



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2026 – 06:08 PM JST

PDB ID : 9VAI / pdb\_00009vai  
Title : Crystal structure of the PDZ tandem of syntenin  
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Deposited on : 2025-06-03  
Resolution : 1.86 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
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

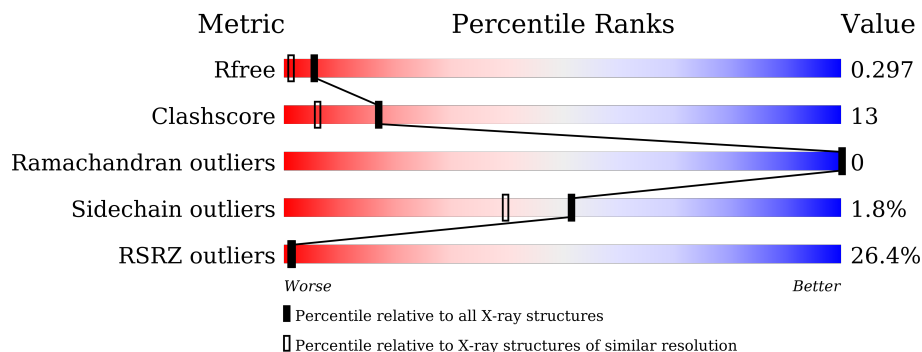
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.86 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	166	<div> <div>19%</div> <div> <div></div> <div>73%</div> <div>25%</div> <div></div> </div> </div>
1	B	166	<div> <div>33%</div> <div> <div></div> <div>68%</div> <div>31%</div> <div></div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2565 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 Syntenin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	164	Total	C	N	O	S	0	0	0
			1248	783	223	236	6			
1	B	166	Total	C	N	O	S	0	0	0
			1270	797	225	242	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	TYR	PHE	engineered mutation	UNP O00560
B	275	TYR	PHE	engineered mutation	UNP O00560

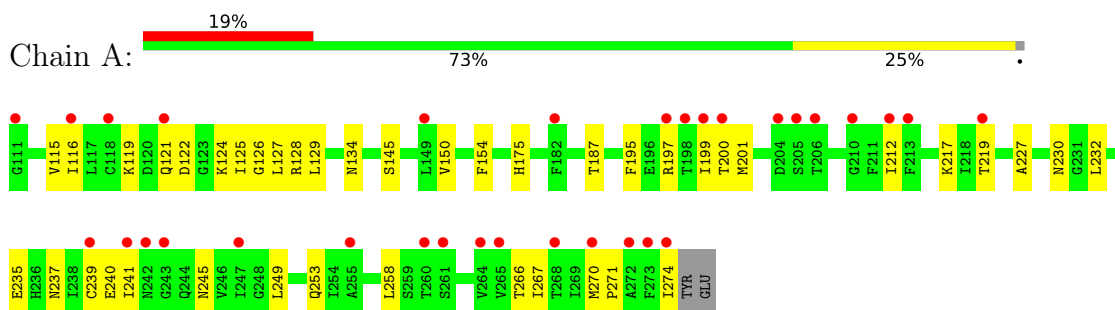
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	25	Total	O	0	0
			25	25		
2	B	22	Total	O	0	0
			22	22		

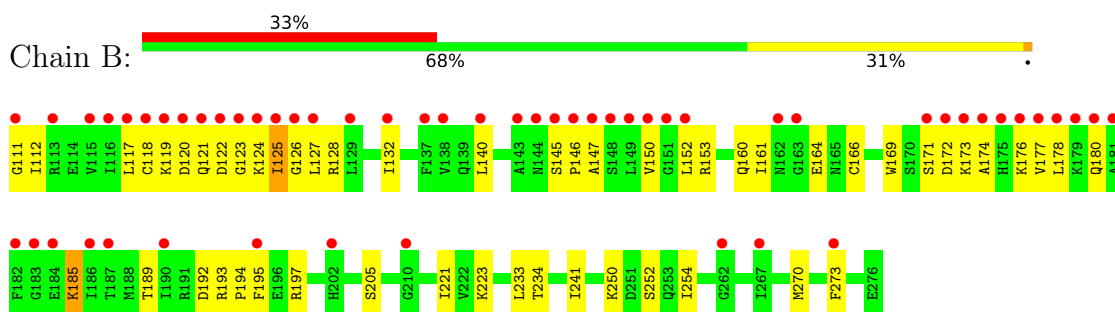
### 3 Residue-property plots [i](#)

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: Syntenin-1



#### • Molecule 1: Syntenin-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.90Å 56.90Å 151.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.87 – 1.86 46.87 – 1.86	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.87-1.86) 96.8 (46.87-1.86)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 1.86Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.249 , 0.297 0.249 , 0.297	Depositor DCC
$R_{free}$ test set	1243 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.2	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 41.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.056 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2565	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% 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

### 5.1 Standard geometry

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	0.38	0/1263	0.59	0/1700
1	B	0.40	0/1286	0.59	0/1730
All	All	0.39	0/2549	0.59	0/3430

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	1248	0	1285	30	0
1	B	1270	0	1300	37	0
2	A	25	0	0	0	0
2	B	22	0	0	0	0
All	All	2565	0	2585	65	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 13.

All (65) 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:193:ARG:HD2	1:B:270:MET:HE1	1.34	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LYS:HE3	1:A:235:GLU:HA	1.51	0.90
1:B:177:VAL:HA	1:B:180:GLN:HG2	1.60	0.81
1:B:153:ARG:HE	1:B:193:ARG:HG3	1.50	0.74
1:A:154:PHE:HZ	1:A:274:ILE:HG22	1.55	0.72
1:B:132:ILE:HD13	1:B:273:PHE:HD2	1.55	0.71
1:B:128:ARG:HB3	1:B:140:LEU:HB3	1.73	0.70
1:A:154:PHE:CZ	1:A:274:ILE:HG22	2.28	0.69
1:A:212:ILE:HG22	1:A:219:THR:OG1	1.93	0.68
1:B:160:GLN:HB2	1:B:189:THR:HB	1.75	0.67
1:A:121:GLN:HG2	1:A:122:ASP:OD2	1.94	0.66
1:A:115:VAL:O	1:A:116:ILE:HD13	1.97	0.64
1:B:145:SER:OG	1:B:146:PRO:HD2	1.98	0.64
1:B:117:LEU:HD23	1:B:125:ILE:HG22	1.80	0.63
1:A:115:VAL:HB	1:A:150:VAL:HG21	1.84	0.59
1:B:147:ALA:HA	1:B:150:VAL:HG22	1.86	0.57
1:A:241:ILE:HD13	1:A:258:LEU:HG	1.87	0.57
1:B:132:ILE:HD13	1:B:273:PHE:CD2	2.39	0.57
1:B:197:ARG:HH22	1:B:233:LEU:HD12	1.69	0.56
1:B:193:ARG:HD2	1:B:270:MET:CE	2.23	0.56
1:A:240:GLU:HG2	1:A:245:ASN:HA	1.88	0.55
1:B:121:GLN:OE1	1:B:122:ASP:OD1	2.25	0.55
1:A:199:ILE:HD11	1:A:230:ASN:HB3	1.89	0.55
1:B:118:CYS:HA	1:B:185:LYS:HD2	1.90	0.54
1:B:161:ILE:HD12	1:B:169:TRP:HZ3	1.73	0.54
1:A:115:VAL:HB	1:A:150:VAL:CG2	2.38	0.53
1:A:127:LEU:O	1:A:128:ARG:HD3	2.07	0.53
1:B:127:LEU:HD21	1:B:152:LEU:CD2	2.39	0.53
1:B:120:ASP:HB3	1:B:123:GLY:O	2.09	0.52
1:B:174:ALA:O	1:B:178:LEU:HD23	2.10	0.52
1:A:115:VAL:C	1:A:116:ILE:HD13	2.36	0.51
1:A:197:ARG:HD2	1:B:194:PRO:O	2.11	0.51
1:A:116:ILE:HD12	1:A:187:THR:HG22	1.95	0.48
1:B:127:LEU:HD21	1:B:152:LEU:HD23	1.95	0.48
1:B:125:ILE:HD12	1:B:126:GLY:H	1.79	0.48
1:B:172:ASP:O	1:B:176:LYS:HG2	2.14	0.48
1:A:239:CYS:SG	1:A:270:MET:HG2	2.55	0.47
1:B:146:PRO:O	1:B:150:VAL:HG13	2.15	0.46
1:A:121:GLN:H	1:A:121:GLN:CD	2.23	0.46
1:B:119:LYS:HD3	1:B:124:LYS:HD2	1.98	0.46
1:B:192:ASP:O	1:B:193:ARG:C	2.58	0.46
1:B:161:ILE:HG13	1:B:166:CYS:SG	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:MET:HE3	1:B:270:MET:HB2	1.87	0.45
1:B:120:ASP:H	1:B:124:LYS:HD3	1.81	0.44
1:A:126:GLY:HA3	1:A:145:SER:HB2	1.99	0.44
1:A:134:ASN:HD21	1:B:223:LYS:NZ	2.16	0.44
1:A:249:LEU:HD22	1:A:253:GLN:NE2	2.32	0.44
1:B:250:LYS:HE3	1:B:252:SER:OG	2.17	0.44
1:A:195:PHE:HB3	1:A:271:PRO:HD2	1.99	0.44
1:B:173:LYS:O	1:B:177:VAL:HG23	2.18	0.43
1:B:111:GLY:O	1:B:112:ILE:HD13	2.19	0.42
1:A:201:MET:SD	1:A:227:ALA:HA	2.60	0.42
1:A:237:ASN:OD1	1:A:274:ILE:HD13	2.20	0.42
1:A:128:ARG:HA	1:A:175:HIS:CE1	2.55	0.42
1:B:150:VAL:HG23	1:B:152:LEU:HD13	2.02	0.42
1:B:111:GLY:C	1:B:112:ILE:HD13	2.45	0.41
1:A:127:LEU:HD13	1:A:129:LEU:HD21	2.01	0.41
1:A:119:LYS:HG2	1:A:125:ILE:HG22	2.03	0.41
1:A:124:LYS:NZ	1:A:128:ARG:NH2	2.68	0.41
1:A:199:ILE:HG21	1:A:232:LEU:HD13	2.02	0.41
1:A:258:LEU:HD21	1:A:267:ILE:HD11	2.02	0.41
1:B:195:PHE:HD2	1:B:273:PHE:CZ	2.39	0.41
1:B:241:ILE:HD11	1:B:254:ILE:HG23	2.02	0.41
1:A:200:THR:OG1	1:A:266:THR:HG22	2.21	0.40
1:B:221:ILE:CD1	1:B:234:THR:HG23	2.52	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	162/166 (98%)	159 (98%)	3 (2%)	0	100	100
1	B	164/166 (99%)	158 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	326/332 (98%)	317 (97%)	9 (3%)	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	139/141 (99%)	139 (100%)	0	100	100
1	B	141/141 (100%)	136 (96%)	5 (4%)	32	16
All	All	280/282 (99%)	275 (98%)	5 (2%)	51	40

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	125	ILE
1	B	164	GLU
1	B	171	SER
1	B	185	LYS
1	B	205	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	134	ASN
1	A	139	GLN
1	A	202	HIS
1	A	215	ASN
1	A	245	ASN
1	B	139	GLN
1	B	165	ASN
1	B	244	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	164/166 (98%)	1.27	32 (19%) 3 2	21, 42, 58, 65	0
1	B	166/166 (100%)	1.80	55 (33%) 1 1	24, 43, 81, 91	0
All	All	330/332 (99%)	1.54	87 (26%) 1 1	21, 42, 72, 91	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	178	LEU	6.9
1	B	117	LEU	6.5
1	B	182	PHE	5.9
1	B	123	GLY	5.7
1	B	181	ALA	5.5
1	B	125	ILE	5.4
1	B	115	VAL	4.6
1	B	150	VAL	4.5
1	A	264	VAL	4.4
1	B	171	SER	4.4
1	B	172	ASP	4.3
1	B	186	ILE	4.0
1	B	151	GLY	4.0
1	B	147	ALA	3.8
1	B	118	CYS	3.7
1	B	120	ASP	3.7
1	B	174	ALA	3.7
1	B	146	PRO	3.6
1	A	199	ILE	3.6
1	B	122	ASP	3.4
1	B	149	LEU	3.4
1	B	176	LYS	3.3
1	A	212	ILE	3.3
1	B	124	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	152	LEU	3.2
1	B	180	GLN	3.1
1	B	116	ILE	3.1
1	B	175	HIS	3.1
1	B	111	GLY	3.1
1	B	195	PHE	3.1
1	A	274	ILE	3.0
1	A	149	LEU	3.0
1	A	273	PHE	3.0
1	B	184	GLU	2.9
1	B	127	LEU	2.9
1	A	243	GLY	2.9
1	B	145	SER	2.9
1	A	260	THR	2.8
1	A	255	ALA	2.8
1	A	121	GLN	2.8
1	A	219	THR	2.8
1	A	265	VAL	2.8
1	A	111	GLY	2.8
1	B	183	GLY	2.8
1	B	121	GLN	2.7
1	B	132	ILE	2.7
1	B	190	ILE	2.7
1	A	247	ILE	2.7
1	B	179	LYS	2.6
1	B	140	LEU	2.6
1	B	163	GLY	2.6
1	A	198	THR	2.6
1	B	273	PHE	2.6
1	A	118	CYS	2.5
1	A	213	PHE	2.5
1	B	144	ASN	2.5
1	A	116	ILE	2.5
1	A	205	SER	2.5
1	B	143	ALA	2.5
1	B	162	ASN	2.4
1	B	202	HIS	2.4
1	B	126	GLY	2.4
1	B	210	GLY	2.3
1	A	239	CYS	2.3
1	B	138	VAL	2.3
1	B	173	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	272	ALA	2.3
1	B	148	SER	2.3
1	B	129	LEU	2.3
1	A	182	PHE	2.2
1	A	241	ILE	2.2
1	A	270	MET	2.2
1	B	119	LYS	2.2
1	B	177	VAL	2.2
1	A	268	THR	2.2
1	B	187	THR	2.2
1	B	267	ILE	2.2
1	A	200	THR	2.2
1	A	206	THR	2.1
1	A	204	ASP	2.1
1	A	197	ARG	2.1
1	B	262	GLY	2.1
1	B	137	PHE	2.0
1	A	261	SER	2.0
1	A	210	GLY	2.0
1	A	242	ASN	2.0
1	B	113	ARG	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.