



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:16 PM UTC

PDB ID : 3PFL / pdb_00003pfl
Title : CRYSTAL STRUCTURE OF PFL FROM E.COLI IN COMPLEX WITH
SUBSTRATE ANALOGUE OXAMATE
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Deposited on : 1999-05-14
Resolution : 2.60 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	:	4-5-2 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

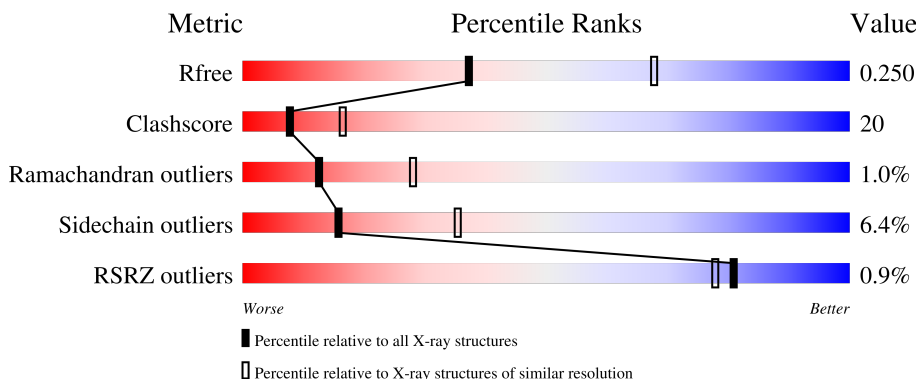
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	759	% 67% 28% 5%
1	B	759	% 63% 32% 5%

2 Entry composition [i](#)

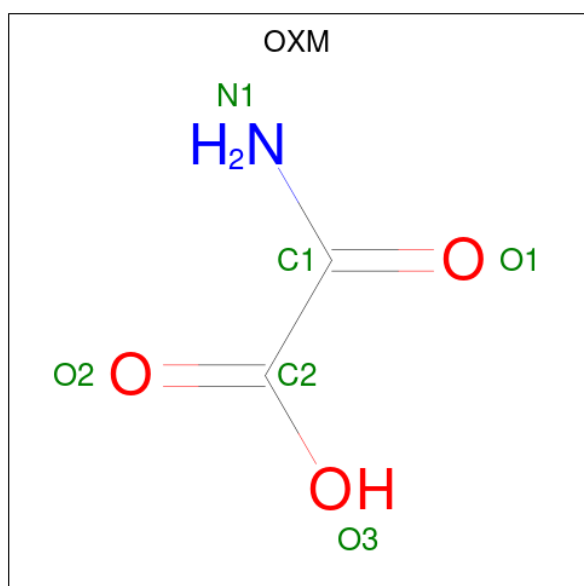
There are 3 unique types of molecules in this entry. The entry contains 12515 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (FORMATE ACETYLTRANSFERASE 1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	759	Total	C	N	O	S	0	0	0
			5988	3784	1023	1145	36			
1	B	759	Total	C	N	O	S	0	0	0
			5988	3784	1023	1145	36			

- Molecule 2 is OXAMIC ACID (CCD ID: OXM) (formula: $C_2H_3NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			6	2	1	3		
2	B	1	Total	C	N	O	0	0
			6	2	1	3		

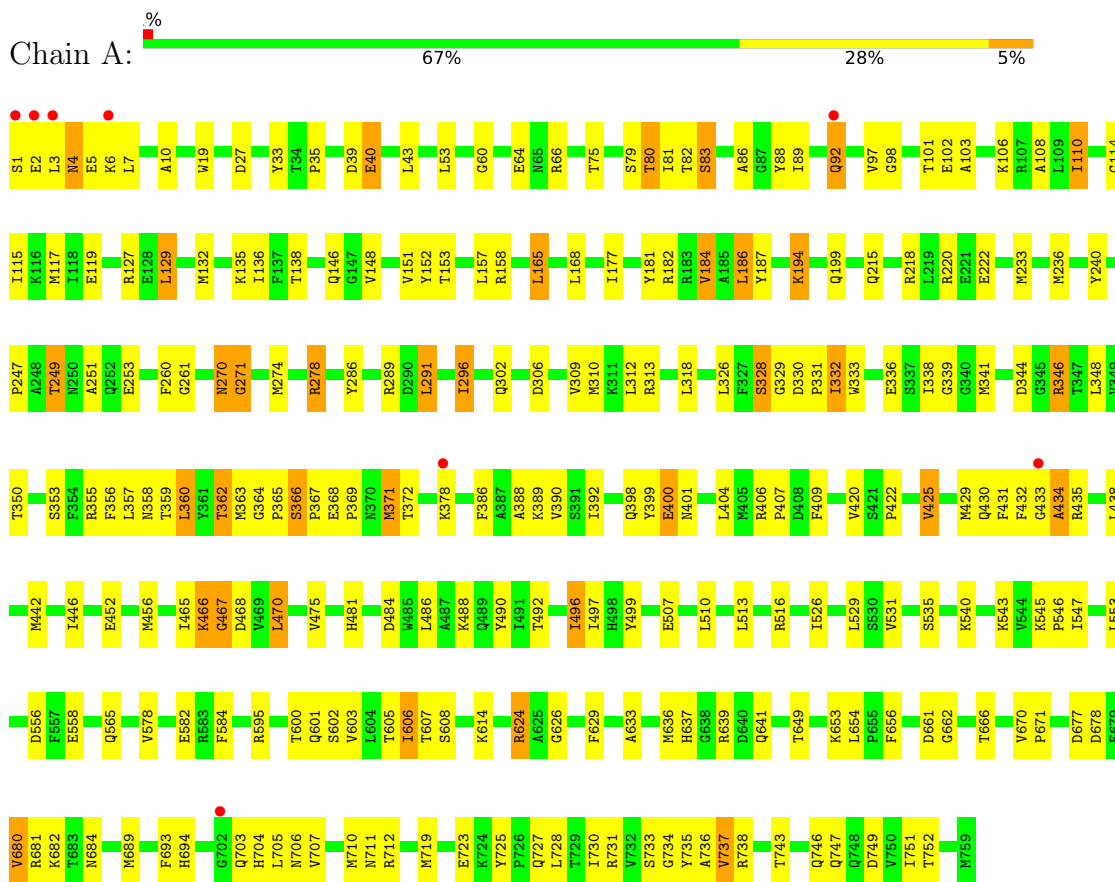
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	294	Total 294	O 294	0	0
3	B	233	Total 233	O 233	0	0

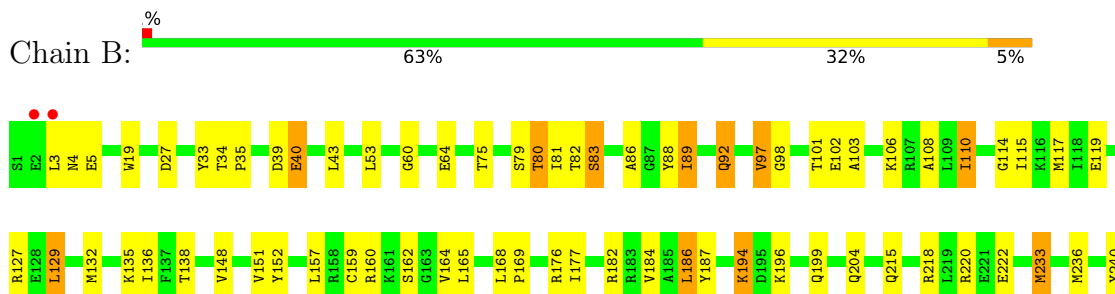
3 Residue-property plots [i](#)

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: PROTEIN (FORMATE ACETYLTRANSFERASE 1)



• Molecule 1: PROTEIN (FORMATE ACETYLTRANSFERASE 1)



I730	A627	S535	L438	F354	T249
R731	P628	L536	A439	R355	I250
V732	F629	K540	T440	F356	A251
S733			T441	L357	Q252
G734	A633	K543	M442	N358	E253
Y735		V544		T359	
A736	H637	K545	A445	L360	
V737	K642	P546	D451	Y361	F260
R738	I547	R548	E452	T362	G261
T743	T649	D549	K453	N363	K267
		E550	L454	P365	
Q746	K653	D551	G467	S366	N270
Q747	L654	G552	D469	P367	G271
Q748	P655	L553	V469	E368	
D749	F656		L470	P369	R278
V750	D661	D556	N471	N370	Y286
I751	G662	F557	Y472	M371	
T752		E558	D473	T372	L291
N759	T666	I559		K378	
	I669	G561	M476	F386	K295
	V670		E477	I296	
			R478	A387	
		Q565	N479	A388	Q302
	D677	F566		K389	D306
	D678	G567	F482	V390	
	E679	N568	M483	S391	V309
	V680	N569		T392	M310
	R681	D570	L486	D393	K311
	K682	P571	A487	T394	L312
	T683	R572	K488	S395	R313
	N684	V573	Q489		
		D574	Y490	Q398	L318
	M689	D575	I491	Y399	
			T492	E400	E322
	F693	V578		M401	
	H694		I496	L404	L326
		E582	I497	M405	F327
	Q703	R583	H498	R406	S328
	H704	F584	Y499	P407	Q329
	L705			D408	D330
	N706	R595	E507	P409	P331
	V707				I332
	N708	T600	L510	V420	W333
	V709	Q601		S421	
	M710	S602	L513	P422	E336
	N711	V603	R516	V425	M341
	R712	L604			D344
	E713	T605	R520	M429	G345
		I606	C524	Q430	R346
	M719	T607	I526	F431	T347
		S608		G433	L348
	E723	K614		A434	V349
	K724	G525		R435	T350
	Y725		L529	A436	S353
	T726	R623	S530		
	Q727	R624	V531		
	L728	A625			
	T729	G626			

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	159.21Å 159.21Å 160.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.1 (50.00-2.60) 96.1 (50.00-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.61Å)	Xtriage
Refinement program	CNS CNS 0.5	Depositor
R, R_{free}	0.212 , 0.251 0.212 , 0.250	Depositor DCC
R_{free} test set	2927 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k 0.005 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12515	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% 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: OXM

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	0.49	0/6109	0.92	17/8253 (0.2%)
1	B	0.50	1/6109 (0.0%)	0.93	15/8253 (0.2%)
All	All	0.50	1/12218 (0.0%)	0.93	32/16506 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	233	MET	SD-CE	-5.17	1.66	1.79

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ILE	N-CA-C	-10.58	102.71	111.81
1	B	89	ILE	N-CA-C	-10.10	103.12	111.81
1	A	468	ASP	N-CA-C	-6.68	105.16	113.38
1	A	2	GLU	N-CA-C	-6.16	106.44	112.97
1	A	366	SER	CA-C-N	6.12	125.68	119.19

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	5988	0	5914	225	0
1	B	5988	0	5914	252	0
2	A	6	0	2	0	0
2	B	6	0	2	0	0
3	A	294	0	0	13	0
3	B	233	0	0	14	0
All	All	12515	0	11832	474	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 20.

The worst 5 of 474 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:332:ILE:HB	3:B:951:HOH:O	1.45	1.12
1:A:602:SER:HB3	1:A:661:ASP:HB3	1.40	1.03
1:B:602:SER:HB3	1:B:661:ASP:HB3	1.43	0.97
1:B:362:THR:HG23	1:B:363:MET:HG3	1.47	0.97
1:A:614:LYS:HA	1:A:626:GLY:HA2	1.47	0.96

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	757/759 (100%)	706 (93%)	44 (6%)	7 (1%)	14	30
1	B	757/759 (100%)	703 (93%)	46 (6%)	8 (1%)	11	25
All	All	1514/1518 (100%)	1409 (93%)	90 (6%)	15 (1%)	12	28

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	434	ALA
1	B	434	ALA
1	B	550	GLU
1	A	271	GLY
1	A	467	GLY

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	638/638 (100%)	597 (94%)	41 (6%)	16	35
1	B	638/638 (100%)	597 (94%)	41 (6%)	16	35
All	All	1276/1276 (100%)	1194 (94%)	82 (6%)	16	35

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	318	LEU
1	B	479	MET
1	B	332	ILE
1	B	371	MET
1	B	529	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	92	GLN
1	B	358	ASN
1	B	711	ASN
1	B	270	ASN
1	B	430	GLN

5.3.3 RNA ⓘ

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](#)

2 ligands are modelled in this entry.

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	$\# Z > 2$
2	OXM	A	761	-	5,5,5	3.17	1 (20%)	2,6,6	1.17	0
2	OXM	B	762	-	5,5,5	3.36	2 (40%)	2,6,6	1.29	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
2	OXM	A	761	-	-	4/4/4/4	-
2	OXM	B	762	-	-	1/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	762	OXM	C1-C2	-7.07	1.47	1.55
2	A	761	OXM	C1-C2	-6.77	1.47	1.55
2	B	762	OXM	O3-C2	-2.27	1.24	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	761	OXM	N1-C1-C2-O2
2	A	761	OXM	N1-C1-C2-O3
2	A	761	OXM	O1-C1-C2-O2
2	A	761	OXM	O1-C1-C2-O3
2	B	762	OXM	O1-C1-C2-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	759/759 (100%)	-0.05	8 (1%) 78 74	27, 45, 65, 100	0
1	B	759/759 (100%)	0.09	6 (0%) 82 80	30, 48, 73, 96	0
All	All	1518/1518 (100%)	0.02	14 (0%) 81 78	27, 47, 70, 100	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	GLU	5.0
1	A	3	LEU	3.6
1	A	1	SER	3.4
1	A	378	LYS	2.7
1	B	270	ASN	2.7

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
2	OXM	A	761	6/6	0.94	0.08	41,43,44,45	0
2	OXM	B	762	6/6	0.96	0.07	42,43,44,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.