



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:56 PM UTC

PDB ID : 5R5B / pdb_00005r5b
Title : PanDDA analysis group deposition – Crystal Structure of human NUDT22 in complex with N13725a
Authors : Diaz-Saez, L.; Talon, R.; Krojer, T.; Burgess-Brown, N.A.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; von Delft, F.; Huber, K.V.M.
Deposited on : 2020-02-28
Resolution : 1.53 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

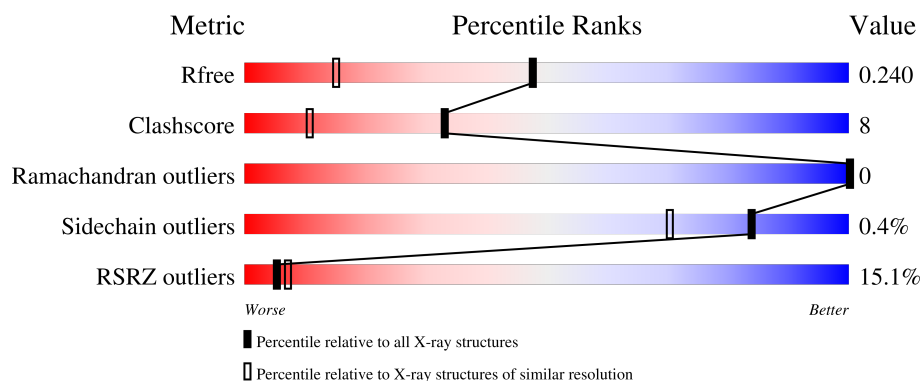
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 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	1003 (1.54-1.54)
Clashscore	190562	1025 (1.54-1.54)
Ramachandran outliers	187476	1007 (1.54-1.54)
Sidechain outliers	187428	1007 (1.54-1.54)
RSRZ outliers	180081	1002 (1.54-1.54)

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	304	

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	DMS	A	403	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DMS	A	405	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2451 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.

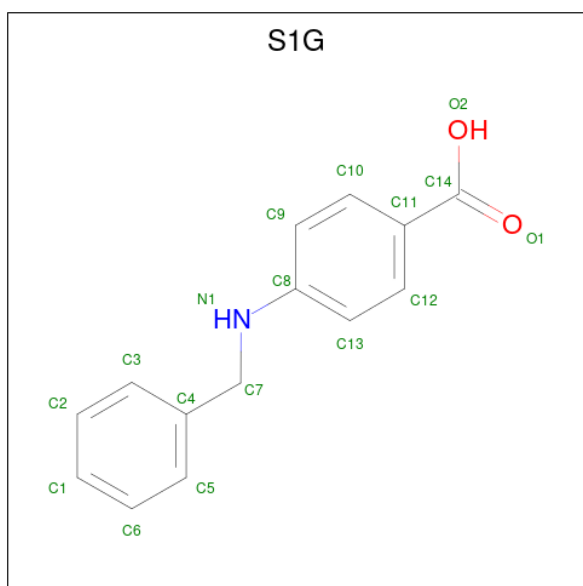
- Molecule 1 is a protein called Uridine diphosphate glucose pyrophosphatase NUDT22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	7	0
			2253	1425	391	432	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q9BRQ3
A	260	ARG	GLN	conflict	UNP Q9BRQ3
A	263	PRO	LEU	conflict	UNP Q9BRQ3

- Molecule 2 is 4-[(phenylmethyl)amino]benzoic acid (CCD ID: S1G) (formula: C₁₄H₁₃NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			17	14	1	2		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



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

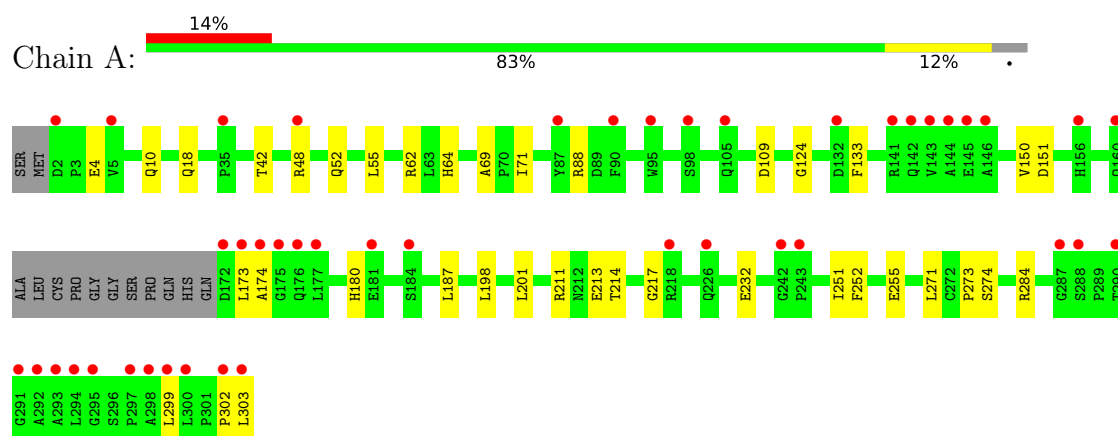
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	165	Total	O	0	0
			165	165		

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: Uridine diphosphate glucose pyrophosphatase NUDT22



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.62Å 52.27Å 101.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.85 – 1.53 50.85 – 1.53	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.85-1.53) 99.8 (50.85-1.53)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.53Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.188 , 0.220 0.207 , 0.240	Depositor DCC
R_{free} test set	2187 reflections (5.37%)	wwPDB-VP
Wilson B-factor (Å ²)	21.1	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.031 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2451	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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: S1G, DMS

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	1.22	1/2307 (0.0%)	1.21	3/3152 (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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	251	ILE	C-O	5.94	1.30	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	ALA	CA-C-N	7.10	128.01	119.99
1	A	174	ALA	C-N-CA	7.10	128.01	119.99
1	A	252	PHE	CA-CB-CG	5.23	119.03	113.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	173	LEU	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	2253	0	2193	34	0
2	A	17	0	0	0	0
3	A	16	0	24	10	0
4	A	165	0	0	13	4
All	All	2451	0	2217	35	4

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 8.

All (35) 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:88:ARG:CD	4:A:501:HOH:O	1.66	1.08
1:A:88:ARG:HD3	4:A:501:HOH:O	1.39	0.99
1:A:255:GLU:OE1	4:A:502:HOH:O	1.93	0.85
1:A:187:LEU:HD13	3:A:403:DMS:H11	1.69	0.74
1:A:4:GLU:HB2	1:A:214:THR:HG23	1.71	0.72
1:A:274:SER:OG	3:A:405:DMS:O	2.08	0.68
1:A:109:ASP:O	3:A:404:DMS:H13	1.94	0.66
1:A:211:ARG:HD3	1:A:213:GLU:OE2	1.96	0.66
1:A:88:ARG:CG	4:A:501:HOH:O	2.21	0.65
1:A:42:THR:OG1	1:A:88:ARG:NH2	2.34	0.59
1:A:198:LEU:CD1	3:A:403:DMS:H12	2.33	0.58
3:A:402:DMS:H13	4:A:548:HOH:O	2.03	0.58
1:A:71:ILE:HG23	4:A:503:HOH:O	2.05	0.57
1:A:302:PRO:O	1:A:303:LEU:CB	2.56	0.54
1:A:4:GLU:HG3	1:A:273:PRO:HG3	1.89	0.53
1:A:211:ARG:CD	1:A:213:GLU:OE2	2.56	0.53
1:A:274:SER:HB2	3:A:405:DMS:H13	1.89	0.53
1:A:4:GLU:HB2	1:A:214:THR:CG2	2.38	0.53
1:A:62:ARG:NH1	4:A:507:HOH:O	2.32	0.52
1:A:69:ALA:O	4:A:503:HOH:O	2.18	0.52
1:A:88:ARG:HG2	4:A:501:HOH:O	2.02	0.52
1:A:198:LEU:HD12	3:A:403:DMS:H12	1.94	0.50
1:A:10:GLN:OE1	1:A:284:ARG:NE	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ILE:N	4:A:503:HOH:O	2.45	0.49
1:A:124:GLY:HA3	3:A:405:DMS:H11	1.95	0.48
1:A:201:LEU:HB2	3:A:403:DMS:H13	1.95	0.48
1:A:18:GLN:HE22	1:A:180:HIS:HD2	1.60	0.47
1:A:64:HIS:HA	4:A:507:HOH:O	2.16	0.47
1:A:299:LEU:N	4:A:509:HOH:O	2.36	0.46
1:A:150:VAL:HB	1:A:271:LEU:HD23	1.99	0.44
1:A:211:ARG:HG3	1:A:217:GLY:HA2	2.00	0.43
1:A:52:GLN:NE2	4:A:512:HOH:O	2.47	0.42
1:A:151:ASP:OD1	3:A:405:DMS:S	2.76	0.42
1:A:48:ARG:HG3	1:A:55:LEU:HD12	2.02	0.42
1:A:133:PHE:CE2	1:A:255:GLU:HG3	2.55	0.41

All (4) 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)
4:A:516:HOH:O	4:A:566:HOH:O[3_655]	1.31	0.89
4:A:546:HOH:O	4:A:651:HOH:O[4_565]	1.81	0.39
4:A:509:HOH:O	4:A:583:HOH:O[3_645]	1.86	0.34
4:A:524:HOH:O	4:A:651:HOH:O[4_565]	2.17	0.03

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	293/304 (96%)	287 (98%)	6 (2%)	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 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	236/244 (97%)	235 (100%)	1 (0%)	84	70

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

Mol	Chain	Res	Type
1	A	232	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	GLN
1	A	176	GLN
1	A	180	HIS
1	A	246	HIS
1	A	257	GLN

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](#)

5 ligands 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	$\# Z > 2$
3	DMS	A	404	-	3,3,3	0.26	0	3,3,3	0.34	0
3	DMS	A	403	-	3,3,3	0.26	0	3,3,3	0.21	0
2	S1G	A	401	-	18,18,18	0.50	0	23,23,23	0.56	0
3	DMS	A	405	-	3,3,3	0.25	0	3,3,3	0.16	0
3	DMS	A	402	-	3,3,3	0.21	0	3,3,3	0.31	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
2	S1G	A	401	-	-	0/9/9/9	0/2/2/2

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.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	404	DMS	1	0
3	A	403	DMS	4	0
3	A	405	DMS	4	0
3	A	402	DMS	1	0

5.7 Other polymers

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	291/304 (95%)	1.03	44 (15%) 5 7	5, 23, 37, 53	19 (6%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	VAL	10.2
1	A	95	TRP	9.7
1	A	90	PHE	9.2
1	A	2[A]	ASP	9.0
1	A	87	TYR	8.5
1	A	144	ALA	8.1
1	A	105[A]	GLN	7.7
1	A	226[A]	GLN	7.7
1	A	146	ALA	7.4
1	A	142	GLN	7.4
1	A	132[A]	ASP	7.4
1	A	184[A]	SER	7.2
1	A	141	ARG	6.9
1	A	98[A]	SER	6.8
1	A	156	HIS	6.6
1	A	181[A]	GLU	6.4
1	A	48	ARG	5.6
1	A	218	ARG	5.5
1	A	290	THR	5.3
1	A	145	GLU	5.0
1	A	173	LEU	4.8
1	A	302	PRO	4.4
1	A	174	ALA	4.4
1	A	300	LEU	4.1
1	A	288	SER	4.0
1	A	293	ALA	4.0
1	A	175	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	160	GLN	3.7
1	A	291	GLY	3.6
1	A	172	ASP	3.4
1	A	287	GLY	3.0
1	A	292	ALA	2.9
1	A	243	PRO	2.8
1	A	297	PRO	2.7
1	A	177	LEU	2.6
1	A	303	LEU	2.5
1	A	294	LEU	2.4
1	A	299	LEU	2.4
1	A	295	GLY	2.4
1	A	298	ALA	2.3
1	A	242	GLY	2.3
1	A	5	VAL	2.2
1	A	176	GLN	2.1
1	A	35	PRO	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	DMS	A	402	4/4	0.67	0.23	72,78,79,79	0
3	DMS	A	405	4/4	0.68	0.22	50,56,57,59	0
2	S1G	A	401	17/17	0.81	0.14	18,20,23,23	17
3	DMS	A	404	4/4	0.82	0.18	54,57,58,63	0
3	DMS	A	403	4/4	0.86	0.15	49,58,59,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.