



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2023 – 09:51 AM EDT

PDB ID : 2ZJG
Title : Crystal structural of mouse kynurenine aminotransferase III
Authors : Han, Q.; Cai, T.; Tagle, D.A.; Robinson, H.; Li, J.
Deposited on : 2008-03-07
Resolution : 3.00 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

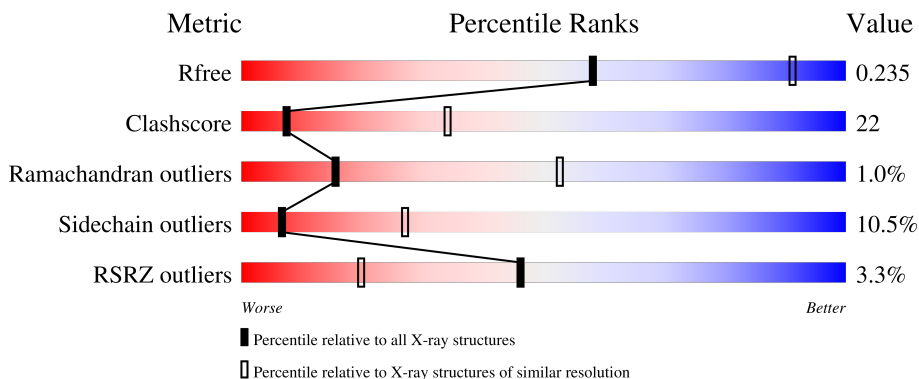
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	410	 2% 62% 31% 6%
1	B	410	 5% 61% 30% 9%

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
2	GOL	A	500	-	-	X	-
2	GOL	A	501	-	-	X	-
2	GOL	B	503	-	X	-	-

2 Entry composition [i](#)

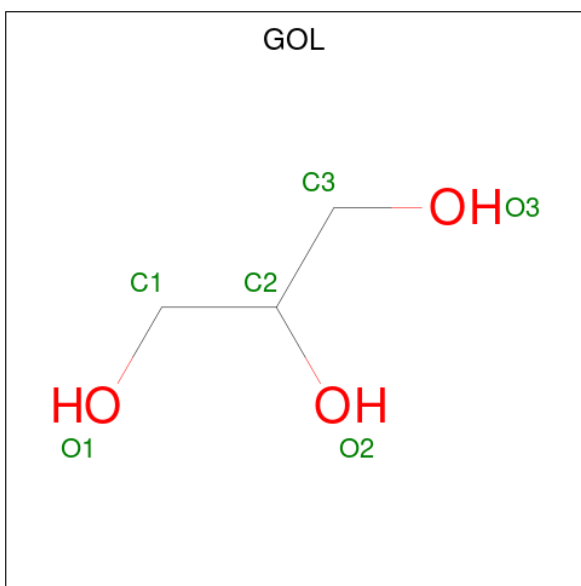
There are 3 unique types of molecules in this entry. The entry contains 6694 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Kynurenine-oxoglutarate transaminase 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	410	Total 3268	C 2108	N 537	O 604	P 1	S 18	0	0	0
1	B	410	Total 3268	C 2108	N 537	O 604	P 1	S 18	0	0	0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	44	Total	O	0	0
			44	44		
3	B	60	Total	O	0	0
			60	60		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.09Å 91.09Å 233.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.58 – 3.00 29.58 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.3 (29.58-3.00) 97.3 (29.58-3.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 3.00Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.222 , 0.233 0.223 , 0.235	Depositor DCC
R_{free} test set	999 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6694	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: LLP, GOL

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	1.15	3/3331 (0.1%)	0.97	7/4525 (0.2%)
1	B	1.13	2/3331 (0.1%)	0.98	9/4525 (0.2%)
All	All	1.14	5/6662 (0.1%)	0.98	16/9050 (0.2%)

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	1	5
1	B	1	9
All	All	2	14

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	102	PHE	CE2-CZ	5.31	1.47	1.37
1	A	314	CYS	CB-SG	-5.29	1.73	1.81
1	A	251	GLU	CG-CD	5.19	1.59	1.51
1	B	110	ALA	CA-CB	-5.17	1.41	1.52
1	A	98	TYR	CD2-CE2	5.06	1.47	1.39

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	48	GLY	N-CA-C	-5.72	98.80	113.10
1	B	335	ASP	CB-CG-OD2	5.70	123.43	118.30
1	B	356	ARG	NE-CZ-NH1	5.61	123.11	120.30
1	B	377	ASP	CB-CG-OD2	5.50	123.25	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	329	ASP	CB-CG-OD2	5.36	123.12	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	256	THR	CB
1	B	286	THR	CB

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	134	GLY	Peptide
1	A	289	LYS	Peptide
1	A	362	GLY	Peptide
1	A	388	MET	Peptide
1	A	52	ASN	Peptide

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	3268	0	3235	154	0
1	B	3268	0	3235	169	0
2	A	24	0	32	9	0
2	B	30	0	40	3	0
3	A	44	0	0	0	0
3	B	60	0	0	8	0
All	All	6694	0	6542	292	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 22.

The worst 5 of 292 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:387:ASP:OD1	1:B:388:MET:HG3	1.12	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:VAL:HG13	1:B:407:LYS:O	1.43	1.19
1:A:88:LYS:HB3	1:A:88:LYS:NZ	1.55	1.12
1:B:334:ASP:HB3	3:B:524:HOH:O	1.48	1.12
1:B:448:ARG:HG3	1:B:448:ARG:HH11	0.97	1.10

There are no symmetry-related clashes.

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	407/410 (99%)	371 (91%)	32 (8%)	4 (1%)	15	53
1	B	407/410 (99%)	369 (91%)	34 (8%)	4 (1%)	15	53
All	All	814/820 (99%)	740 (91%)	66 (8%)	8 (1%)	15	53

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	64	PRO
1	B	65	SER
1	B	312	TYR
1	A	86	LEU
1	A	203	SER

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	357/357 (100%)	315 (88%)	42 (12%)	5	22
1	B	357/357 (100%)	324 (91%)	33 (9%)	9	34
All	All	714/714 (100%)	639 (90%)	75 (10%)	7	27

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	271	GLU
1	B	387	ASP
1	B	286	THR
1	B	360	SER
1	A	271	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	240	HIS
1	B	405	HIS
1	B	359	ASN
1	A	451	ASN
1	B	97	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](#)

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	A	281	1	23,24,25	1.94	4 (17%)	25,32,34	1.82	7 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LLP	B	281	1	23,24,25	2.06	9 (39%)	25,32,34	2.13	6 (24%)

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	A	281	1	-	8/16/17/19	0/1/1/1
1	LLP	B	281	1	-	8/16/17/19	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	281	LLP	O3-C3	-5.74	1.23	1.37
1	B	281	LLP	O3-C3	-4.13	1.27	1.37
1	A	281	LLP	C3-C2	-3.26	1.37	1.40
1	B	281	LLP	P-OP3	-3.20	1.42	1.54
1	B	281	LLP	CE-NZ	3.19	1.53	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	281	LLP	OP4-C5'-C5	4.93	118.75	109.35
1	B	281	LLP	C4-C4'-NZ	-4.86	101.99	124.31
1	B	281	LLP	C4-C3-C2	-4.78	117.23	120.19
1	A	281	LLP	OP4-C5'-C5	4.08	117.13	109.35
1	A	281	LLP	C3-C4-C5	3.55	120.98	118.26

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	281	LLP	C5'-OP4-P-OP2
1	A	281	LLP	C5'-OP4-P-OP3
1	A	281	LLP	O-C-CA-CB
1	B	281	LLP	C5'-OP4-P-OP1
1	B	281	LLP	C5'-OP4-P-OP2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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
2	GOL	A	501	-	5,5,5	0.36	0	5,5,5	1.06	0
2	GOL	B	501	-	5,5,5	0.59	0	5,5,5	0.51	0
2	GOL	B	504	-	5,5,5	0.39	0	5,5,5	0.31	0
2	GOL	B	503	-	5,5,5	0.68	0	5,5,5	2.08	4 (80%)
2	GOL	A	500	-	5,5,5	0.87	0	5,5,5	2.46	4 (80%)
2	GOL	B	500	-	5,5,5	0.53	0	5,5,5	0.85	0
2	GOL	A	503	-	5,5,5	0.48	0	5,5,5	0.69	0
2	GOL	B	502	-	5,5,5	0.46	0	5,5,5	0.50	0
2	GOL	A	502	-	5,5,5	0.52	0	5,5,5	0.25	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	GOL	A	501	-	-	1/4/4/4	-
2	GOL	B	501	-	-	3/4/4/4	-
2	GOL	B	504	-	-	2/4/4/4	-
2	GOL	B	503	-	-	2/4/4/4	-
2	GOL	A	500	-	-	0/4/4/4	-
2	GOL	B	500	-	-	2/4/4/4	-
2	GOL	A	503	-	-	1/4/4/4	-
2	GOL	B	502	-	-	2/4/4/4	-
2	GOL	A	502	-	-	2/4/4/4	-

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	GOL	C3-C2-C1	-3.30	98.87	111.70
2	A	500	GOL	O3-C3-C2	-2.80	96.78	110.20
2	A	500	GOL	O2-C2-C1	-2.71	97.21	109.12
2	B	503	GOL	C3-C2-C1	-2.43	102.26	111.70
2	B	503	GOL	O2-C2-C3	2.28	119.18	109.12

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	502	GOL	O1-C1-C2-O2
2	A	502	GOL	O1-C1-C2-C3
2	B	500	GOL	O1-C1-C2-C3
2	B	502	GOL	O1-C1-C2-C3
2	B	503	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GOL	5	0
2	B	501	GOL	1	0
2	A	500	GOL	5	0
2	B	502	GOL	2	0
2	A	502	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	409/410 (99%)	-0.24	7 (1%) 70 41	12, 25, 56, 76	0
1	B	409/410 (99%)	-0.16	20 (4%) 29 11	13, 28, 66, 80	0
All	All	818/820 (99%)	-0.20	27 (3%) 46 20	12, 26, 58, 80	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	387	ASP	5.1
1	B	386	SER	4.9
1	B	389	ASN	4.3
1	B	384	ASP	4.0
1	B	385	LEU	3.3

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	A	281	24/25	0.96	0.23	17,24,31,32	0
1	LLP	B	281	24/25	0.97	0.22	19,23,29,31	0

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, 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
2	GOL	B	504	6/6	0.48	0.31	88,90,90,91	0
2	GOL	A	503	6/6	0.55	0.36	75,75,77,77	0
2	GOL	B	500	6/6	0.59	0.27	57,66,67,69	0
2	GOL	B	502	6/6	0.75	0.40	49,55,57,58	0
2	GOL	B	501	6/6	0.81	0.27	55,57,58,59	0
2	GOL	A	502	6/6	0.85	0.27	37,48,53,54	0
2	GOL	A	501	6/6	0.87	0.25	43,48,49,51	0
2	GOL	B	503	6/6	0.96	0.29	38,40,46,52	0
2	GOL	A	500	6/6	0.96	0.19	17,20,23,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.