

Full wwPDB X-ray Structure Validation Report (i)

Sep 17, 2023 – 11:15 PM EDT

PDB ID	:	4ZI8
Title	:	Structure of mouse clustered PcdhgC3 EC1-3
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Deposited on		
Resolution	:	1.70 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 (i) 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 (1)) were used in the production of this report:

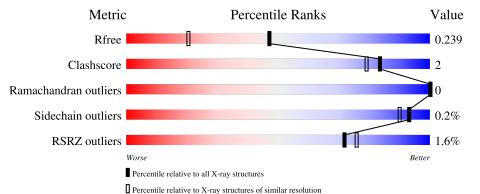
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.70 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	А	334	% 	6% 6%					
1	В	334	^{2%} 91%	6% •					



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5655 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	313	Total	С	Ν	0	S	0	2	0
	I A	313	2455	1537	425	487	6	0		
1	В	202	Total	С	Ν	0	S	0	4	0
1	I B	323	2546	1595	442	504	5	0	4	0

• Molecule 1 is a protein called Protein Pcdhgc3.

Chain	Residue	Modelled	Actual	Actual Comment	
А	-19	MET	-	initiating methionine	UNP Q91XX1
А	-18	GLY	-	expression tag	UNP Q91XX1
А	-17	SER	-	expression tag	UNP Q91XX1
А	-16	ASP	-	expression tag	UNP Q91XX1
А	-15	LYS	-	expression tag	UNP Q91XX1
А	-14	ILE	-	expression tag	UNP Q91XX1
А	-13	HIS	-	expression tag	UNP Q91XX1
A	-12	HIS	-	expression tag	UNP Q91XX1
А	-11	HIS	-	expression tag	UNP Q91XX1
A	-10	HIS	-	expression tag	UNP Q91XX1
А	-9	HIS	-	expression tag	UNP Q91XX1
А	-8	HIS	-	expression tag	UNP Q91XX1
А	-7	GLU	-	expression tag	UNP Q91XX1
А	-6	ASN	-	expression tag	UNP Q91XX1
A	-5	LEU	-	expression tag	UNP Q91XX1
А	-4	TYR	-	expression tag	UNP Q91XX1
А	-3	PHE	-	expression tag	UNP Q91XX1
А	-2	GLN	-	expression tag	UNP Q91XX1
А	-1	GLY	-	expression tag	UNP Q91XX1
В	-19	MET	-	initiating methionine	UNP Q91XX1
В	-18	GLY	-	expression tag	UNP Q91XX1
В	-17	SER	-	expression tag	UNP Q91XX1
В	-16	ASP	-	expression tag	UNP Q91XX1
В	-15	LYS	-	expression tag	UNP Q91XX1
В	-14	ILE	-	expression tag	UNP Q91XX1

There are 38 discrepancies between the modelled and reference sequences:

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Chain	Residue	Modelled	Actual	Comment	Reference
В	-13	HIS	-	expression tag	UNP Q91XX1
В	-12	HIS	-	expression tag	UNP Q91XX1
В	-11	HIS	-	expression tag	UNP Q91XX1
В	-10	HIS	-	expression tag	UNP Q91XX1
В	-9	HIS	-	expression tag	UNP Q91XX1
В	-8	HIS	-	expression tag	UNP Q91XX1
В	-7	GLU	-	expression tag	UNP Q91XX1
В	-6	ASN	-	expression tag	UNP Q91XX1
В	-5	LEU	-	expression tag	UNP Q91XX1
В	-4	TYR	-	expression tag	UNP Q91XX1
В	-3	PHE	-	expression tag	UNP Q91XX1
В	-2	GLN	-	expression tag	UNP Q91XX1
В	-1	GLY	-	expression tag	UNP Q91XX1

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• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

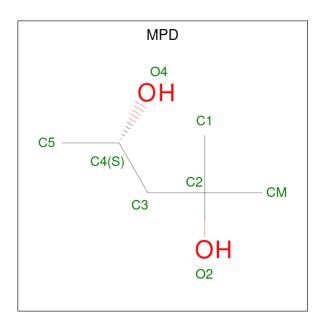
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	9	Total Ca 9 9	0	0
2	В	6	Total Ca 6 6	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

• Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).





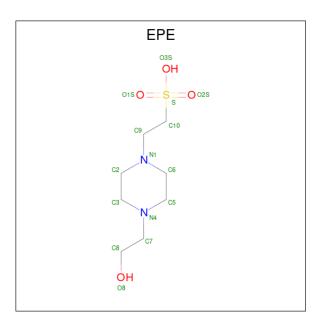
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0

• Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total Na 1 1	0	0

• Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	В	1	Total	С	Ν	0	S	0	0
0	D	L	15	8	2	4	1	0	U

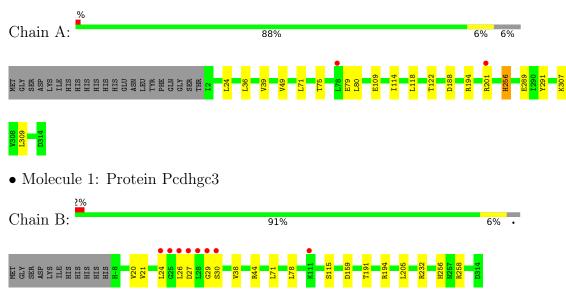
• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	294	Total O 294 294	0	0
7	В	312	Total O 312 312	0	0



3 Residue-property plots (i)

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: Protein Pcdhgc3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	44.12Å 82.29Å 237.69Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 - 1.70	Depositor
Resolution (A)	48.17 - 1.70	EDS
% Data completeness	86.0 (48.17-1.70)	Depositor
(in resolution range)	69.7 (48.17 - 1.70)	EDS
R _{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.51 (at 1.70 \text{\AA})$	Xtriage
Refinement program	PHENIX	Depositor
D D.	0.204 , 0.239	Depositor
R, R_{free}	0.204 , 0.239	DCC
R_{free} test set	1869 reflections (2.37%)	wwPDB-VP
Wilson B-factor $(Å^2)$	19.5	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32 , 37.7	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5655	wwPDB-VP
Average B, all atoms $(Å^2)$	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, CA, NA, EPE, 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	Iol Chain Bond lengths		Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.52	0/2504	0.63	0/3403
1	В	0.55	0/2604	0.63	1/3539~(0.0%)
All	All	0.54	0/5108	0.63	1/6942~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	В	194	ARG	NE-CZ-NH1	-5.47	117.57	120.30

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	А	2455	0	2408	12	0
1	В	2546	0	2499	14	0
2	А	9	0	0	0	0
2	В	6	0	0	0	0
3	А	1	0	0	0	0
4	А	8	0	14	2	0
4	В	8	0	14	1	0
5	В	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes		
6	В	15	0	17	0	0		
7	А	294	0	0	0	0		
7	В	312	0	0	3	1		
All	All	5655	0	4952	24	1		

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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 2.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 4 1	A + 0	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:75:THR:O	1:B:258:ARG:NH2	2.33	0.58
1:B:232[B]:ARG:NH2	7:B:503:HOH:O	2.32	0.53
1:B:115:SER:HA	1:B:205:LEU:HB2	1.89	0.53
1:B:27:ASP:OD1	1:B:30:SER:N	2.42	0.47
1:B:21:VAL:HG13	1:B:26:LEU:HB2	1.97	0.46
4:A:411:MPD:H31	1:B:159:ASP:HB2	1.97	0.45
1:A:109:GLU:OE1	1:A:201:ARG:NH1	2.44	0.44
1:A:291:TYR:CZ	1:A:307:LYS:HD3	2.53	0.44
1:A:289:GLU:HG2	1:A:309:LEU:CD2	2.48	0.43
1:A:114:ILE:HG23	1:A:118:LEU:HD12	2.00	0.43
1:B:38:VAL:HG13	1:B:78:LEU:HD12	2.00	0.43
1:B:256:HIS:ND1	4:B:409:MPD:H31	2.34	0.43
1:A:39:VAL:HB	1:A:79:GLU:HB2	2.00	0.43
1:A:256:HIS:CD2	1:B:71:LEU:HD23	2.53	0.43
1:A:24:LEU:HD11	1:A:80:LEU:HD13	2.02	0.42
1:A:71:LEU:HD23	1:B:256:HIS:CD2	2.54	0.42
1:A:188:ASP:OD2	1:A:194:ARG:HB2	2.19	0.42
1:B:20:VAL:O	1:B:24:LEU:HB2	2.20	0.42
4:A:411:MPD:H12	4:A:411:MPD:H4	1.85	0.41
1:A:36:LEU:HD21	1:A:49:VAL:HG21	2.03	0.41
1:A:118:LEU:HD13	1:A:122:THR:HG21	2.03	0.40
1:B:191:THR:HG23	7:B:679:HOH:O	2.20	0.40
1:B:27:ASP:OD1	1:B:29:GLY:CA	2.70	0.40
1:B:44:ARG:NH1	7:B:508:HOH:O	2.39	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.



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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:645:HOH:O	7:B:666:HOH:O[4_466]	2.08	0.12

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	Percentile	es
1	А	313/334~(94%)	313~(100%)	0	0	100 100)
1	В	325/334~(97%)	323~(99%)	2(1%)	0	100 100)
All	All	638/668~(96%)	636 (100%)	2~(0%)	0	100 100)

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	269/286~(94%)	268 (100%)	1 (0%)	91 87
1	В	280/286~(98%)	280 (100%)	0	100 100
All	All	549/572~(96%)	548 (100%)	1 (0%)	93 90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	256	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are



no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 17 are monoatomic - leaving 3 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	Turne	Гуре Chain		Link	Bo	Bond lengths			Bond angles		
	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
4	MPD	А	411	-	7,7,7	0.29	0	$9,\!10,\!10$	0.40	0	
4	MPD	В	409	-	7,7,7	0.25	0	9,10,10	0.43	0	
6	EPE	В	408	-	$15,\!15,\!15$	0.79	1 (6%)	18,20,20	1.70	4 (22%)	

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	MPD	А	411	-	-	0/5/5/5	-
4	MPD	В	409	-	-	3/5/5/5	-
6	EPE	В	408	-	-	6/9/19/19	0/1/1/1



All ((1)	bond	length	outliers	are	listed	below:
\		10 0 11 01		0.0101010	002.0	110000	0010111

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	В	408	EPE	C10-S	2.71	1.81	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
6	В	408	EPE	C5-N4-C3	4.23	118.36	108.83
6	В	408	EPE	C7-N4-C3	3.22	119.47	111.23
6	В	408	EPE	C7-N4-C5	2.80	118.40	111.23
6	В	408	EPE	O3S-S-C10	2.22	109.35	105.77

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	В	408	EPE	C9-C10-S-O2S
6	В	408	EPE	C9-C10-S-O3S
6	В	408	EPE	C10-C9-N1-C2
6	В	408	EPE	C10-C9-N1-C6
4	В	409	MPD	C2-C3-C4-C5
6	В	408	EPE	C9-C10-S-O1S
4	В	409	MPD	CM-C2-C3-C4
6	В	408	EPE	N4-C7-C8-O8
4	В	409	MPD	C2-C3-C4-O4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	411	MPD	2	0
4	В	409	MPD	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, 95^{th} 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	$\langle RSRZ \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	А	313/334~(93%)	-0.26	2 (0%) 89 91	19, 35, 55, 74	0
1	В	323/334~(96%)	-0.14	8 (2%) 57 61	18, 31, 51, 92	0
All	All	636/668~(95%)	-0.20	10 (1%) 72 76	18, 33, 54, 92	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	28	LEU	3.6
1	В	29	GLY	3.5
1	В	24	LEU	3.5
1	В	27	ASP	3.3
1	В	26	LEU	3.0
1	В	25	GLY	2.6
1	А	201	ARG	2.4
1	А	78	LEU	2.3
1	В	111	LYS	2.1
1	В	30	SER	2.0

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 monosaccharides 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, 95^{th} 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
6	EPE	В	408	15/15	0.78	0.14	47,54,75,79	0
4	MPD	В	409	8/8	0.82	0.17	71,74,76,78	0
4	MPD	А	411	8/8	0.84	0.16	61,62,68,69	0
3	CL	А	410	1/1	0.90	0.09	$55,\!55,\!55,\!55$	0
2	CA	А	402	1/1	0.96	0.03	37,37,37,37	0
2	CA	А	403	1/1	0.97	0.03	38, 38, 38, 38	0
2	CA	В	404	1/1	0.97	0.05	32,32,32,32	0
2	CA	В	405	1/1	0.97	0.08	29,29,29,29	0
2	CA	В	406	1/1	0.97	0.05	28,28,28,28	0
2	CA	А	407	1/1	0.98	0.08	30,30,30,30	0
2	CA	А	401	1/1	0.98	0.03	32,32,32,32	0
2	CA	В	403	1/1	0.99	0.08	20,20,20,20	0
2	CA	А	405	1/1	0.99	0.08	21,21,21,21	0
2	CA	А	406	1/1	0.99	0.06	20,20,20,20	0
2	CA	А	404	1/1	0.99	0.07	20,20,20,20	0
2	CA	А	408	1/1	0.99	0.05	31,31,31,31	0
2	CA	А	409	1/1	0.99	0.06	30,30,30,30	0
2	CA	В	401	1/1	0.99	0.10	18,18,18,18	0
5	NA	В	407	1/1	0.99	0.11	18,18,18,18	0
2	CA	В	402	1/1	0.99	0.09	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.

