



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:32 PM UTC

PDB ID : 6EBA / pdb\_00006eba  
Title : Crystal Structure of A Bacterial Homolog to Human Lysosomal Transporter, Spinster, in Inward-facing And Unoccupied Conformation  
Authors : Zhou, F.; Yao, D.; Rao, B.; Zhang, L.; Cao, Y.  
Deposited on : 2018-08-06  
Resolution : 3.81 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

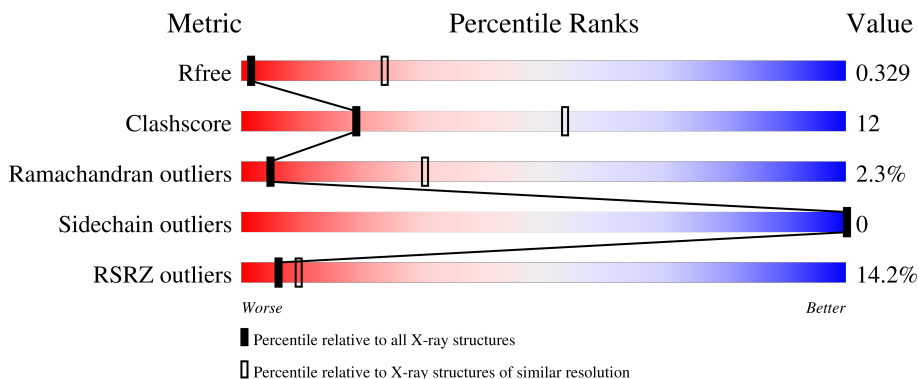
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.81 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	1043 (3.98-3.66)
Clashscore	190562	1075 (3.98-3.66)
Ramachandran outliers	187476	1029 (3.98-3.66)
Sidechain outliers	187428	1024 (3.98-3.66)
RSRZ outliers	180081	1042 (3.98-3.66)

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	508	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3628 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 Major facilitator family transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	479	3628	2412	582	614	20	0	0	0

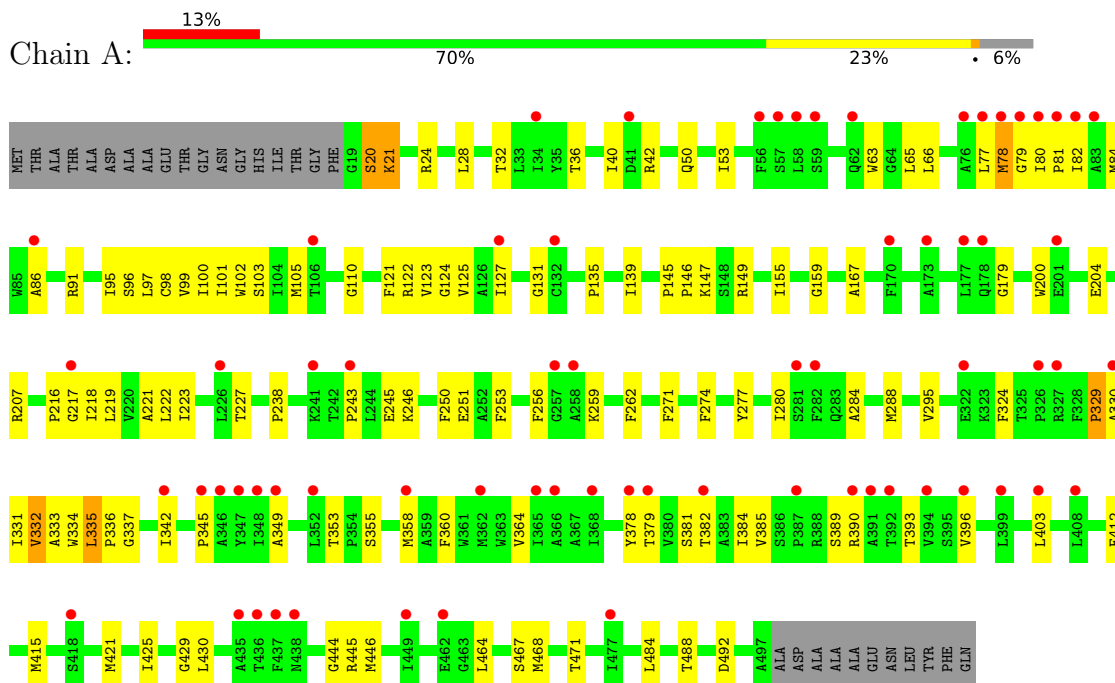
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	500	ALA	-	expression tag	UNP Q0C3L7
A	501	ALA	-	expression tag	UNP Q0C3L7
A	502	ALA	-	expression tag	UNP Q0C3L7
A	503	GLU	-	expression tag	UNP Q0C3L7
A	504	ASN	-	expression tag	UNP Q0C3L7
A	505	LEU	-	expression tag	UNP Q0C3L7
A	506	TYR	-	expression tag	UNP Q0C3L7
A	507	PHE	-	expression tag	UNP Q0C3L7
A	508	GLN	-	expression tag	UNP Q0C3L7

### 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: Major facilitator family transporter



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.63Å 98.49Å 125.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.24 – 3.81 49.24 – 3.81	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.24-3.81) 84.3 (49.24-3.81)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.57 (at 3.77Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.315 , 0.326 0.320 , 0.329	Depositor DCC
$R_{free}$ test set	1107 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	144.1	Xtrriage
Anisotropy	0.509	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 145.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.78	EDS
Total number of atoms	3628	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	189.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.09% 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	0.18	0/3735	0.42	0/5095

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 [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	3628	0	3688	86	0
All	All	3628	0	3688	86	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 12.

All (86) 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:A:100:ILE:HG13	1:A:218:ILE:HD12	1.59	0.84
1:A:332:VAL:HG21	1:A:337:GLY:HA2	1.63	0.81
1:A:20:SER:O	1:A:24:ARG:NH1	2.22	0.72
1:A:86:ALA:O	1:A:91:ARG:NH2	2.23	0.70
1:A:467:SER:O	1:A:471:THR:HG23	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:VAL:HG11	1:A:393:THR:HG21	1.77	0.67
1:A:99:VAL:HB	1:A:221:ALA:HB2	1.77	0.66
1:A:421:MET:O	1:A:425:ILE:HG12	1.95	0.66
1:A:349:ALA:O	1:A:353:THR:OG1	2.14	0.66
1:A:379:THR:O	1:A:382:THR:HG22	1.97	0.64
1:A:146:PRO:HA	1:A:149:ARG:HG3	1.79	0.64
1:A:95:ILE:HD11	1:A:135:PRO:HB2	1.79	0.63
1:A:464:LEU:O	1:A:468:MET:HG2	1.99	0.62
1:A:78:MET:O	1:A:82:ILE:HG13	2.01	0.60
1:A:100:ILE:HG22	1:A:101:ILE:HD12	1.84	0.59
1:A:288:MET:HE1	1:A:295:VAL:HG22	1.85	0.58
1:A:259:LYS:NZ	1:A:384:ILE:O	2.32	0.58
1:A:204:GLU:OE1	1:A:204:GLU:N	2.36	0.56
1:A:42:ARG:O	1:A:122:ARG:NH2	2.39	0.55
1:A:484:LEU:O	1:A:488:THR:HG22	2.06	0.55
1:A:77:LEU:O	1:A:79:GLY:N	2.39	0.55
1:A:425:ILE:HG23	1:A:430:LEU:HD12	1.89	0.54
1:A:412:PHE:CD1	1:A:471:THR:HG22	2.43	0.54
1:A:65:LEU:HD21	1:A:415:MET:HE3	1.89	0.53
1:A:20:SER:OG	1:A:21:LYS:N	2.40	0.53
1:A:425:ILE:O	1:A:429:GLY:N	2.40	0.53
1:A:219:LEU:HA	1:A:222:LEU:HD12	1.90	0.53
1:A:444:GLY:O	1:A:446:MET:N	2.41	0.53
1:A:105:MET:HE2	1:A:124:GLY:HA3	1.92	0.52
1:A:334:TRP:CE3	1:A:335:LEU:HG	2.45	0.52
1:A:382:THR:O	1:A:390:ARG:NH2	2.38	0.51
1:A:32:THR:HG21	1:A:155:ILE:HD12	1.91	0.51
1:A:335:LEU:H	1:A:336:PRO:HD2	1.75	0.51
1:A:91:ARG:O	1:A:95:ILE:HD12	2.11	0.51
1:A:145:PRO:HB2	1:A:147:LYS:HD2	1.93	0.51
1:A:82:ILE:HD13	1:A:131:GLY:HA2	1.92	0.50
1:A:147:LYS:HD2	1:A:147:LYS:H	1.76	0.50
1:A:91:ARG:HB2	1:A:139:ILE:HD11	1.94	0.50
1:A:223:ILE:O	1:A:227:THR:OG1	2.26	0.50
1:A:84:MET:SD	1:A:84:MET:N	2.85	0.49
1:A:253:PHE:HA	1:A:256:PHE:CE2	2.47	0.49
1:A:353:THR:HG22	1:A:355:SER:H	1.77	0.49
1:A:28:LEU:O	1:A:32:THR:HG23	2.13	0.48
1:A:412:PHE:HD1	1:A:471:THR:HG22	1.77	0.48
1:A:342:ILE:O	1:A:345:PRO:HD2	2.14	0.47
1:A:40:ILE:HA	1:A:167:ALA:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:MET:HE3	1:A:121:PHE:HA	1.95	0.47
1:A:179:GLY:O	1:A:200:TRP:HB3	2.15	0.47
1:A:335:LEU:H	1:A:336:PRO:CD	2.28	0.47
1:A:103:SER:OG	1:A:217:GLY:HA3	2.15	0.46
1:A:121:PHE:O	1:A:125:VAL:HG23	2.14	0.46
1:A:251:GLU:N	1:A:251:GLU:OE2	2.49	0.46
1:A:218:ILE:HG23	1:A:219:LEU:N	2.31	0.46
1:A:250:PHE:O	1:A:253:PHE:HB3	2.16	0.46
1:A:332:VAL:HG22	1:A:333:ALA:H	1.79	0.46
1:A:100:ILE:HG13	1:A:218:ILE:CD1	2.40	0.44
1:A:91:ARG:H	1:A:91:ARG:HG2	1.64	0.44
1:A:219:LEU:O	1:A:223:ILE:HG22	2.18	0.44
1:A:36:THR:HG22	1:A:159:GLY:HA2	1.99	0.44
1:A:358:MET:HE2	1:A:358:MET:HB2	1.84	0.44
1:A:123:VAL:O	1:A:127:ILE:HG12	2.17	0.43
1:A:389:SER:O	1:A:393:THR:HG23	2.18	0.43
1:A:284:ALA:O	1:A:288:MET:HG2	2.18	0.43
1:A:329:PRO:O	1:A:331:ILE:N	2.52	0.43
1:A:360:PHE:O	1:A:364:VAL:HG13	2.19	0.43
1:A:216:PRO:HA	1:A:219:LEU:HD21	2.01	0.43
1:A:262:PHE:HZ	1:A:396:VAL:HG23	1.84	0.42
1:A:271:PHE:HA	1:A:274:PHE:HB3	2.01	0.42
1:A:50:GLN:NE2	1:A:53:ILE:HD11	2.35	0.42
1:A:96:SER:HA	1:A:221:ALA:HB1	2.02	0.42
1:A:21:LYS:HD3	1:A:24:ARG:HH12	1.84	0.42
1:A:97:LEU:O	1:A:101:ILE:HD13	2.19	0.42
1:A:110:GLY:O	1:A:207:ARG:NH2	2.44	0.42
1:A:80:ILE:HB	1:A:81:PRO:HD3	2.01	0.42
1:A:99:VAL:HG22	1:A:102:TRP:CZ2	2.54	0.42
1:A:28:LEU:HG	1:A:155:ILE:HD11	2.02	0.42
1:A:243:PRO:C	1:A:245:GLU:H	2.27	0.42
1:A:384:ILE:HD11	1:A:492:ASP:HB3	2.02	0.41
1:A:277:TYR:HA	1:A:280:ILE:HG22	2.02	0.41
1:A:146:PRO:HG3	1:A:149:ARG:NH1	2.36	0.41
1:A:256:PHE:HB3	1:A:385:VAL:HG21	2.02	0.41
1:A:63:TRP:CZ3	1:A:66:LEU:HD23	2.56	0.40
1:A:95:ILE:O	1:A:99:VAL:HG23	2.21	0.40
1:A:98:CYS:O	1:A:102:TRP:CD1	2.75	0.40
1:A:378:TYR:O	1:A:381:SER:OG	2.39	0.40
1:A:403:LEU:HD23	1:A:403:LEU:HA	1.88	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	477/508 (94%)	430 (90%)	36 (8%)	11 (2%)	5 30

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	ALA
1	A	445	ARG
1	A	78	MET
1	A	332	VAL
1	A	20	SER
1	A	21	LYS
1	A	238	PRO
1	A	246	LYS
1	A	324	PHE
1	A	329	PRO
1	A	335	LEU

### 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	366/384 (95%)	366 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	377	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](#)

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	479/508 (94%)	0.71	68 (14%) <b>6</b>   <b>9</b>	143, 184, 241, 282	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	ALA	10.1
1	A	365	ILE	7.9
1	A	435	ALA	7.9
1	A	78	MET	6.0
1	A	349	ALA	5.9
1	A	436	THR	5.8
1	A	326	PRO	5.8
1	A	342	ILE	5.8
1	A	394	VAL	5.7
1	A	352	LEU	5.7
1	A	81	PRO	5.6
1	A	80	ILE	5.3
1	A	438	ASN	4.4
1	A	59	SER	4.3
1	A	83	ALA	4.3
1	A	62	GLN	4.2
1	A	390	ARG	4.2
1	A	77	LEU	4.0
1	A	362	MET	4.0
1	A	327	ARG	3.9
1	A	449	ILE	3.8
1	A	57	SER	3.8
1	A	392	THR	3.7
1	A	58	LEU	3.7
1	A	346	ALA	3.7
1	A	391	ALA	3.6
1	A	226	LEU	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	127	ILE	3.5
1	A	201	GLU	3.3
1	A	132	CYS	3.2
1	A	177	LEU	3.1
1	A	173	ALA	3.1
1	A	82	ILE	3.0
1	A	178	GLN	3.0
1	A	366	ALA	3.0
1	A	347	TYR	2.9
1	A	86	ALA	2.9
1	A	170	PHE	2.9
1	A	345	PRO	2.9
1	A	79	GLY	2.8
1	A	379	THR	2.8
1	A	217	GLY	2.7
1	A	358	MET	2.7
1	A	41	ASP	2.6
1	A	281	SER	2.6
1	A	418	SER	2.6
1	A	387	PRO	2.5
1	A	243	PRO	2.4
1	A	382	THR	2.4
1	A	34	ILE	2.4
1	A	257	GLY	2.4
1	A	282	PHE	2.3
1	A	408	LEU	2.3
1	A	348	ILE	2.3
1	A	477	ILE	2.3
1	A	322	GLU	2.3
1	A	106	THR	2.2
1	A	241	LYS	2.2
1	A	378	TYR	2.2
1	A	462	GLU	2.2
1	A	399	LEU	2.2
1	A	396	VAL	2.1
1	A	403	LEU	2.1
1	A	330	ALA	2.1
1	A	368	ILE	2.1
1	A	437	PHE	2.1
1	A	258	ALA	2.0
1	A	56	PHE	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.