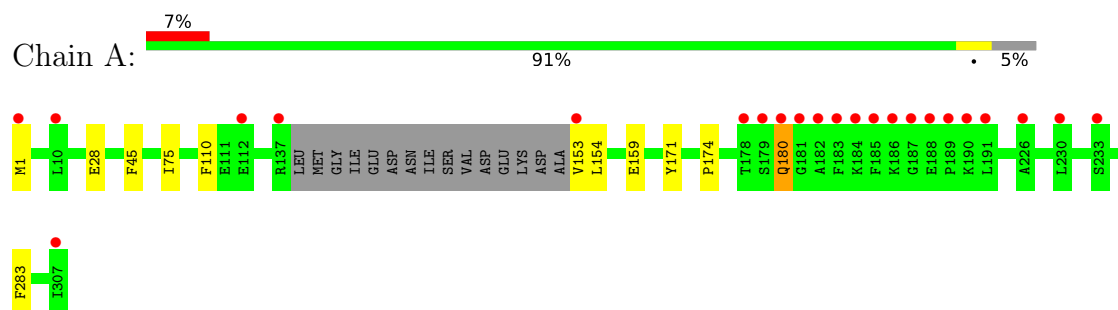
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	198	Total	O	0	0
			198	198		
5	B	198	Total	O	0	0
			198	198		

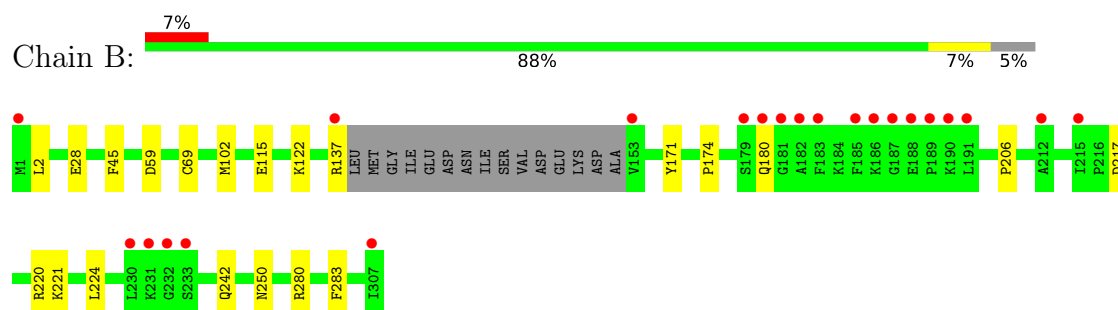
3 Residue-property plots [i](#)

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: Fructose-bisphosphate aldolase



- Molecule 1: Fructose-bisphosphate aldolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	39.41Å 63.09Å 64.79Å 82.51° 75.96° 74.39°	Depositor
Resolution (Å)	35.78 – 1.77 35.78 – 1.77	Depositor EDS
% Data completeness (in resolution range)	83.3 (35.78-1.77) 83.4 (35.78-1.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 1.77Å)	Xtriage
Refinement program	PHENIX (dev_2481)	Depositor
R, R_{free}	0.193 , 0.216 (Not available) , 0.211	Depositor DCC
R_{free} test set	2483 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	13.2	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.237 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9616	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.45% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, 13P, 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	0.17	0/2340	0.33	0/3145
1	B	0.18	0/2340	0.32	0/3145
All	All	0.17	0/4680	0.32	0/6290

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

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	2299	2293	2314	6	0
1	B	2299	2293	2314	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	10	5	5	1	0
4	B	10	5	5	0	0
5	A	198	0	0	3	0
5	B	198	0	0	11	1
All	All	5020	4596	4638	22	1

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 (22) 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:180:GLN:HB3	5:B:548:HOH:O	1.80	0.81
1:B:242:GLN:NE2	5:B:503:HOH:O	2.16	0.77
1:B:217:ASP:OD2	5:B:501:HOH:O	2.09	0.70
1:B:221:LYS:NZ	5:B:505:HOH:O	2.27	0.67
1:B:180:GLN:HG2	5:B:657:HOH:O	1.94	0.67
1:A:174:PRO:O	5:A:502:HOH:O	2.14	0.66
4:A:404:13P:O2	5:A:501:HOH:O	2.14	0.66
1:B:137:ARG:NH1	5:B:508:HOH:O	2.28	0.66
1:A:1:MET:N	1:A:75:ILE:O	2.28	0.65
1:B:69[B]:CYS:SG	5:B:623:HOH:O	2.36	0.64
1:B:280:ARG:NH1	5:B:509:HOH:O	2.31	0.63
1:B:174:PRO:O	5:B:502:HOH:O	2.15	0.63
1:A:180:GLN:HG2	5:A:554:HOH:O	2.05	0.55
1:B:115:GLU:OE2	5:B:504:HOH:O	2.21	0.45
1:A:153:VAL:HG12	1:A:154:LEU:O	2.17	0.45
1:B:28:GLU:HG2	1:B:283:PHE:HB3	2.00	0.44
1:B:220:ARG:O	1:B:224:LEU:HD23	2.18	0.43
1:A:110:PHE:CD2	1:A:159:GLU:HG2	2.53	0.43
1:B:122:LYS:NZ	5:B:520:HOH:O	2.47	0.42
1:B:59:ASP:OD2	1:B:59:ASP:N	2.52	0.41
1:A:28:GLU:HG2	1:A:283:PHE:HB3	2.03	0.41
1:B:206:PRO:HA	1:B:250:ASN:OD1	2.22	0.40

All (1) 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)
5:B:576:HOH:O	5:B:658:HOH:O[1_455]	2.01	0.19

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	293/307 (95%)	287 (98%)	6 (2%)	0	100	100
1	B	293/307 (95%)	286 (98%)	7 (2%)	0	100	100
All	All	586/614 (95%)	573 (98%)	13 (2%)	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	246/254 (97%)	243 (99%)	3 (1%)	63	49
1	B	246/254 (97%)	242 (98%)	4 (2%)	55	38
All	All	492/508 (97%)	485 (99%)	7 (1%)	57	44

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	PHE
1	A	171	TYR
1	A	180	GLN
1	B	2	LEU
1	B	45	PHE
1	B	102	MET
1	B	171	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	180	GLN
1	A	287	GLN

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Mol	Chain	Res	Type
1	B	31	ASN
1	B	168	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	$\# Z > 2$
4	13P	B	404	3	9,9,9	0.62	0	10,12,12	1.08	0
4	13P	A	404	3	9,9,9	0.53	0	10,12,12	1.08	0

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
4	13P	B	404	3	-	5/8/8/8	-
4	13P	A	404	3	-	1/8/8/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	404	13P	C1-O1-P-O1P
4	B	404	13P	C1-O1-P-O2P
4	B	404	13P	C1-O1-P-O3P
4	B	404	13P	O1-C1-C2-C3
4	A	404	13P	O1-C1-C2-C3
4	B	404	13P	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	13P	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

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	292/307 (95%)	0.40	23 (7%) 18 22	9, 19, 58, 132	5 (1%)
1	B	292/307 (95%)	0.35	22 (7%) 20 24	8, 19, 56, 112	5 (1%)
All	All	584/614 (95%)	0.37	45 (7%) 19 23	8, 19, 57, 132	10 (1%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	153	VAL	6.7
1	A	183	PHE	6.7
1	A	182	ALA	6.2
1	B	153	VAL	5.7
1	A	187	GLY	5.3
1	A	181	GLY	5.1
1	B	187	GLY	4.9
1	A	307	ILE	4.8
1	A	180	GLN	4.6
1	B	180	GLN	4.5
1	A	189	PRO	4.4
1	B	183	PHE	4.4
1	A	185	PHE	4.2
1	B	181	GLY	4.2
1	B	182	ALA	4.2
1	B	186	LYS	3.7
1	A	188	GLU	3.5
1	B	231	LYS	3.2
1	B	185	PHE	3.2
1	A	233	SER	3.2
1	A	1	MET	3.2
1	B	137	ARG	3.2
1	B	189	PRO	3.0
1	A	186	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	184	LYS	2.9
1	B	233	SER	2.9
1	B	232	GLY	2.8
1	A	10	LEU	2.8
1	B	1	MET	2.7
1	B	191	LEU	2.6
1	A	137	ARG	2.6
1	A	190	LYS	2.5
1	B	307	ILE	2.5
1	A	191	LEU	2.4
1	B	179	SER	2.4
1	B	212	ALA	2.4
1	B	215	ILE	2.4
1	B	188	GLU	2.3
1	A	226	ALA	2.3
1	B	190	LYS	2.3
1	A	178	THR	2.2
1	A	230	LEU	2.2
1	A	112	GLU	2.1
1	A	179	SER	2.0
1	B	230	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	ZN	B	402[A]	1/1	0.92	0.07	32,32,32,32	1
3	ZN	B	403[B]	1/1	0.92	0.16	25,25,25,25	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	13P	B	404	10/10	0.92	0.10	22,30,37,37	0
4	13P	A	404	10/10	0.94	0.08	22,29,37,37	0
3	ZN	A	403[B]	1/1	0.94	0.06	24,24,24,24	1
2	NA	A	401	1/1	0.97	0.05	25,25,25,25	0
3	ZN	A	402[A]	1/1	0.98	0.06	37,37,37,37	1
2	NA	B	401	1/1	0.98	0.04	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.