



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 01:55 PM UTC

PDB ID : 2HQQ / pdb_00002hqq
Title : Crystal structure of a monomeric cyan fluorescent protein derived from *Clavul-
laria*
Authors : Henderson, J.N.; Campbell, R.E.; Ai, H.; Remington, S.J.
Deposited on : 2006-07-18
Resolution : 1.19 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

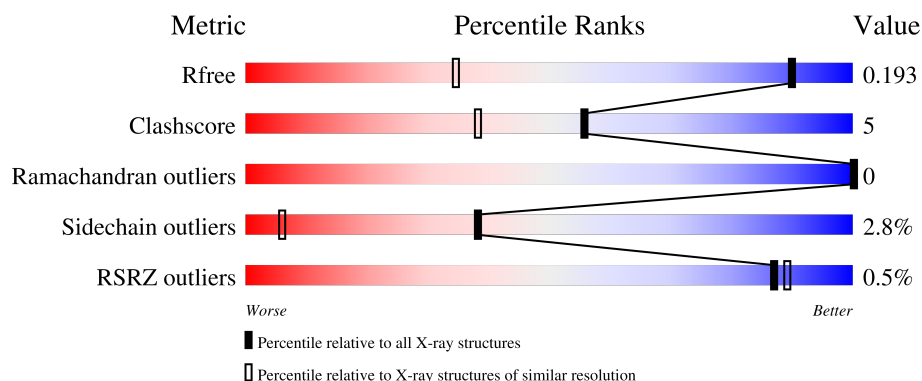
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.19 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}	180053	1216 (1.20-1.20)
Clashscore	190562	1265 (1.20-1.20)
Ramachandran outliers	187476	1226 (1.20-1.20)
Sidechain outliers	187428	1226 (1.20-1.20)
RSRZ outliers	180081	1214 (1.20-1.20)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	219	

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
4	ACT	A	405	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2154 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 Cyan fluorescent chromoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	22	0
			1810	1177	289	335	9			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ASN	HIS	engineered mutation	UNP Q9U6Y3
A	44	ILE	LEU	engineered mutation	UNP Q9U6Y3
A	62	THR	SER	engineered mutation	UNP Q9U6Y3
A	63	THR	ASN	engineered mutation	UNP Q9U6Y3
A	66	PIA	GLN	chromophore	UNP Q9U6Y3
A	66	PIA	TYR	chromophore	UNP Q9U6Y3
A	66	PIA	GLY	chromophore	UNP Q9U6Y3
A	72	PHE	LEU	engineered mutation	UNP Q9U6Y3
A	80	PRO	ALA	engineered mutation	UNP Q9U6Y3
A	81	ASN	ASP	engineered mutation	UNP Q9U6Y3
A	123	HIS	ARG	engineered mutation	UNP Q9U6Y3
A	124	LEU	PHE	engineered mutation	UNP Q9U6Y3
A	125	LYS	ASP	engineered mutation	UNP Q9U6Y3
A	127	GLU	MET	engineered mutation	UNP Q9U6Y3
A	141	THR	LEU	engineered mutation	UNP Q9U6Y3
A	142	GLY	LYS	engineered mutation	UNP Q9U6Y3
A	144	ASP	GLU	engineered mutation	UNP Q9U6Y3
A	145	ALA	PRO	engineered mutation	UNP Q9U6Y3
A	149	ARG	ILE	engineered mutation	UNP Q9U6Y3
A	158	LYS	VAL	engineered mutation	UNP Q9U6Y3
A	161	VAL	ILE	engineered mutation	UNP Q9U6Y3
A	162	LYS	SER	engineered mutation	UNP Q9U6Y3
A	164	LYS	SER	engineered mutation	UNP Q9U6Y3
A	173	HIS	TYR	engineered mutation	UNP Q9U6Y3
A	175	VAL	CYS	engineered mutation	UNP Q9U6Y3
A	179	THR	SER	engineered mutation	UNP Q9U6Y3
A	182	ARG	LYS	engineered mutation	UNP Q9U6Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	186	ALA	VAL	engineered mutation	UNP Q9U6Y3
A	213	VAL	LEU	engineered mutation	UNP Q9U6Y3
A	216	SER	ASN	engineered mutation	UNP Q9U6Y3
A	221	ASN	TYR	engineered mutation	UNP Q9U6Y3
A	223	THR	LEU	engineered mutation	UNP Q9U6Y3
A	224	ASP	LEU	engineered mutation	UNP Q9U6Y3
A	225	GLY	PRO	engineered mutation	UNP Q9U6Y3
A	226	MET	SER	engineered mutation	UNP Q9U6Y3

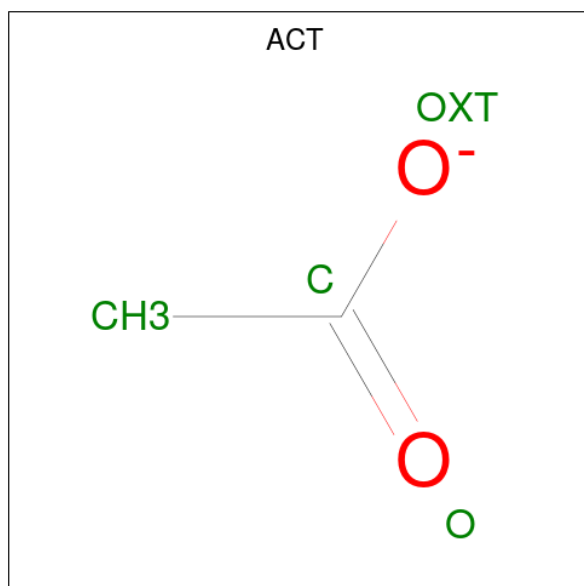
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0

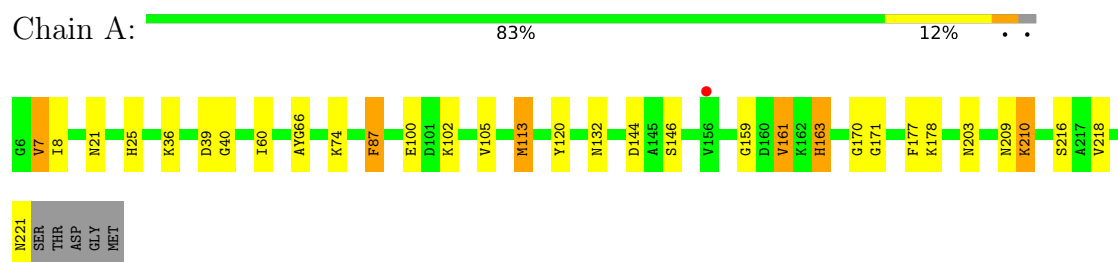
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	336	Total 336	O 336	0	7

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Cyan fluorescent chromoprotein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.83Å 38.02Å 61.12Å 90.00° 90.81° 90.00°	Depositor
Resolution (Å)	10.00 – 1.19 10.00 – 1.19	Depositor EDS
% Data completeness (in resolution range)	93.2 (10.00-1.19) 91.2 (10.00-1.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 1.19Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.137 , 0.206 0.140 , 0.193	Depositor DCC
R_{free} test set	3271 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	14.7	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 66.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2154	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.81% 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, ACT, PIA, CL

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	0.81	0/1887	1.34	12/2546 (0.5%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	ASN	CA-CB-CG	-13.70	98.91	112.60
1	A	87	PHE	CA-CB-CG	-6.97	106.83	113.80
1	A	221	ASN	OD1-CG-ND2	6.44	129.04	122.60
1	A	144	ASP	CA-CB-CG	6.35	118.95	112.60
1	A	170	GLY	O-C-N	-5.83	115.62	122.50
1	A	210	LYS	CB-CG-CD	5.48	123.90	111.30
1	A	100[A]	GLU	N-CA-C	5.33	117.84	111.71
1	A	102	LYS	CA-C-N	-5.20	115.16	120.10
1	A	102	LYS	C-N-CA	-5.20	115.16	120.10
1	A	171	GLY	O-C-N	-5.19	118.34	122.81
1	A	132	ASN	CA-CB-CG	-5.07	107.53	112.60
1	A	170	GLY	CA-C-O	5.06	124.63	119.01

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	1810	0	1779	17	0
2	A	3	0	0	0	0
3	A	1	0	0	0	0
4	A	4	0	3	0	0
5	A	336	0	0	1	0
All	All	2154	0	1782	17	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 5.

All (17) 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:A:74:LYS:HB3	1:A:218[B]:VAL:HG12	1.80	0.63
1:A:87:PHE:CD1	1:A:113[A]:MET:HE3	2.41	0.56
1:A:146[A]:SER:HB3	1:A:163:HIS:CE1	2.43	0.54
1:A:60[A]:ILE:CG2	1:A:105:VAL:HG21	2.39	0.53
1:A:36[B]:LYS:HD3	1:A:39:ASP:OD2	2.12	0.49
1:A:21[B]:ASN:HA	1:A:25:HIS:O	2.12	0.48
1:A:8:ILE:HD13	1:A:113[A]:MET:HE1	1.97	0.47
1:A:40:GLY:O	1:A:216[B]:SER:HA	2.16	0.46
1:A:203:ASN:ND2	5:A:661:HOH:O	2.48	0.45
1:A:178[A]:LYS:HE2	1:A:178[A]:LYS:HB3	1.78	0.44
1:A:161:VAL:HG13	1:A:177:PHE:HB2	2.00	0.43
1:A:209:ASN:C	1:A:210:LYS:HD2	2.43	0.42
1:A:7:VAL:HB	1:A:113[B]:MET:HE1	2.01	0.42
1:A:113[A]:MET:HE2	1:A:113[A]:MET:HB2	1.87	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	228/219 (104%)	224 (98%)	4 (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	194/190 (102%)	188 (97%)	6 (3%)	35	5

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

Mol	Chain	Res	Type
1	A	7	VAL
1	A	113[A]	MET
1	A	113[B]	MET
1	A	120	TYR
1	A	161	VAL
1	A	163	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	128	ASN

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	PIA	A	66	1	20,21,22	1.87	5 (25%)	28,29,31	1.47	3 (10%)

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	PIA	A	66	1	-	1/8/27/28	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	PIA	CG2-CB2	-3.90	1.39	1.46
1	A	66	PIA	CE1-CZ	3.41	1.45	1.39
1	A	66	PIA	CA2-C2	-3.14	1.45	1.48
1	A	66	PIA	OH-CZ	-2.93	1.30	1.37
1	A	66	PIA	C1-N3	2.44	1.41	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	PIA	O2-C2-CA2	4.24	133.73	131.02
1	A	66	PIA	CD2-CE2-CZ	2.57	122.59	119.88
1	A	66	PIA	CB1-CA1-C1	2.12	114.41	111.43

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	66	PIA	C3-CA3-N3-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	ACT	A	405	-	3,3,3	1.83	1 (33%)	3,3,3	1.91	2 (66%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	405	ACT	O-C	2.85	1.34	1.22

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	405	ACT	OXT-C-CH3	2.37	125.00	115.05
4	A	405	ACT	OXT-C-O	-2.29	113.53	122.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 [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	213/219 (97%)	-0.12	1 (0%) 87 89	9, 19, 29, 46	27 (12%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	156	VAL	2.2

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(Å ²)	Q<0.9
1	PIA	A	66	20/21	0.98	0.04	12,14,16,18	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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(Å ²)	Q<0.9
4	ACT	A	405	4/4	0.91	0.10	29,31,31,39	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	A	403	1/1	0.97	0.05	38,38,38,38	1
2	ZN	A	402	1/1	0.99	0.03	27,27,27,27	0
3	CL	A	404	1/1	1.00	0.06	24,24,24,24	0
2	ZN	A	401	1/1	1.00	0.01	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.