



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 12, 2018 – 01:47 PM EST

PDB ID : 6HG1
Title : Hybrid dihydroorotase domain of human CAD with E. coli flexible loop in apo state
Authors : Ramon-Maiques, S.; Del Cano-Ochoa, F.
Deposited on : 2018-08-22
Resolution : 2.12 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031633
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

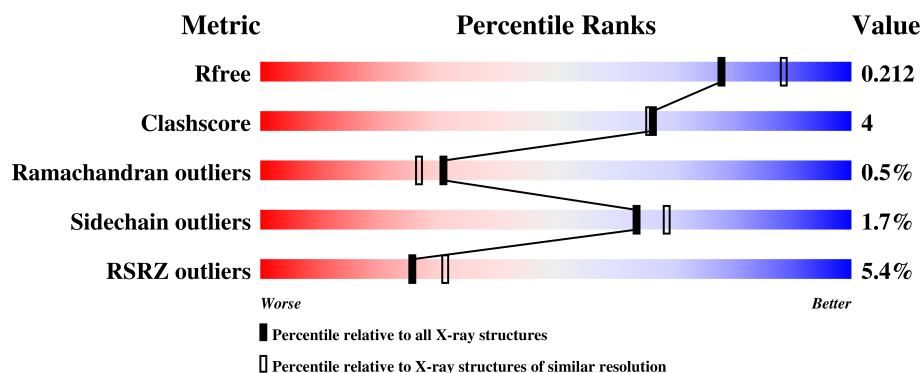
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.12 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}	111664	5449 (2.14-2.10)
Clashscore	122126	5972 (2.14-2.10)
Ramachandran outliers	120053	5914 (2.14-2.10)
Sidechain outliers	120020	5915 (2.14-2.10)
RSRZ outliers	108989	5321 (2.14-2.10)

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 ≥ 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	371	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FMT	A	1904	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5903 atoms, of which 2929 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 CAD protein,Dihydroorotase,CAD protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	371	Total	C	H	N	O	S	0	17	0
			5824	1847	2921	518	525	13			

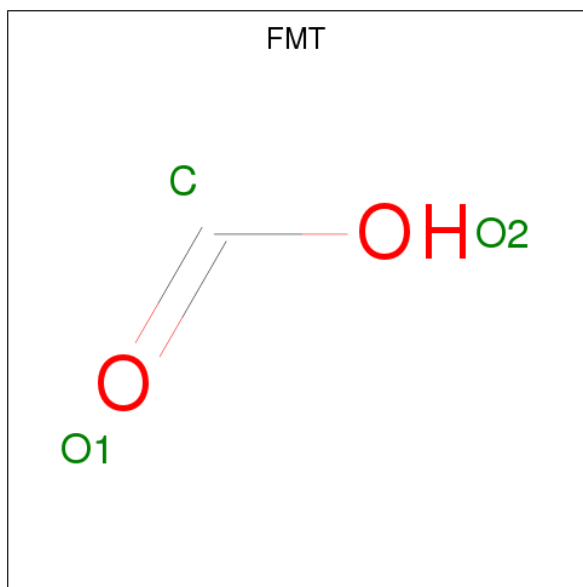
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1459	ALA	-	expression tag	UNP P27708
A	1595	GLU	GLN	conflict	UNP P27708
A	1829	ALA	-	expression tag	UNP P27708

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

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

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			5	1	2	2		
3	A	1	Total	C	H	O	0	0
			5	1	2	2		
3	A	1	Total	C	H	O	0	0
			5	1	2	2		
3	A	1	Total	C	H	O	0	0
			5	1	2	2		

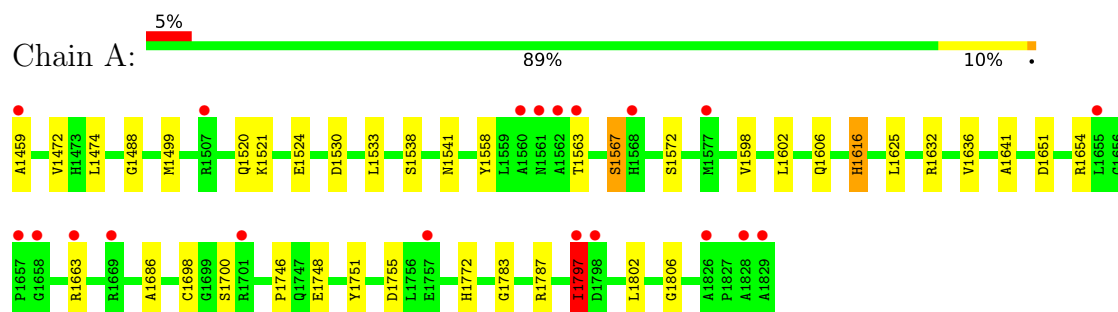
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		

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 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: CAD protein, Dihydroorotase, CAD protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	81.05Å 160.59Å 58.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.36 – 2.12 72.36 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.5 (72.36-2.12) 99.5 (72.36-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.12Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.174 , 0.209 0.176 , 0.212	Depositor DCC
R_{free} test set	1047 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	41.7	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 71.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5903	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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

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	0.39	2/3024 (0.1%)	0.62	4/4128 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1797[A]	ILE	CA-C	5.48	1.67	1.52
1	A	1797[B]	ILE	CA-C	5.48	1.67	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1797[A]	ILE	CA-C-N	-9.43	96.47	117.20
1	A	1797[B]	ILE	CA-C-N	-9.43	96.47	117.20
1	A	1797[A]	ILE	CB-CA-C	-8.01	95.59	111.60
1	A	1797[B]	ILE	CB-CA-C	-8.01	95.59	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1797[A]	ILE	Mainchain

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Mol	Chain	Res	Type	Group
1	A	1797[B]	ILE	Mainchain

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	2903	2921	2901	24	1
2	A	2	0	0	0	0
3	A	12	8	4	2	0
4	A	57	0	0	4	0
All	All	2974	2929	2905	25	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 4.

All (25) 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)
3:A:1905:FMT:O2	4:A:2001:HOH:O	1.81	0.97
1:A:1558:TYR:OH	1:A:1663:ARG:NH1	2.21	0.73
1:A:1521:LYS:NZ	1:A:1524:GLU:OE1	2.22	0.71
1:A:1806:GLY:O	4:A:2002:HOH:O	2.13	0.66
1:A:1602:LEU:HD21	1:A:1636:VAL:HG21	1.81	0.61
1:A:1751:TYR:OH	1:A:1787:ARG:NH1	2.33	0.61
1:A:1563:THR:HG23	1:A:1563:THR:O	2.05	0.56
1:A:1755:ASP:O	1:A:1783:GLY:HA2	2.06	0.54
1:A:1598[B]:VAL:HG23	1:A:1625:LEU:CD2	2.38	0.54
1:A:1598[B]:VAL:HG23	1:A:1625:LEU:HD23	1.90	0.53
1:A:1651:ASP:OD1	1:A:1654:ARG:NH1	2.41	0.51
1:A:1602:LEU:HD21	1:A:1636:VAL:CG2	2.42	0.49
1:A:1558:TYR:HB3	1:A:1567:SER:HA	1.95	0.49
1:A:1472:VAL:HG12	1:A:1474:LEU:HG	1.98	0.46
1:A:1748:GLU:HG3	4:A:2021:HOH:O	2.16	0.46
1:A:1563:THR:O	1:A:1563:THR:CG2	2.65	0.45
1:A:1746:PRO:HB2	3:A:1903:FMT:O1	2.17	0.44
1:A:1499:MET:HA	1:A:1530:ASP:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1474:LEU:HD22	1:A:1488:GLY:HA3	1.99	0.43
1:A:1520:GLN:HG2	1:A:1533:LEU:HD12	2.00	0.43
1:A:1606:GLN:NE2	4:A:2003:HOH:O	2.35	0.42
1:A:1538:SER:OG	1:A:1541:ASN:N	2.52	0.42
1:A:1459:ALA:HB1	1:A:1755:ASP:OD1	2.21	0.41
1:A:1797[B]:ILE:HG22	1:A:1802:LEU:HD11	2.04	0.40
1:A:1641:ALA:HA	1:A:1686:ALA:O	2.21	0.40

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:A:1698:CYS:SG	1:A:1698:CYS:HG[3_454]	1.20	0.40

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	385/371 (104%)	371 (96%)	11 (3%)	3 (1%)	21 15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1616	HIS
1	A	1700[A]	SER
1	A	1700[B]	SER

5.3.2 Protein sidechains [i](#)

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	312/298 (105%)	306 (98%)	6 (2%)	60	65

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1567	SER
1	A	1572	SER
1	A	1616	HIS
1	A	1632[A]	ARG
1	A	1632[B]	ARG
1	A	1772	HIS

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 molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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
1	KCX	A	1556	1,2	8,11,12	1.25	1 (12%)	6,12,14	1.19	1 (16%)

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
1	KCX	A	1556	1,2	-	0/6/10/12	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1556	KCX	CA-C	2.96	1.54	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1556	KCX	CE-NZ-CX	-2.38	120.16	123.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z > 2$
3	FMT	A	1903	-	2,2,2	0.63	0	1,1,1	0.28	0
3	FMT	A	1904	-	2,2,2	0.63	0	1,1,1	0.35	0
3	FMT	A	1905	-	2,2,2	0.65	0	1,1,1	0.50	0
3	FMT	A	1906	-	2,2,2	1.02	0	1,1,1	0.25	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
3	FMT	A	1903	-	-	0/0/0/0	0/0/0/0
3	FMT	A	1904	-	-	0/0/0/0	0/0/0/0
3	FMT	A	1905	-	-	0/0/0/0	0/0/0/0
3	FMT	A	1906	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1903	FMT	1	0
3	A	1905	FMT	1	0

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, 95th 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 ²)	Q<0.9
1	A	370/371 (99%)	0.50	20 (5%) 26 31	30, 44, 84, 127	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1563	THR	5.9
1	A	1829	ALA	5.6
1	A	1561	ASN	4.3
1	A	1562	ALA	4.2
1	A	1828	ALA	3.7
1	A	1701	ARG	3.2
1	A	1663	ARG	3.0
1	A	1459	ALA	3.0
1	A	1657	PRO	2.9
1	A	1757	GLU	2.8
1	A	1568	HIS	2.8
1	A	1797[A]	ILE	2.6
1	A	1655	LEU	2.6
1	A	1798	ASP	2.5
1	A	1658	GLY	2.4
1	A	1507	ARG	2.3
1	A	1560	ALA	2.2
1	A	1577	MET	2.1
1	A	1669	ARG	2.1
1	A	1826	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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. The B-factors column lists the minimum, median, 95th 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	KCX	A	1556	12/13	0.96	0.14	34,46,57,58	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95th 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	FMT	A	1904	3/3	0.78	0.43	64,66,77,80	0
3	FMT	A	1903	3/3	0.81	0.35	95,95,114,114	5
3	FMT	A	1905	3/3	0.93	0.26	43,45,54,56	0
3	FMT	A	1906	3/3	0.93	0.11	33,36,40,43	5
2	ZN	A	1902	1/1	0.97	0.18	39,39,39,39	1
2	ZN	A	1901	1/1	0.99	0.17	38,38,38,38	1

6.5 Other polymers [i](#)

There are no such residues in this entry.