



# Full wwPDB X-ray Structure Validation Report

Mar 31, 2014 – 03:14 PM BST

PDB ID : 4OGE  
Title : Crystal structure of the Type II-C Cas9 enzyme from *Actinomyces naeslundii*  
Authors : Jiang, F.; Ma, E.; Lin, S.; Doudna, J.A.  
Deposited on : 2014-01-15  
Resolution : 2.20 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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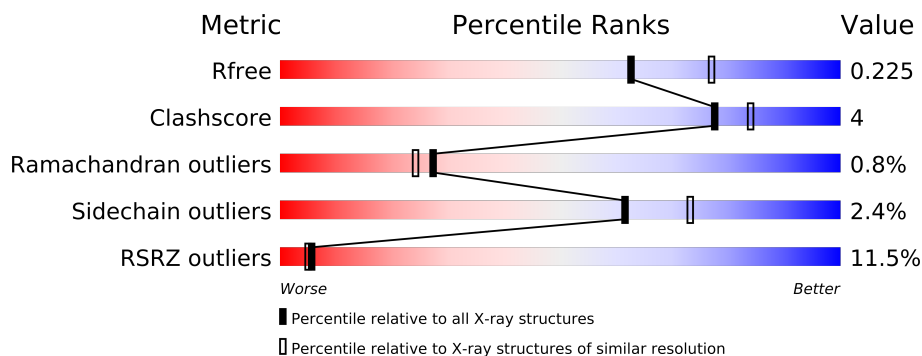
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable23004
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)	:	stable23004

# 1 Overall quality at a glance


The reported resolution of this entry is 2.20 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	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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	1101	

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	MG	A	1204	-	X
4	SPD	A	1205	-	X
4	SPD	A	1206	-	X

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7799 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 HNH endonuclease domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	977	Total	C	N	O	S	0	0	0
			7432	4620	1392	1391	29			

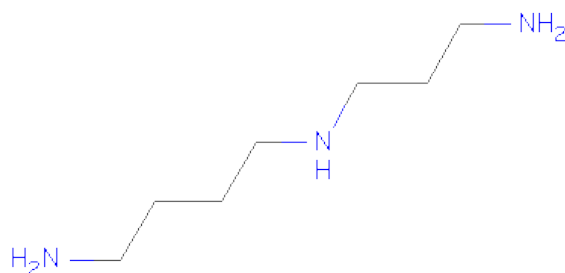
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Mg	0	0
			3	3		

- Molecule 4 is SPERMIDINE (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			10	7	3		
4	A	1	Total	C	N	0	0
			10	7	3		

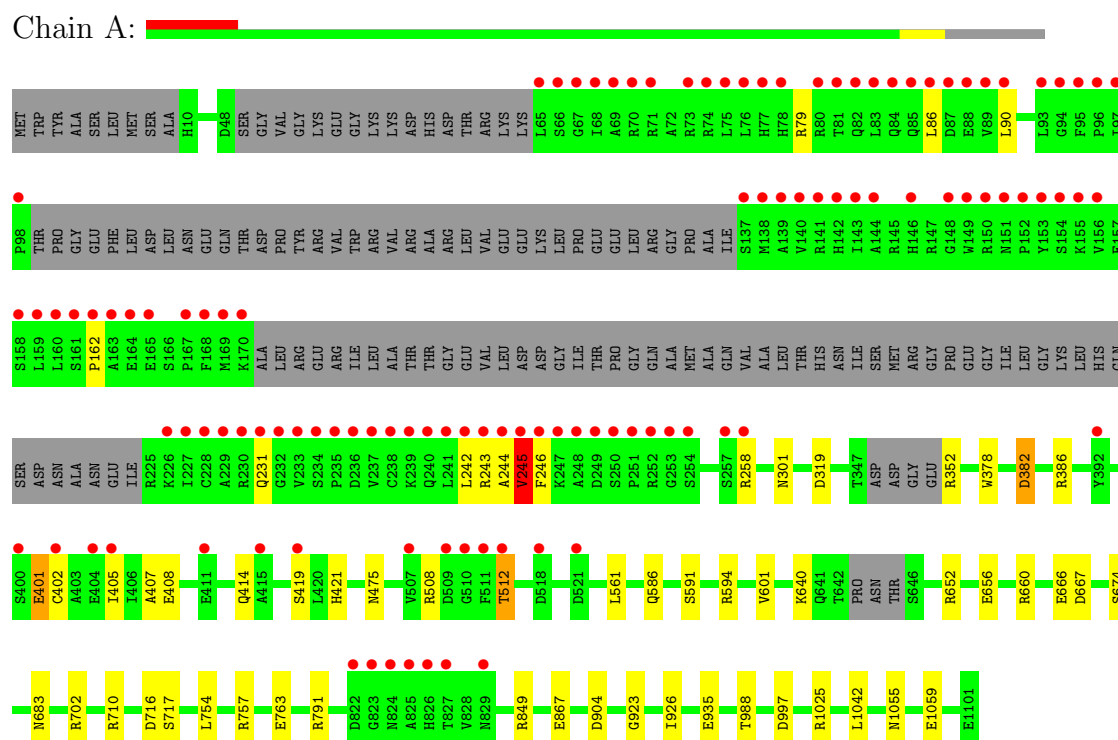
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	343	Total	O	0	0
			343	343		

### 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: HNH endonuclease domain protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.42Å 133.03Å 80.69Å 90.00° 96.22° 90.00°	Depositor
Resolution (Å)	68.69 – 2.20 68.69 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.9 (68.69-2.20) 97.9 (68.69-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.186 , 0.226 0.186 , 0.225	Depositor DCC
$R_{free}$ test set	3927 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.4	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 42.4	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 78398 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7799	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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, SPD, MG

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	0.41	0/7575	0.56	0/10287

There are no bond length outliers.

There are no bond angle outliers.

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	7432	0	0	28	0
2	A	1	0	0	0	0
3	A	3	0	0	0	0
4	A	20	0	38	3	0
5	A	343	0	0	7	0
All	All	7799	0	38	28	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 4.

All (28) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1055:ASN:ND2	1:A:1059:GLU:OE2	2.24	0.70
1:A:710:ARG:NH1	5:A:1584:HOH:O	2.23	0.70
1:A:319:ASP:OD2	1:A:652:ARG:NH2	2.26	0.68
1:A:378:TRP:O	1:A:386:ARG:NH1	2.29	0.66
1:A:660:ARG:NH2	1:A:667:ASP:OD2	2.29	0.65
1:A:1025:ARG:NH2	5:A:1357:HOH:O	2.29	0.64
1:A:382:ASP:OD1	1:A:382:ASP:N	2.31	0.64
1:A:757:ARG:CB	4:A:1205:SPD:H72	2.32	0.59
1:A:301:ASN:ND2	5:A:1417:HOH:O	2.35	0.59
1:A:352:ARG:NH2	1:A:683:ASN:OD1	2.36	0.58
1:A:1025:ARG:NH1	5:A:1534:HOH:O	2.36	0.58
1:A:754:LEU:O	4:A:1205:SPD:H81	2.04	0.57
1:A:242:LEU:O	1:A:245:VAL:N	2.36	0.57
1:A:242:LEU:O	1:A:244:ALA:N	2.38	0.56
1:A:849:ARG:NH2	1:A:904:ASP:OD2	2.40	0.54
1:A:421:HIS:NE2	1:A:512:THR:O	2.41	0.54
1:A:591:SER:OG	1:A:763:GLU:OE2	2.28	0.52
1:A:935:GLU:OE2	1:A:988:THR:OG1	2.28	0.51
1:A:674:SER:O	1:A:702:ARG:NH1	2.45	0.50
1:A:594:ARG:NH2	1:A:656:GLU:OE1	2.45	0.49
1:A:666:GLU:OE2	5:A:1387:HOH:O	2.20	0.48
1:A:710:ARG:NE	1:A:716:ASP:OD2	2.49	0.46
1:A:926:ILE:O	4:A:1206:SPD:H52	2.17	0.45
1:A:586:GLN:NE2	5:A:1437:HOH:O	2.52	0.43
1:A:401:GLU:O	1:A:405:ILE:N	2.52	0.42
1:A:419:SER:O	1:A:421:HIS:ND1	2.53	0.41
1:A:791:ARG:NH2	5:A:1482:HOH:O	2.53	0.41
1:A:716:ASP:O	1:A:717:SER:OG	2.39	0.40

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	965/1101 (88%)	914 (95%)	43 (4%)	8 (1%)	27	24



All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	243	ARG
1	A	508	ARG
1	A	407	ALA
1	A	414	GLN
1	A	923	GLY
1	A	162	PRO
1	A	231	GLN
1	A	245	VAL

### 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	759/931 (82%)	741 (98%)	18 (2%)	61	73

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

Mol	Chain	Res	Type
1	A	79	ARG
1	A	86	LEU
1	A	90	LEU
1	A	245	VAL
1	A	246	PHE
1	A	258	ARG
1	A	382	ASP
1	A	401	GLU
1	A	402	CYS
1	A	408	GLU
1	A	475	ASN
1	A	512	THR
1	A	561	LEU
1	A	601	VAL
1	A	640	LYS
1	A	867	GLU
1	A	997	ASP
1	A	1042	LEU

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

### 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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SPD	A	1205	-	9,9,9	0.45	0	8,8,8	1.37	2 (25%)
4	SPD	A	1206	-	9,9,9	0.43	0	8,8,8	0.77	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SPD	A	1205	-	-	0/7/7/7	0/0/0/0
4	SPD	A	1206	-	-	0/7/7/7	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1205	SPD	C4-C5-N6	-2.43	105.62	112.09
4	A	1205	SPD	C7-C8-C9	-2.15	105.64	114.61

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	977/1101 (88%)	0.60	113 (11%) 5 5	20, 42, 147, 199	0

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	160	LEU	10.7
1	A	98	PRO	10.6
1	A	227	ILE	10.3
1	A	233	VAL	9.6
1	A	245	VAL	9.5
1	A	143	ILE	9.4
1	A	161	SER	9.0
1	A	244	ALA	8.6
1	A	248	ALA	8.6
1	A	65	LEU	8.4
1	A	163	ALA	8.1
1	A	149	TRP	8.1
1	A	226	LYS	8.1
1	A	169	MET	8.0
1	A	228	CYS	7.3
1	A	249	ASP	7.3
1	A	823	GLY	7.1
1	A	162	PRO	6.8
1	A	151	ASN	6.8
1	A	144	ALA	6.8
1	A	827	THR	6.7
1	A	139	ALA	6.4
1	A	89	VAL	6.4
1	A	231	GLN	6.0
1	A	152	PRO	6.0
1	A	73	ARG	5.8
1	A	234	SER	5.7

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Mol	Chain	Res	Type	RSRZ
1	A	76	LEU	5.6
1	A	66	SER	5.5
1	A	140	VAL	5.5
1	A	824	ASN	5.5
1	A	822	ASP	5.4
1	A	86	LEU	5.4
1	A	257	SER	5.4
1	A	97	ILE	5.4
1	A	239	LYS	5.3
1	A	511	PHE	5.2
1	A	138	MET	5.1
1	A	237	VAL	5.1
1	A	155	LYS	5.0
1	A	235	PRO	4.9
1	A	241	LEU	4.8
1	A	826	HIS	4.8
1	A	168	PHE	4.7
1	A	415	ALA	4.6
1	A	238	CYS	4.6
1	A	146	HIS	4.5
1	A	153	TYR	4.4
1	A	142	HIS	4.4
1	A	68	ILE	4.3
1	A	77	HIS	4.1
1	A	154	SER	4.0
1	A	69	ALA	4.0
1	A	96	PRO	4.0
1	A	246	PHE	3.9
1	A	230	ARG	3.8
1	A	509	ASP	3.8
1	A	170	LYS	3.8
1	A	81	THR	3.7
1	A	93	LEU	3.6
1	A	165	GLU	3.6
1	A	236	ASP	3.6
1	A	250	SER	3.6
1	A	159	LEU	3.5
1	A	242	LEU	3.5
1	A	419	SER	3.5
1	A	141	ARG	3.5
1	A	229	ALA	3.5
1	A	518	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	825	ALA	3.4
1	A	87	ASP	3.4
1	A	164	GLU	3.4
1	A	253	GLY	3.4
1	A	251	PRO	3.3
1	A	80	ARG	3.3
1	A	404	GLU	3.3
1	A	78	HIS	3.3
1	A	158	SER	3.2
1	A	90	LEU	3.1
1	A	247	LYS	3.0
1	A	521	ASP	2.9
1	A	400	SER	2.8
1	A	510	GLY	2.8
1	A	512	THR	2.8
1	A	70	ARG	2.8
1	A	67	GLY	2.8
1	A	75	LEU	2.7
1	A	258	ARG	2.7
1	A	85	GLN	2.7
1	A	507	VAL	2.7
1	A	83	LEU	2.7
1	A	94	GLY	2.7
1	A	137	SER	2.7
1	A	240	GLN	2.6
1	A	402	CYS	2.6
1	A	88	GLU	2.6
1	A	95	PHE	2.6
1	A	392	TYR	2.5
1	A	829	ASN	2.5
1	A	405	ILE	2.4
1	A	71	ARG	2.3
1	A	252	ARG	2.3
1	A	74	ARG	2.3
1	A	254	SER	2.3
1	A	167	PRO	2.3
1	A	150	ARG	2.3
1	A	148	GLY	2.2
1	A	243	ARG	2.2
1	A	411	GLU	2.2
1	A	232	GLY	2.2
1	A	156	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	82	GLN	2.0
1	A	84	GLN	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
4	SPD	A	1206	10/10	0.38	8.19	41,70,89,90	0
4	SPD	A	1205	10/10	0.22	3.60	26,45,49,53	0
3	MG	A	1204	1/1	0.17	2.34	14,14,14,14	0
3	MG	A	1203	1/1	0.17	1.78	53,53,53,53	0
2	ZN	A	1201	1/1	0.17	1.52	28,28,28,28	0
3	MG	A	1202	1/1	0.15	0.23	19,19,19,19	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.