



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 30, 2026 – 10:53 AM UTC

PDB ID : 8AFV / pdb_00008afv
Title : DaArgC3 - Engineered Formyl Phosphate Reductase with 3 substitutions (S178V, G182V, L233I)
Authors : Pfister, P.; Nattermann, M.; Zarzycki, J.; Erb, T.J.
Deposited on : 2022-07-18
Resolution : 2.19 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

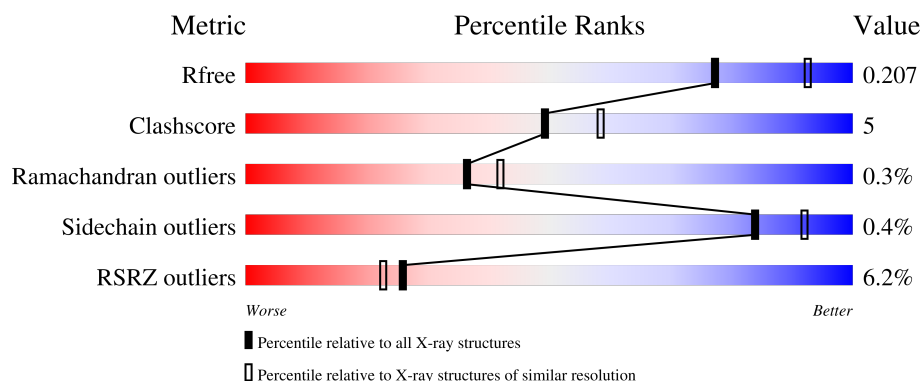
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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	342	0% 88% 9% .
1	B	342	2% 87% 8% 5%
1	C	342	5% 80% 13% 6%
1	D	342	16% 76% 15% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10561 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 N-acetyl-gamma-glutamyl-phosphate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2594	1666	422	492	14			
1	B	325	Total	C	N	O	S	0	0	0
			2514	1612	410	478	14			
1	C	321	Total	C	N	O	S	0	0	0
			2481	1593	404	470	14			
1	D	316	Total	C	N	O	S	0	0	0
			2434	1562	395	463	14			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	178	VAL	SER	engineered mutation	UNP D4H3H4
A	182	VAL	GLY	engineered mutation	UNP D4H3H4
A	233	ILE	LEU	engineered mutation	UNP D4H3H4
A	335	LEU	-	expression tag	UNP D4H3H4
A	336	GLU	-	expression tag	UNP D4H3H4
A	337	HIS	-	expression tag	UNP D4H3H4
A	338	HIS	-	expression tag	UNP D4H3H4
A	339	HIS	-	expression tag	UNP D4H3H4
A	340	HIS	-	expression tag	UNP D4H3H4
A	341	HIS	-	expression tag	UNP D4H3H4
A	342	HIS	-	expression tag	UNP D4H3H4
B	178	VAL	SER	engineered mutation	UNP D4H3H4
B	182	VAL	GLY	engineered mutation	UNP D4H3H4
B	233	ILE	LEU	engineered mutation	UNP D4H3H4
B	335	LEU	-	expression tag	UNP D4H3H4
B	336	GLU	-	expression tag	UNP D4H3H4
B	337	HIS	-	expression tag	UNP D4H3H4
B	338	HIS	-	expression tag	UNP D4H3H4
B	339	HIS	-	expression tag	UNP D4H3H4
B	340	HIS	-	expression tag	UNP D4H3H4
B	341	HIS	-	expression tag	UNP D4H3H4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	342	HIS	-	expression tag	UNP D4H3H4
C	178	VAL	SER	engineered mutation	UNP D4H3H4
C	182	VAL	GLY	engineered mutation	UNP D4H3H4
C	233	ILE	LEU	engineered mutation	UNP D4H3H4
C	335	LEU	-	expression tag	UNP D4H3H4
C	336	GLU	-	expression tag	UNP D4H3H4
C	337	HIS	-	expression tag	UNP D4H3H4
C	338	HIS	-	expression tag	UNP D4H3H4
C	339	HIS	-	expression tag	UNP D4H3H4
C	340	HIS	-	expression tag	UNP D4H3H4
C	341	HIS	-	expression tag	UNP D4H3H4
C	342	HIS	-	expression tag	UNP D4H3H4
D	178	VAL	SER	engineered mutation	UNP D4H3H4
D	182	VAL	GLY	engineered mutation	UNP D4H3H4
D	233	ILE	LEU	engineered mutation	UNP D4H3H4
D	335	LEU	-	expression tag	UNP D4H3H4
D	336	GLU	-	expression tag	UNP D4H3H4
D	337	HIS	-	expression tag	UNP D4H3H4
D	338	HIS	-	expression tag	UNP D4H3H4
D	339	HIS	-	expression tag	UNP D4H3H4
D	340	HIS	-	expression tag	UNP D4H3H4
D	341	HIS	-	expression tag	UNP D4H3H4
D	342	HIS	-	expression tag	UNP D4H3H4

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Na 2 2	0	0
2	B	1	Total Na 1 1	0	0
2	C	1	Total Na 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	159	Total O 159 159	0	0
3	B	171	Total O 171 171	0	0

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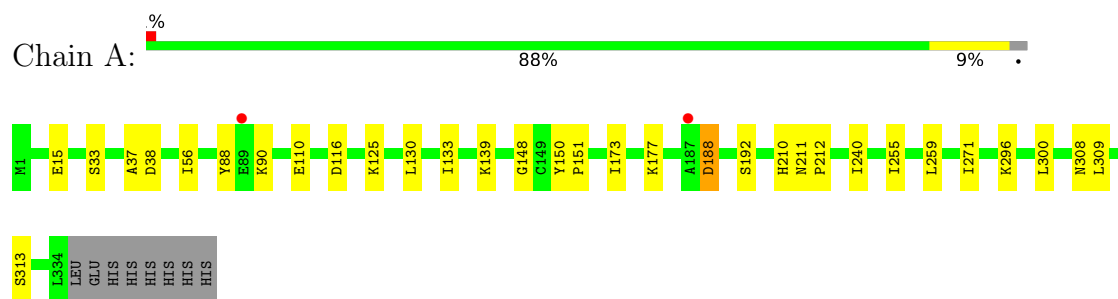
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	112	Total 112	O 112	0	0
3	D	92	Total 92	O 92	0	0

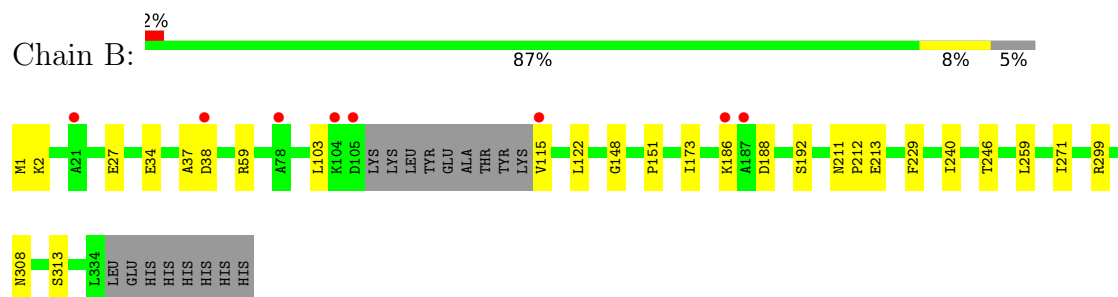
3 Residue-property plots [i](#)

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.

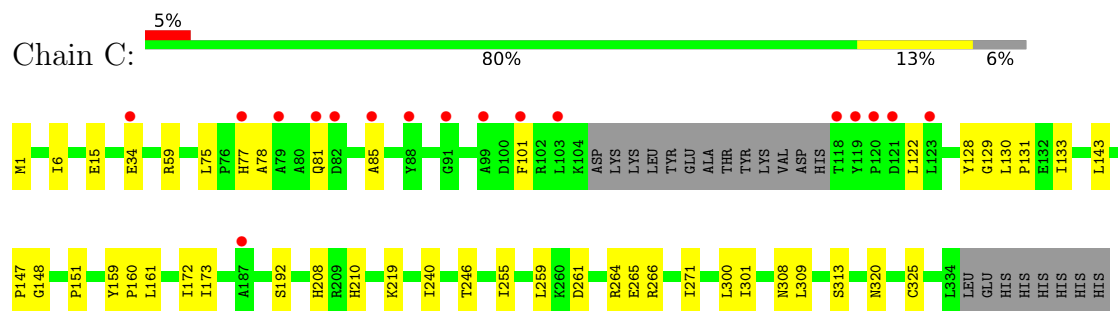
- Molecule 1: N-acetyl-gamma-glutamyl-phosphate reductase



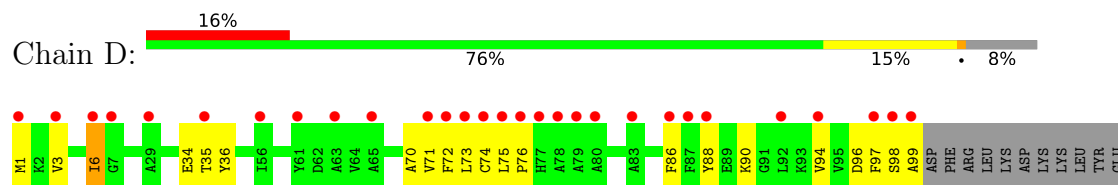
- Molecule 1: N-acetyl-gamma-glutamyl-phosphate reductase

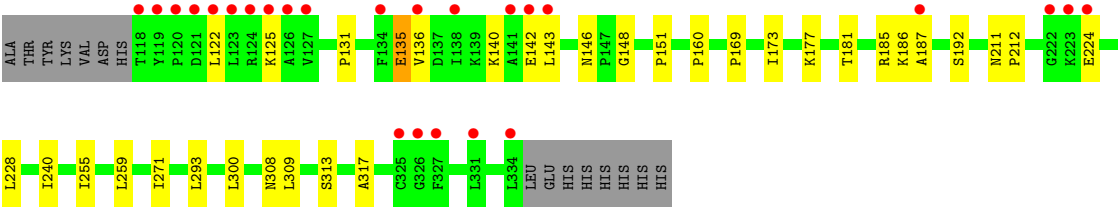


- Molecule 1: N-acetyl-gamma-glutamyl-phosphate reductase



- Molecule 1: N-acetyl-gamma-glutamyl-phosphate reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.88Å 109.55Å 133.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.36 – 2.19 42.36 – 2.19	Depositor EDS
% Data completeness (in resolution range)	96.4 (42.36-2.19) 96.3 (42.36-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.37 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.189 , 0.207 0.188 , 0.207	Depositor DCC
R_{free} test set	1998 reflections (2.88%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.2	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	0.95	EDS
Total number of atoms	10561	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.23	0/2648	0.38	0/3593
1	B	0.26	0/2565	0.39	0/3481
1	C	0.28	0/2531	0.45	0/3434
1	D	0.40	0/2483	0.57	1/3371 (0.0%)
All	All	0.30	0/10227	0.45	1/13879 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	142	GLU	N-CA-C	-5.08	107.05	114.12

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	A	2594	0	2600	20	0
1	B	2514	0	2513	17	0
1	C	2481	0	2489	29	0
1	D	2434	0	2439	48	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
3	A	159	0	0	3	1
3	B	171	0	0	4	0
3	C	112	0	0	0	0
3	D	92	0	0	1	0
All	All	10561	0	10041	109	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 5.

The worst 5 of 109 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:D:125:LYS:HG3	1:D:143:LEU:HD23	1.74	0.69
1:B:2:LYS:NZ	3:B:501:HOH:O	2.24	0.67
1:A:173:ILE:HD12	1:B:173:ILE:HD12	1.77	0.67
1:A:192:SER:HA	1:D:192:SER:HA	1.80	0.64
1:C:255:ILE:HD13	1:C:300:LEU:HD22	1.81	0.63

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)
3:A:502:HOH:O	3:A:583:HOH:O[4_455]	2.11	0.09

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	332/342 (97%)	323 (97%)	8 (2%)	1 (0%)	36 42
1	B	321/342 (94%)	312 (97%)	8 (2%)	1 (0%)	36 42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	317/342 (93%)	303 (96%)	13 (4%)	1 (0%)	36	42
1	D	312/342 (91%)	296 (95%)	15 (5%)	1 (0%)	36	42
All	All	1282/1368 (94%)	1234 (96%)	44 (3%)	4 (0%)	36	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	313	SER
1	D	313	SER
1	A	313	SER
1	B	313	SER

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	282/290 (97%)	281 (100%)	1 (0%)	84	92
1	B	274/290 (94%)	273 (100%)	1 (0%)	84	92
1	C	270/290 (93%)	270 (100%)	0	100	100
1	D	265/290 (91%)	263 (99%)	2 (1%)	73	85
All	All	1091/1160 (94%)	1087 (100%)	4 (0%)	84	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	ASP
1	B	115	VAL
1	D	6	ILE
1	D	135	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	211	ASN
1	A	320	ASN
1	B	211	ASN
1	C	211	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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.

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 [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	334/342 (97%)	-0.12	2 (0%) 85 83	18, 28, 45, 72	0
1	B	325/342 (95%)	0.09	8 (2%) 58 55	18, 32, 53, 107	0
1	C	321/342 (93%)	0.33	17 (5%) 32 29	20, 38, 73, 126	0
1	D	316/342 (92%)	0.84	54 (17%) 4 3	22, 45, 82, 127	0
All	All	1296/1368 (94%)	0.28	81 (6%) 26 23	18, 35, 67, 127	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	115	VAL	6.3
1	C	187	ALA	5.6
1	D	122	LEU	5.0
1	D	97	PHE	4.6
1	C	119	TYR	4.4

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 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($\text{\AA}^2$)	Q<0.9
2	NA	B	401	1/1	0.92	0.10	51,51,51,51	0
2	NA	C	401	1/1	0.93	0.07	24,24,24,24	0
2	NA	A	401	1/1	0.97	0.10	25,25,25,25	0
2	NA	A	402	1/1	0.98	0.08	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.