



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:37 PM EST

PDB ID : 5TEB  
Title : Crystal Structure of the TIR domain from the Arabidopsis Thaliana disease resistance protein RPP1  
Authors : Bentham, A.R.; Zhang, X.; Croll, T.; Williams, S.; Kobe, B.  
Deposited on : 2016-09-20  
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

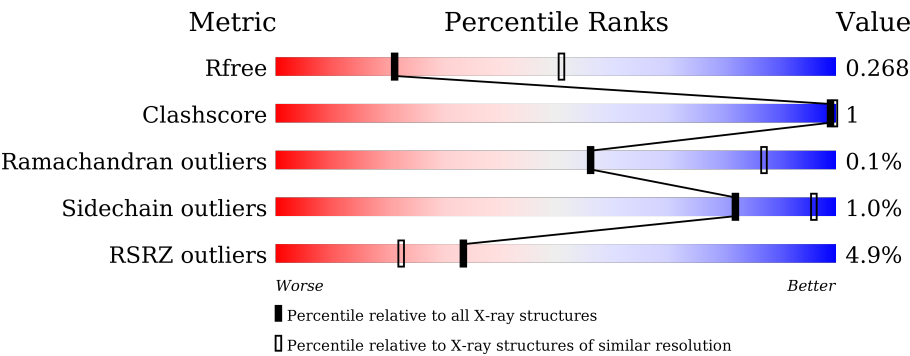
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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  $\geq 3$ , 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	168	<div><div>4%</div><div>95%</div><div>..</div></div>
1	B	168	<div><div>7%</div><div>97%</div><div>..</div></div>
1	C	168	<div><div>7%</div><div>97%</div><div>...</div></div>
1	D	168	<div><div>4%</div><div>95%</div><div>..</div></div>
1	E	168	<div><div>3%</div><div>97%</div><div>...</div></div>
1	F	168	<div><div>2%</div><div>97%</div><div>...</div></div>

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Mol	Chain	Length	Quality of chain
1	G	168	<div><div></div><div>7%</div><div>92%</div><div>5%</div></div>
1	H	168	<div><div></div><div>4%</div><div>92%</div><div>5%</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10533 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 Recognition of Peronospora parasitica 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	B	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	C	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	D	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	E	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	F	166	Total	C	N	O	S	0	0	0
			1331	843	231	249	8			
1	G	159	Total	C	N	O	S	0	0	0
			1271	804	218	241	8			
1	H	160	Total	C	N	O	S	0	0	0
			1276	807	219	242	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	87	SER	-	expression tag	UNP D9IW02
A	88	ASN	-	expression tag	UNP D9IW02
A	89	ALA	-	expression tag	UNP D9IW02
B	87	SER	-	expression tag	UNP D9IW02
B	88	ASN	-	expression tag	UNP D9IW02
B	89	ALA	-	expression tag	UNP D9IW02
C	87	SER	-	expression tag	UNP D9IW02
C	88	ASN	-	expression tag	UNP D9IW02
C	89	ALA	-	expression tag	UNP D9IW02
D	87	SER	-	expression tag	UNP D9IW02
D	88	ASN	-	expression tag	UNP D9IW02
D	89	ALA	-	expression tag	UNP D9IW02
E	87	SER	-	expression tag	UNP D9IW02

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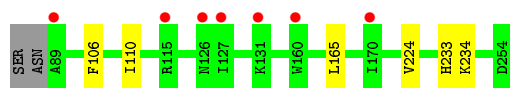
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Chain	Residue	Modelled	Actual	Comment	Reference
E	88	ASN	-	expression tag	UNP D9IW02
E	89	ALA	-	expression tag	UNP D9IW02
F	87	SER	-	expression tag	UNP D9IW02
F	88	ASN	-	expression tag	UNP D9IW02
F	89	ALA	-	expression tag	UNP D9IW02
G	87	SER	-	expression tag	UNP D9IW02
G	88	ASN	-	expression tag	UNP D9IW02
G	89	ALA	-	expression tag	UNP D9IW02
H	87	SER	-	expression tag	UNP D9IW02
H	88	ASN	-	expression tag	UNP D9IW02
H	89	ALA	-	expression tag	UNP D9IW02

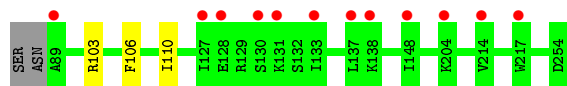
### 3 Residue-property plots [i](#)

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.

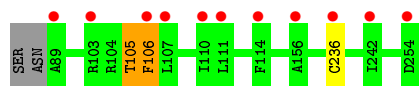
- Molecule 1: Recognition of *Peronospora parasitica* 1



- Molecule 1: Recognition of *Peronospora parasitica* 1



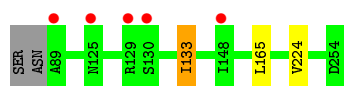
- Molecule 1: Recognition of *Peronospora parasitica* 1



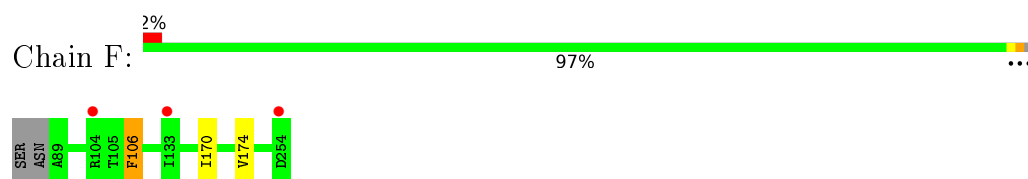
- Molecule 1: Recognition of *Peronospora parasitica* 1



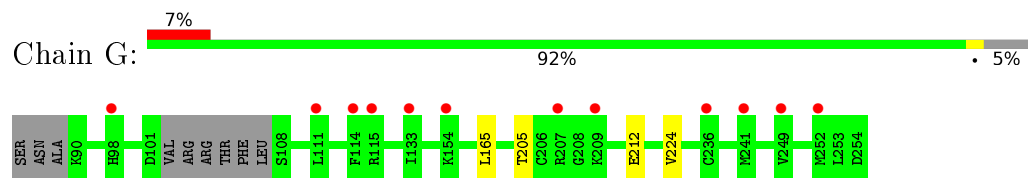
- Molecule 1: Recognition of *Peronospora parasitica* 1



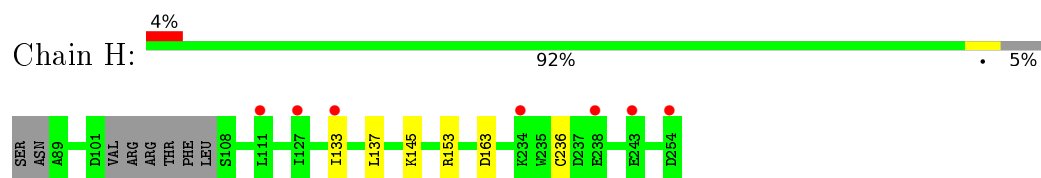
- Molecule 1: Recognition of *Peronospora parasitica* 1



- Molecule 1: Recognition of *Peronospora parasitica* 1



- Molecule 1: Recognition of *Peronospora parasitica* 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.89Å 84.33Å 122.75Å 90.00° 90.10° 90.00°	Depositor
Resolution (Å)	40.95 – 2.80 42.47 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.95-2.80) 99.3 (42.47-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.81Å)	Xtriage
Refinement program	PHENIX (1.11rc2_2531: ???)	Depositor
R, $R_{free}$	0.218 , 0.269 0.217 , 0.268	Depositor DCC
$R_{free}$ test set	1979 reflections (4.78%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.8	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l 0.000 for k,h,-l 0.125 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10533	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.10 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3845e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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	0.36	0/1356	0.58	0/1821
1	B	0.34	0/1356	0.56	0/1821
1	C	0.32	0/1356	0.55	0/1821
1	D	0.37	0/1356	0.62	0/1821
1	E	0.37	0/1356	0.62	0/1821
1	F	0.35	0/1356	0.55	0/1821
1	G	0.33	0/1294	0.53	0/1736
1	H	0.31	0/1299	0.53	0/1743
All	All	0.34	0/10729	0.57	0/14405

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	1331	0	1337	3	0
1	B	1331	0	1337	1	0
1	C	1331	0	1337	1	0
1	D	1331	0	1337	2	1
1	E	1331	0	1337	2	0
1	F	1331	0	1337	2	0
1	G	1271	0	1269	1	0
1	H	1276	0	1274	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10533	0	10565	14	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 1.

All (14) 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:165:LEU:HD11	1:D:224:VAL:HG11	1.70	0.74
1:A:165:LEU:HD11	1:A:224:VAL:HG21	1.70	0.72
1:G:165:LEU:HD11	1:G:224:VAL:HG21	1.73	0.69
1:E:165:LEU:HD11	1:E:224:VAL:HG11	1.79	0.64
1:B:106:PHE:CE2	1:B:110:ILE:HD11	2.46	0.51
1:F:170:ILE:O	1:F:174:VAL:HG22	2.13	0.48
1:H:133:ILE:CG1	1:H:163:ASP:HB3	2.43	0.48
1:H:133:ILE:HG23	1:H:137:LEU:HD23	1.97	0.47
1:C:105:THR:HG22	1:C:106:PHE:H	1.80	0.45
1:F:106:PHE:CD1	1:F:106:PHE:N	2.86	0.43
1:A:233:HIS:CD2	1:A:234:LYS:HG3	2.53	0.43
1:D:241:MET:O	1:D:245:ILE:HG12	2.19	0.43
1:A:106:PHE:CZ	1:A:110:ILE:HD11	2.55	0.42
1:E:133:ILE:O	1:E:133:ILE:HG13	2.20	0.42

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)
1:D:118:GLY:O	1:D:207:ARG:NE[2_545]	2.16	0.04

## 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	164/168 (98%)	156 (95%)	8 (5%)	0	100	100
1	B	164/168 (98%)	156 (95%)	8 (5%)	0	100	100
1	C	164/168 (98%)	159 (97%)	5 (3%)	0	100	100
1	D	164/168 (98%)	158 (96%)	6 (4%)	0	100	100
1	E	164/168 (98%)	157 (96%)	6 (4%)	1 (1%)	30	65
1	F	164/168 (98%)	160 (98%)	4 (2%)	0	100	100
1	G	155/168 (92%)	147 (95%)	8 (5%)	0	100	100
1	H	156/168 (93%)	152 (97%)	4 (3%)	0	100	100
All	All	1295/1344 (96%)	1245 (96%)	49 (4%)	1 (0%)	56	87

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	133	ILE

### 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	146/148 (99%)	146 (100%)	0	100	100
1	B	146/148 (99%)	145 (99%)	1 (1%)	88	97
1	C	146/148 (99%)	143 (98%)	3 (2%)	61	90
1	D	146/148 (99%)	145 (99%)	1 (1%)	88	97
1	E	146/148 (99%)	146 (100%)	0	100	100
1	F	146/148 (99%)	145 (99%)	1 (1%)	88	97
1	G	140/148 (95%)	138 (99%)	2 (1%)	74	94
1	H	140/148 (95%)	137 (98%)	3 (2%)	61	90
All	All	1156/1184 (98%)	1145 (99%)	11 (1%)	82	96

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	103	ARG
1	C	105	THR
1	C	106	PHE
1	C	236	CYS
1	D	218	ARG
1	F	106	PHE
1	G	205	THR
1	G	212	GLU
1	H	145	LYS
1	H	153	ARG
1	H	236	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates 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	166/168 (98%)	0.30	7 (4%) 40 28	37, 65, 135, 220	0
1	B	166/168 (98%)	0.52	12 (7%) 18 10	42, 79, 149, 208	0
1	C	166/168 (98%)	0.33	11 (6%) 22 13	39, 76, 137, 169	0
1	D	166/168 (98%)	0.42	7 (4%) 40 28	34, 68, 133, 205	0
1	E	166/168 (98%)	0.28	5 (3%) 54 41	37, 62, 106, 236	0
1	F	166/168 (98%)	0.20	3 (1%) 71 61	35, 64, 98, 138	0
1	G	159/168 (94%)	0.51	12 (7%) 17 9	42, 87, 136, 217	0
1	H	160/168 (95%)	0.44	7 (4%) 38 26	54, 89, 143, 174	0
All	All	1315/1344 (97%)	0.37	64 (4%) 33 22	34, 72, 137, 236	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	127	ILE	15.8
1	E	130	SER	13.2
1	B	127	ILE	9.4
1	G	209	LYS	8.4
1	D	89	ALA	8.0
1	B	128	GLU	7.4
1	D	127	ILE	7.4
1	D	128	GLU	7.3
1	E	89	ALA	6.6
1	C	89	ALA	5.9
1	B	89	ALA	4.8
1	C	254	ASP	4.5
1	A	126	ASN	4.0
1	G	115	ARG	4.0
1	B	131	LYS	3.9
1	F	254	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	126	ASN	3.8
1	H	127	ILE	3.8
1	E	125	ASN	3.8
1	H	254	ASP	3.7
1	H	111	LEU	3.7
1	G	111	LEU	3.7
1	A	160	TRP	3.4
1	C	106	PHE	3.4
1	B	133	ILE	3.3
1	D	129	ARG	3.3
1	F	133	ILE	3.3
1	G	133	ILE	3.2
1	G	236	CYS	3.1
1	G	98	HIS	3.0
1	A	89	ALA	2.9
1	G	249	VAL	2.9
1	D	131	LYS	2.9
1	E	129	ARG	2.9
1	C	156	ALA	2.9
1	F	104	ARG	2.8
1	C	103	ARG	2.7
1	A	131	LYS	2.6
1	G	154	LYS	2.5
1	A	170	ILE	2.4
1	B	137	LEU	2.4
1	G	207	ARG	2.4
1	G	252	MET	2.3
1	H	133	ILE	2.3
1	H	243	GLU	2.2
1	C	110	ILE	2.2
1	A	115	ARG	2.2
1	E	148	ILE	2.2
1	B	217	TRP	2.2
1	B	204	LYS	2.2
1	B	130	SER	2.2
1	C	111	LEU	2.2
1	H	234	LYS	2.2
1	C	114	PHE	2.2
1	B	214	VAL	2.1
1	C	242	ILE	2.1
1	B	148	ILE	2.1
1	C	107	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	236	CYS	2.1
1	G	114	PHE	2.0
1	G	241	MET	2.0
1	D	119	ILE	2.0
1	H	238	GLU	2.0
1	B	138	LYS	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.