



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 03:17 PM UTC

PDB ID : 2O0R / pdb_00002o0r
Title : The three-dimensional structure of N-Succinyldiaminopimelate aminotransferase from Mycobacterium tuberculosis
Authors : Weyand, S.; Kefala, G.; Weiss, M.S.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2006-11-28
Resolution : 2.00 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
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

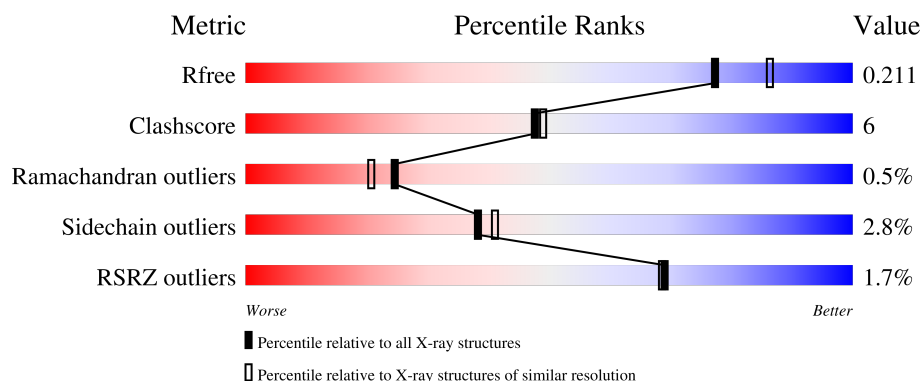
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

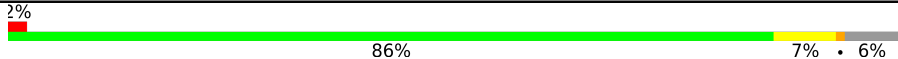
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	411	
1	B	411	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6319 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 Rv0858c (N-Succinyldiaminopimelate aminotransferase).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	P	S	0	5	0
			2931	1856	517	545	1	12			
1	B	384	Total	C	N	O	P	S	0	5	0
			2916	1848	507	548	1	12			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP O53870
A	1	ALA	-	cloning artifact	UNP O53870
A	232	LLP	LYS	modified residue	UNP O53870
A	398	GLY	-	cloning artifact	UNP O53870
A	399	VAL	-	cloning artifact	UNP O53870
A	400	PRO	-	cloning artifact	UNP O53870
A	401	ARG	-	cloning artifact	UNP O53870
A	402	GLY	-	cloning artifact	UNP O53870
A	403	LEU	-	cloning artifact	UNP O53870
A	404	GLU	-	cloning artifact	UNP O53870
A	405	HIS	-	expression tag	UNP O53870
A	406	HIS	-	expression tag	UNP O53870
A	407	HIS	-	expression tag	UNP O53870
A	408	HIS	-	expression tag	UNP O53870
A	409	HIS	-	expression tag	UNP O53870
A	410	HIS	-	expression tag	UNP O53870
B	0	MET	-	initiating methionine	UNP O53870
B	1	ALA	-	cloning artifact	UNP O53870
B	232	LLP	LYS	modified residue	UNP O53870
B	398	GLY	-	cloning artifact	UNP O53870
B	399	VAL	-	cloning artifact	UNP O53870
B	400	PRO	-	cloning artifact	UNP O53870
B	401	ARG	-	cloning artifact	UNP O53870
B	402	GLY	-	cloning artifact	UNP O53870
B	403	LEU	-	cloning artifact	UNP O53870

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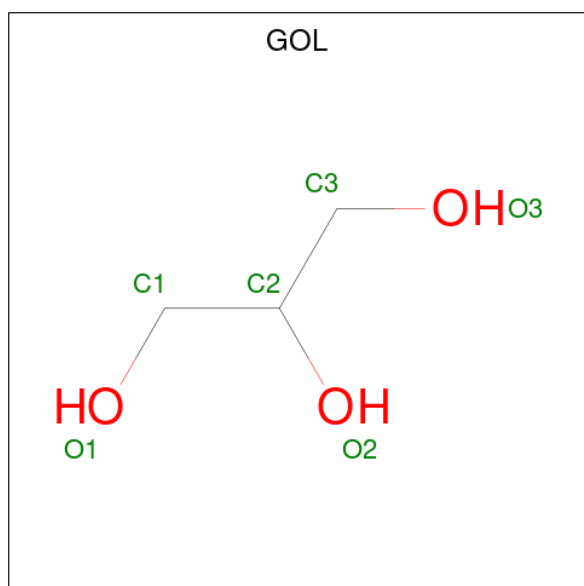
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Chain	Residue	Modelled	Actual	Comment	Reference
B	404	GLU	-	cloning artifact	UNP O53870
B	405	HIS	-	expression tag	UNP O53870
B	406	HIS	-	expression tag	UNP O53870
B	407	HIS	-	expression tag	UNP O53870
B	408	HIS	-	expression tag	UNP O53870
B	409	HIS	-	expression tag	UNP O53870
B	410	HIS	-	expression tag	UNP O53870

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

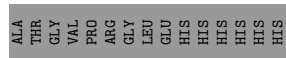
- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Na 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	225	Total 225	O 225	0	0
5	B	232	Total 232	O 232	0	0

- Molecule 1: Rv0858c (N-Succinyldiaminopimelate aminotransferase)



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	54.34Å 56.13Å 247.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.00) 99.7 (20.00-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.164 , 0.213 0.167 , 0.211	Depositor DCC
R_{free} test set	1080 reflections (2.06%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6319	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: CL, GOL, LLP, 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	0.95	0/2992	1.01	6/4084 (0.1%)
1	B	1.01	0/2977	1.04	4/4066 (0.1%)
All	All	0.98	0/5969	1.03	10/8150 (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	B	0	3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	GLN	CA-C-N	-6.85	112.64	119.56
1	A	270	GLN	C-N-CA	-6.85	112.64	119.56
1	B	24	ILE	N-CA-C	-6.16	103.98	113.16
1	B	141	ASP	O-C-N	-5.41	118.11	123.62
1	B	246	GLY	CA-C-N	5.30	125.22	119.76

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	141	ASP	Peptide
1	B	23	ARG	Peptide
1	B	364	ASP	Peptide

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	2931	0	2896	29	0
1	B	2916	0	2871	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	1	0
4	B	1	0	0	0	0
5	A	225	0	0	5	0
5	B	232	0	0	2	0
All	All	6319	0	5783	65	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 6.

The worst 5 of 65 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:B:23:ARG:HH11	1:B:23:ARG:HG2	1.34	0.92
1:A:292:ARG:HD3	5:A:906:HOH:O	1.79	0.82
1:B:120:ASP:OD2	3:B:702:GOL:H31	1.82	0.79
1:A:379:ASP:HB2	5:A:842:HOH:O	1.85	0.77
1:B:197[B]:THR:HG21	5:B:733:HOH:O	1.84	0.76

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	385/411 (94%)	373 (97%)	10 (3%)	2 (0%)	24	21
1	B	384/411 (93%)	372 (97%)	10 (3%)	2 (0%)	24	21
All	All	769/822 (94%)	745 (97%)	20 (3%)	4 (0%)	24	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	365	VAL
1	A	263	TYR
1	B	263	TYR
1	A	354	PRO

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	295/309 (96%)	288 (98%)	7 (2%)	43	47
1	B	294/309 (95%)	283 (96%)	11 (4%)	30	30
All	All	589/618 (95%)	571 (97%)	18 (3%)	38	37

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	316	TYR
1	B	381	LEU
1	B	365	VAL
1	B	23	ARG
1	B	292	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	73	GLN
1	B	166	ASN

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Mol	Chain	Res	Type
1	B	235	ASN
1	A	367	ASN
1	A	73	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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	LLP	B	232	1	23,24,25	1.62	4 (17%)	25,32,34	2.22	8 (32%)
1	LLP	A	232	1	23,24,25	1.70	2 (8%)	25,32,34	1.87	7 (28%)

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	LLP	B	232	1	-	5/16/17/19	0/1/1/1
1	LLP	A	232	1	-	6/16/17/19	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	LLP	O3-C3	-5.57	1.24	1.36
1	B	232	LLP	O3-C3	-4.38	1.26	1.36
1	B	232	LLP	C2-N1	3.76	1.40	1.33
1	B	232	LLP	C6-N1	2.68	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	LLP	C6-N1	2.27	1.39	1.34

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	232	LLP	OP4-C5'-C5	5.91	120.43	109.36
1	B	232	LLP	C3-C4-C5	4.44	121.84	118.28
1	A	232	LLP	C4-C4'-NZ	-4.39	103.77	124.04
1	B	232	LLP	C4-C4'-NZ	-3.69	107.02	124.04
1	A	232	LLP	C3-C4-C5	3.63	121.19	118.28

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	232	LLP	CG-CD-CE-NZ
1	A	232	LLP	C4-C4'-NZ-CE
1	B	232	LLP	C4-C4'-NZ-CE
1	B	232	LLP	C3-C4-C4'-NZ
1	B	232	LLP	CA-CB-CG-CD

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	232	LLP	1	0
1	A	232	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 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	$\# Z > 2$
3	GOL	A	701	-	5,5,5	0.46	0	5,5,5	0.68	0
3	GOL	B	702	-	5,5,5	0.36	0	5,5,5	0.56	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	GOL	A	701	-	-	2/4/4/4	-
3	GOL	B	702	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	GOL	C1-C2-C3-O3
3	A	701	GOL	O2-C2-C3-O3
3	B	702	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	702	GOL	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	384/411 (93%)	-0.36	8 (2%) 63 63	7, 14, 31, 60	5 (1%)
1	B	383/411 (93%)	-0.33	5 (1%) 75 74	7, 14, 32, 51	5 (1%)
All	All	767/822 (93%)	-0.34	13 (1%) 69 68	7, 14, 33, 60	10 (1%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	365	VAL	3.7
1	A	1	ALA	3.3
1	B	355	ALA	2.8
1	A	15	ALA	2.7
1	B	23	ARG	2.7

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	LLP	B	232	24/25	0.97	0.06	11,14,19,24	0
1	LLP	A	232	24/25	0.98	0.05	9,14,23,28	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
3	GOL	A	701	6/6	0.74	0.13	30,36,41,44	0
3	GOL	B	702	6/6	0.84	0.12	33,37,39,46	0
4	NA	B	603	1/1	0.87	0.08	32,32,32,32	0
2	CL	A	601	1/1	0.98	0.15	11,11,11,11	0
2	CL	B	602	1/1	0.99	0.15	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.