



# Full wwPDB X-ray Structure Validation Report

Sep 3, 2014 – 04:58 PM EDT

PDB ID : 1XOC  
Title : The structure of the oligopeptide-binding protein, AppA, from *Bacillus subtilis* in complex with a nonapeptide.  
Authors : Levnikov, V.M.; Blagova, E.V.; Brannigan, J.A.; Wright, L.; Vagin, A.A.; Wilkinson, A.J.  
Deposited on : 2004-10-06  
Resolution : 1.55 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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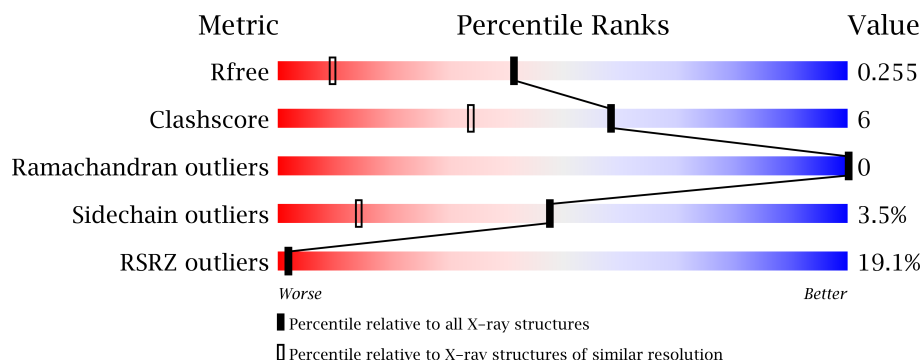
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 1.55 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))
$R_{free}$	66092	1117 (1.58-1.54)
Clashscore	79885	1249 (1.58-1.54)
Ramachandran outliers	78287	1212 (1.58-1.54)
Sidechain outliers	78261	1210 (1.58-1.54)
RSRZ outliers	66119	1117 (1.58-1.54)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	520	
2	B	9	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	ZN	A	525	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4650 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Oligopeptide-binding protein appA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	504	Total	C	N	O	S	0	9	0
			4118	2648	660	801	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	CYS	CLONING ARTIFACT	UNP P42061

- Molecule 2 is a protein called Nonapeptide VDSKNTSSW.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	2	0
			76	46	13	17			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	Zn	0	2
			15	15		

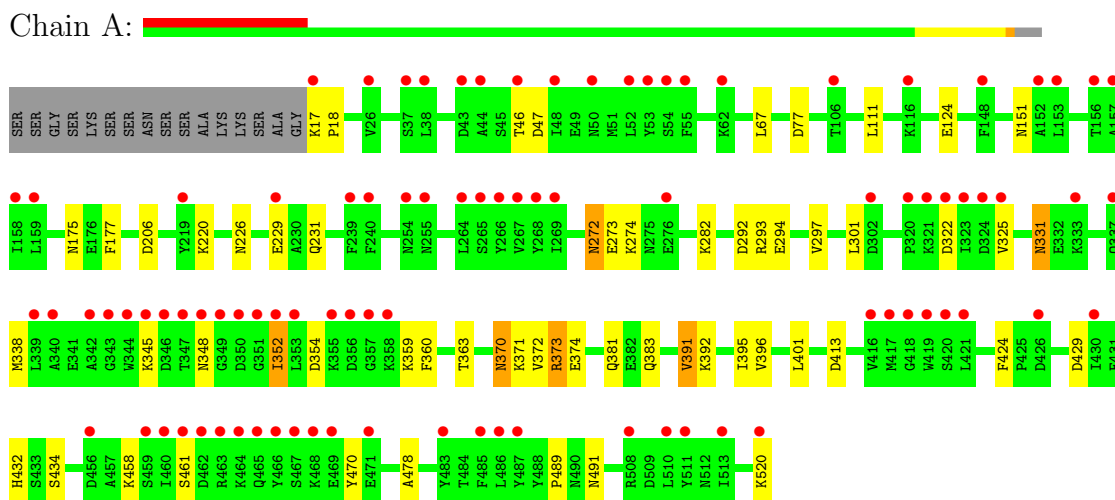
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	435	Total	O	0	6
			435	435		
4	B	6	Total	O	0	1
			6	6		

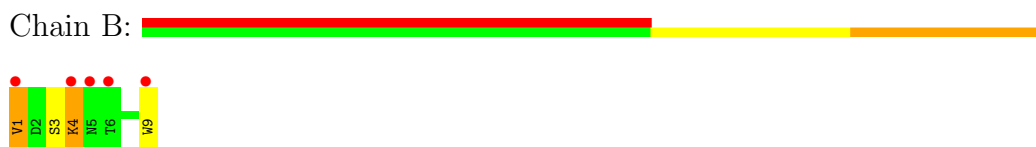
### 3 Residue-property plots

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: Oligopeptide-binding protein appA



- Molecule 2: Nonapeptide VDSKNTSSW



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	120.95Å 90.78Å 54.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.57 – 1.55 30.56 – 1.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.57-1.55) 99.3 (30.56-1.55)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 1.54Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.176 , 0.206 0.235 , 0.255	Depositor DCC
$R_{free}$ test set	4411 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.6	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 54.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 88019 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4650	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.63	0/4256	0.71	5/5748 (0.1%)
2	B	0.64	0/114	0.61	0/148
All	All	0.63	0/4370	0.71	5/5896 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	354	ASP	CB-CG-OD2	8.39	125.85	118.30
1	A	373	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	77	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	47	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	A	293	ARG	NE-CZ-NH2	-5.09	117.75	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4118	0	4058	47	0
2	B	76	0	68	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	15	0	0	0	0
4	A	435	0	0	14	0
4	B	6	0	0	0	0
All	All	4650	0	4126	52	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (52) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:226:ASN:ND2	1:A:371[A]:LYS:HZ2	1.55	1.03
1:A:226:ASN:HD21	1:A:371[A]:LYS:NZ	1.72	0.88
1:A:226:ASN:HD21	1:A:371[A]:LYS:HZ2	0.87	0.85
1:A:226:ASN:ND2	1:A:371[A]:LYS:NZ	2.30	0.79
1:A:371[B]:LYS:HD2	4:A:927:HOH:O	1.82	0.78
4:A:655:HOH:O	2:B:1:VAL:HG21	1.93	0.68
1:A:352:ILE:HD11	1:A:359:LYS:HB2	1.75	0.67
1:A:458:LYS:NZ	4:A:538:HOH:O	2.30	0.63
1:A:371[B]:LYS:CD	4:A:927:HOH:O	2.43	0.63
4:A:656[B]:HOH:O	2:B:4[B]:LYS:HD2	1.99	0.62
1:A:17:LYS:NZ	4:A:935:HOH:O	2.33	0.60
1:A:46:THR:HG21	2:B:4[A]:LYS:HE2	1.83	0.59
1:A:175:ASN:HD22	1:A:177:PHE:H	1.52	0.56
1:A:151:ASN:ND2	1:A:424:PHE:HB3	2.20	0.56
1:A:396:VAL:HG22	1:A:401:LEU:HB2	1.87	0.56
1:A:371[B]:LYS:NZ	1:A:374:GLU:OE1	2.14	0.55
1:A:17:LYS:HB3	1:A:18:PRO:HD3	1.89	0.55
1:A:292:ASP:H	1:A:383:GLN:HE22	1.55	0.55
1:A:297:VAL:HA	1:A:301:LEU:HD23	1.88	0.55
1:A:292:ASP:H	1:A:383:GLN:NE2	2.05	0.55
1:A:282:LYS:NZ	1:A:338:MET:O	2.35	0.54
1:A:371[B]:LYS:NZ	1:A:374:GLU:CD	2.62	0.54
1:A:432:HIS:HD2	1:A:434:SER:H	1.58	0.52
1:A:331:ASN:C	1:A:331:ASN:HD22	2.13	0.51
4:A:798:HOH:O	2:B:1:VAL:HG11	2.09	0.51
1:A:371[B]:LYS:NZ	1:A:374:GLU:OE2	2.45	0.49
1:A:370:ASN:C	1:A:370:ASN:HD22	2.15	0.49
4:A:656[B]:HOH:O	2:B:4[B]:LYS:CD	2.59	0.49
1:A:363:THR:OG1	1:A:392:LYS:HE3	2.13	0.48
1:A:206:ASP:OD2	4:A:836:HOH:O	2.20	0.48
1:A:151:ASN:HD21	1:A:424:PHE:HB3	1.77	0.47
1:A:429:ASP:CG	4:A:910:HOH:O	2.52	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:489:PRO:HB3	2:B:9[A]:TRP:HB3	1.96	0.47
1:A:371[B]:LYS:NZ	4:A:815:HOH:O	2.48	0.47
1:A:374:GLU:HG2	1:A:395[B]:ILE:HD12	1.97	0.46
1:A:322:ASP:N	1:A:322:ASP:OD2	2.49	0.46
1:A:272:ASN:HD22	1:A:272:ASN:C	2.18	0.45
1:A:175:ASN:ND2	1:A:177:PHE:H	2.15	0.44
1:A:229:GLU:HB3	4:A:740:HOH:O	2.15	0.44
1:A:272:ASN:ND2	1:A:274:LYS:H	2.13	0.44
1:A:373:ARG:NE	2:B:9[B]:TRP:O	2.48	0.44
1:A:413:ASP:OD2	4:A:715:HOH:O	2.21	0.44
1:A:381:GLN:HA	1:A:391:VAL:HG13	1.99	0.44
1:A:272:ASN:HD22	1:A:273:GLU:N	2.17	0.42
1:A:370:ASN:ND2	1:A:373:ARG:H	2.17	0.42
1:A:432:HIS:CD2	1:A:434:SER:H	2.37	0.42
2:B:3:SER:C	2:B:4[A]:LYS:HD3	2.40	0.42
1:A:220:LYS:NZ	1:A:231:GLN:HE22	2.18	0.41
1:A:124:GLU:CG	4:A:959:HOH:O	2.68	0.41
1:A:370:ASN:HD21	1:A:372:VAL:HB	1.84	0.41
1:A:325:VAL:HG13	1:A:478:ALA:HB1	2.01	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	511/520 (98%)	501 (98%)	10 (2%)	0	100	100
2	B	8/9 (89%)	8 (100%)	0	0	100	100
All	All	519/529 (98%)	509 (98%)	10 (2%)	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	452/455 (99%)	437 (97%)	15 (3%)	50	16
2	B	12/9 (133%)	9 (75%)	3 (25%)	1	0
All	All	464/464 (100%)	446 (96%)	18 (4%)	48	11

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67[A]	LEU
1	A	67[B]	LEU
1	A	111	LEU
1	A	272	ASN
1	A	294	GLU
1	A	331	ASN
1	A	345	LYS
1	A	348	ASN
1	A	352	ILE
1	A	360	PHE
1	A	370	ASN
1	A	391	VAL
1	A	461	SER
1	A	470	TYR
1	A	520	LYS
2	B	1	VAL
2	B	4[A]	LYS
2	B	4[B]	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	175	ASN
1	A	226	ASN
1	A	231	GLN
1	A	233	GLN
1	A	272	ASN

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Mol	Chain	Res	Type
1	A	285	GLN
1	A	331	ASN
1	A	368	GLN
1	A	370	ASN
1	A	383	GLN
1	A	409	ASN
1	A	432	HIS
1	A	435	GLN
1	A	465	GLN
1	A	475	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 15 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	504/520 (96%)	1.02	93 (18%) 2 2	26, 31, 37, 44	0
2	B	9/9 (100%)	2.51	5 (55%) 0 0	30, 31, 34, 34	3 (33%)
All	All	513/529 (96%)	1.05	98 (19%) 2 2	26, 31, 37, 44	3 (0%)

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	9[A]	TRP	9.3
1	A	322	ASP	8.4
1	A	461	SER	6.8
1	A	352	ILE	6.8
1	A	349	GLY	6.1
1	A	323	ILE	5.6
1	A	324	ASP	5.2
1	A	348	ASN	5.2
1	A	321	LYS	5.2
1	A	333	LYS	5.0
1	A	357	GLY	5.0
1	A	358	LYS	4.8
1	A	520	LYS	4.7
1	A	351	GLY	4.6
1	A	340	ALA	4.6
1	A	462	ASP	4.6
1	A	465	GLN	4.5
1	A	345	LYS	4.5
1	A	464	LYS	4.4
1	A	347	THR	4.3
1	A	55	PHE	4.3
1	A	460	ILE	4.2
1	A	459	SER	4.2
1	A	267	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	158	ILE	4.1
1	A	419	TRP	4.1
1	A	337	GLN	4.1
1	A	510	LEU	4.0
1	A	421	LEU	3.9
1	A	350	ASP	3.7
1	A	44	ALA	3.7
1	A	325	VAL	3.6
1	A	468	LYS	3.5
1	A	356	ASP	3.5
1	A	469	GLU	3.4
1	A	48	ILE	3.3
1	A	320	PRO	3.3
1	A	46	THR	3.3
1	A	486	LEU	3.2
1	A	53	TYR	3.1
1	A	157	ALA	3.1
1	A	513	ILE	3.1
1	A	342	ALA	3.1
1	A	487	TYR	3.1
1	A	344	TRP	3.0
1	A	467	SER	3.0
1	A	343	GLY	2.9
1	A	52	LEU	2.9
1	A	266	TYR	2.9
1	A	116	LYS	2.8
1	A	264	LEU	2.8
1	A	276	GLU	2.8
1	A	268	TYR	2.7
1	A	463	ARG	2.7
1	A	153	LEU	2.7
1	A	430	ILE	2.7
1	A	17	LYS	2.6
1	A	50	ASN	2.6
1	A	471	GLU	2.6
1	A	339	LEU	2.6
1	A	156	THR	2.6
1	A	346	ASP	2.6
1	A	466	TYR	2.6
1	A	418	GLY	2.6
1	A	38	LEU	2.5
1	A	37[A]	SER	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	5	ASN	2.5
1	A	159	LEU	2.5
1	A	269	ILE	2.5
1	A	239	PHE	2.4
1	A	355	LYS	2.4
1	A	426	ASP	2.3
1	A	420	SER	2.3
1	A	456	ASP	2.3
1	A	483	TYR	2.3
1	A	54	SER	2.3
1	A	508	ARG	2.3
1	A	353	LEU	2.3
1	A	416	VAL	2.2
1	A	485	PHE	2.2
1	A	255	ASN	2.2
1	A	152	ALA	2.2
1	A	26	VAL	2.2
2	B	1	VAL	2.2
1	A	219	TYR	2.2
1	A	254	ASN	2.2
1	A	43	ASP	2.1
2	B	4[A]	LYS	2.1
1	A	148	PHE	2.1
1	A	240	PHE	2.1
1	A	62	LYS	2.1
1	A	229	GLU	2.1
1	A	302	ASP	2.1
1	A	106	THR	2.0
2	B	6	THR	2.0
1	A	511	TYR	2.0
1	A	417	MET	2.0
1	A	265[A]	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	ZN	A	525	1/1	0.17	4.70	39,39,39,39	0
3	ZN	A	526	1/1	0.17	1.07	48,48,48,48	1
3	ZN	A	524[C]	1/1	0.17	0.75	30,30,30,30	1
3	ZN	A	531	1/1	0.28	0.24	45,45,45,45	0
3	ZN	A	530	1/1	0.13	-0.14	38,38,38,38	0
3	ZN	A	528	1/1	0.10	-0.60	35,35,35,35	0
3	ZN	A	534	1/1	0.09	-0.72	93,93,93,93	0
3	ZN	A	527	1/1	0.08	-0.79	30,30,30,30	0
3	ZN	A	532	1/1	0.05	-1.32	82,82,82,82	0
3	ZN	A	522[A]	1/1	0.06	-2.65	19,19,19,19	1
3	ZN	A	533	1/1	0.11	-2.78	88,88,88,88	0
3	ZN	A	521	1/1	0.04	-3.07	18,18,18,18	1
3	ZN	A	523	1/1	0.06	-3.44	20,20,20,20	0
3	ZN	A	529	1/1	0.17	-5.00	36,36,36,36	1
3	ZN	A	535	1/1	0.10	-7.14	100,100,100,100	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.