



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:45 PM GMT

PDB ID : 3RST  
Title : Crystal structure of Bacillus subtilis signal peptide peptidase A  
Authors : Nam, S.E.; Paetzel, M.  
Deposited on : 2011-05-02  
Resolution : 2.37 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](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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

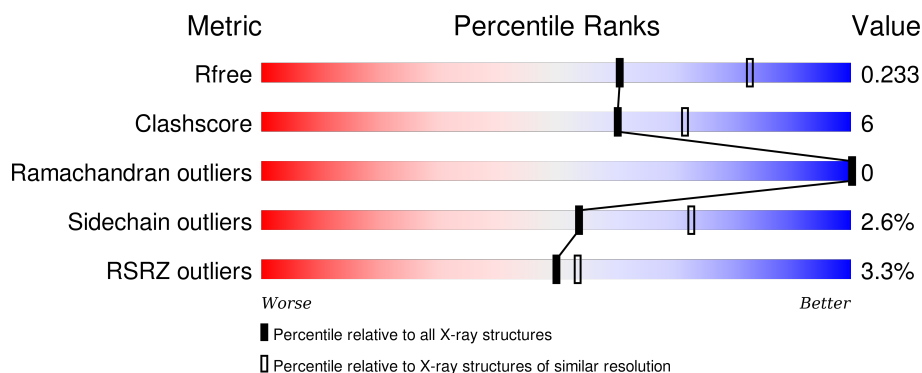
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.37 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	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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	240	<div> <div>5%</div> <div>83% 12% 5%</div> </div>
1	B	240	<div> <div>5%</div> <div>85% 8% 7%</div> </div>
1	C	240	<div> <div>3%</div> <div>81% 13% 5%</div> </div>
1	D	240	<div> <div>4%</div> <div>83% 10% 7%</div> </div>
1	E	240	<div> <div>5%</div> <div>82% 10% 7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	240	<div><div></div><div>2%</div><div>83%</div><div>12%</div><div>6%</div></div>
1	G	240	<div><div></div><div>4%</div><div>86%</div><div>7%</div><div>6%</div></div>
1	H	240	<div><div></div><div>%</div><div>86%</div><div>8%</div><div>6%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13957 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 Signal peptide peptidase sppA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	1	0
			1726	1084	288	345	9			
1	B	223	Total	C	N	O	S	0	0	0
			1699	1069	286	335	9			
1	C	229	Total	C	N	O	S	0	0	0
			1740	1092	291	348	9			
1	D	223	Total	C	N	O	S	0	0	0
			1687	1058	282	338	9			
1	E	223	Total	C	N	O	S	12	1	0
			1701	1068	286	338	9			
1	F	226	Total	C	N	O	S	5	1	0
			1706	1071	282	343	10			
1	G	226	Total	C	N	O	S	7	1	0
			1714	1076	289	340	9			
1	H	226	Total	C	N	O	S	0	0	0
			1727	1086	290	342	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
B	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
C	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
D	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
E	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
F	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
G	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525
H	199	ALA	LYS	ENGINEERED MUTATION	UNP O34525

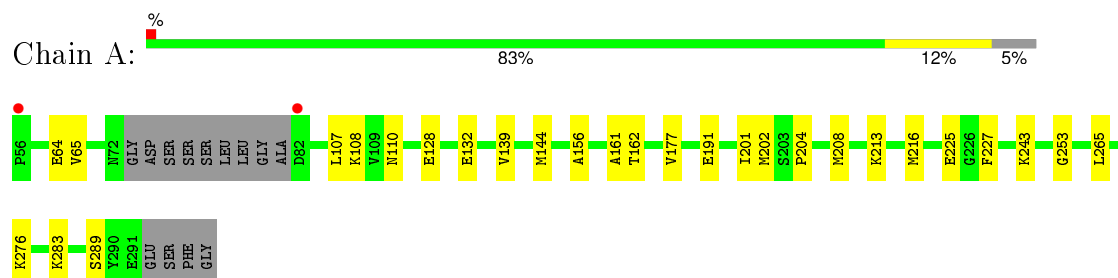
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total 45	O 45	0	0
2	B	18	Total 18	O 18	0	0
2	C	33	Total 33	O 33	0	0
2	D	23	Total 23	O 23	0	0
2	E	27	Total 27	O 27	0	0
2	F	46	Total 46	O 46	0	0
2	G	35	Total 35	O 35	0	0
2	H	30	Total 30	O 30	0	0

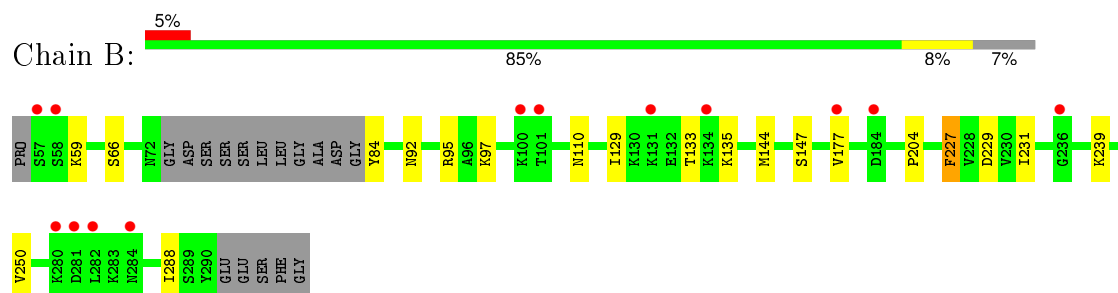
### 3 Residue-property plots [i](#)

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.

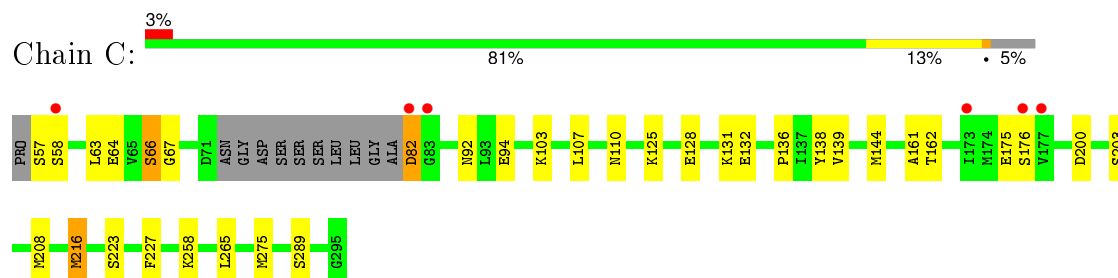
- Molecule 1: Signal peptide peptidase sppA



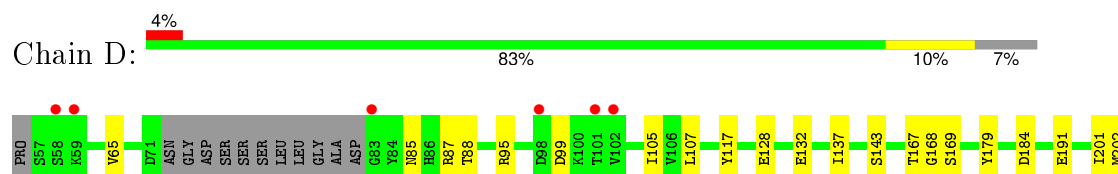
- Molecule 1: Signal peptide peptidase sppA

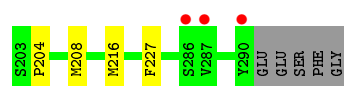


- Molecule 1: Signal peptide peptidase sppA

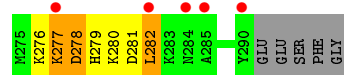
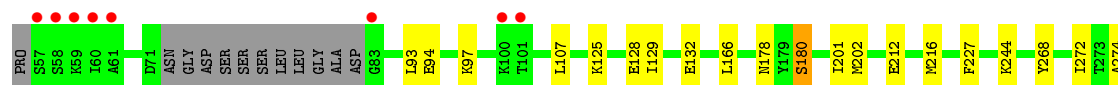
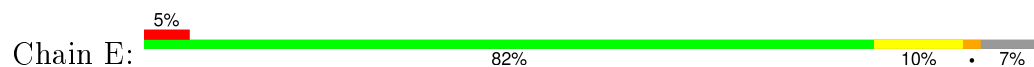


- Molecule 1: Signal peptide peptidase sppA

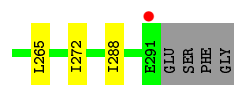
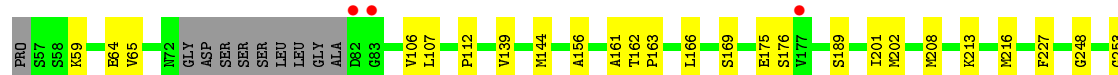
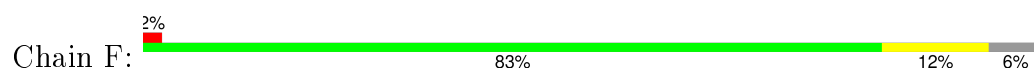




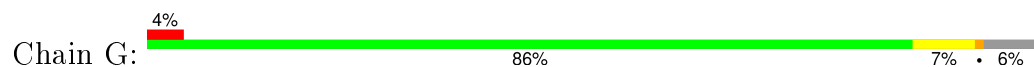
- Molecule 1: Signal peptide peptidase sppA



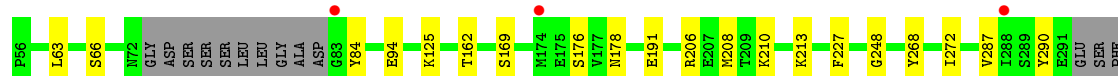
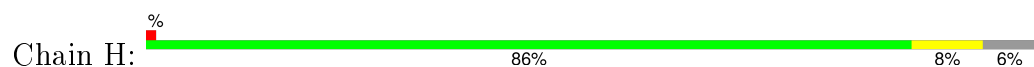
- Molecule 1: Signal peptide peptidase sppA



- Molecule 1: Signal peptide peptidase sppA



- Molecule 1: Signal peptide peptidase sppA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.78Å 131.07Å 207.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.37 40.65 – 2.37	Depositor EDS
% Data completeness (in resolution range)	98.2 (50.00-2.37) 98.1 (40.65-2.37)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.33 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.206 , 0.241 0.200 , 0.233	Depositor DCC
$R_{free}$ test set	4817 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.1	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 96456 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13957	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.50	0/1752	0.59	0/2350
1	B	0.43	0/1721	0.55	0/2307
1	C	0.49	0/1763	0.57	0/2364
1	D	0.49	0/1709	0.55	0/2293
1	E	0.51	0/1729	0.56	0/2317
1	F	0.53	0/1733	0.58	0/2327
1	G	0.49	0/1743	0.59	0/2337
1	H	0.51	0/1750	0.59	0/2344
All	All	0.49	0/13900	0.57	0/18639

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	1726	0	1721	20	0
1	B	1699	0	1718	11	0
1	C	1740	0	1739	23	0
1	D	1687	0	1676	16	0
1	E	1701	0	1709	33	0
1	F	1706	0	1692	29	0
1	G	1714	0	1714	24	0
1	H	1727	0	1750	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	45	0	0	0	0
2	B	18	0	0	1	0
2	C	33	0	0	0	0
2	D	23	0	0	0	0
2	E	27	0	0	1	0
2	F	46	0	0	0	0
2	G	35	0	0	0	0
2	H	30	0	0	0	0
All	All	13957	0	13719	154	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 6.

The worst 5 of 154 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:E:281:ASP:C	1:E:282:LEU:HD22	1.53	1.27
1:E:281:ASP:O	1:E:282:LEU:HD22	1.38	1.19
1:E:281:ASP:C	1:E:282:LEU:CD2	2.14	1.15
1:G:201:ILE:CD1	1:G:216:MET:HE1	1.87	1.03
1:G:201:ILE:HD13	1:G:216:MET:HE1	1.38	1.00

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	224/240 (93%)	219 (98%)	5 (2%)	0	100	100
1	B	219/240 (91%)	212 (97%)	7 (3%)	0	100	100
1	C	225/240 (94%)	219 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	219/240 (91%)	213 (97%)	6 (3%)	0	100	100
1	E	220/240 (92%)	213 (97%)	7 (3%)	0	100	100
1	F	223/240 (93%)	218 (98%)	5 (2%)	0	100	100
1	G	223/240 (93%)	218 (98%)	5 (2%)	0	100	100
1	H	222/240 (92%)	215 (97%)	7 (3%)	0	100	100
All	All	1775/1920 (92%)	1727 (97%)	48 (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	185/201 (92%)	183 (99%)	2 (1%)	80	91
1	B	184/201 (92%)	183 (100%)	1 (0%)	92	97
1	C	188/201 (94%)	177 (94%)	11 (6%)	24	36
1	D	180/201 (90%)	176 (98%)	4 (2%)	60	78
1	E	184/201 (92%)	175 (95%)	9 (5%)	31	46
1	F	183/201 (91%)	179 (98%)	4 (2%)	60	78
1	G	184/201 (92%)	179 (97%)	5 (3%)	52	71
1	H	188/201 (94%)	184 (98%)	4 (2%)	61	79
All	All	1476/1608 (92%)	1436 (97%)	40 (3%)	54	71

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	107	LEU
1	E	244	LYS
1	H	162	THR
1	E	180	SER
1	E	277	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	198	HIS
1	D	217	GLN
1	F	217	GLN
1	D	70	GLN
1	G	70	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 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 [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, 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	227/240 (94%)	-0.00	2 (0%) 85 87	26, 38, 60, 77	0
1	B	223/240 (92%)	0.18	13 (5%) 26 31	32, 50, 89, 105	0
1	C	229/240 (95%)	0.05	6 (2%) 59 62	29, 43, 63, 74	0
1	D	223/240 (92%)	0.30	9 (4%) 42 47	34, 55, 102, 112	0
1	E	223/240 (92%)	0.22	13 (5%) 26 31	27, 50, 111, 169	2 (0%)
1	F	226/240 (94%)	-0.11	4 (1%) 71 74	27, 40, 64, 81	1 (0%)
1	G	226/240 (94%)	-0.00	9 (3%) 42 47	27, 45, 81, 101	1 (0%)
1	H	226/240 (94%)	-0.06	3 (1%) 79 81	27, 43, 72, 84	0
All	All	1803/1920 (93%)	0.07	59 (3%) 50 53	26, 45, 82, 169	4 (0%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	82	ASP	5.4
1	D	83	GLY	5.0
1	E	282	LEU	4.4
1	G	58	SER	4.4
1	E	57	SER	4.3

### 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

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.