



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 8, 2024 – 12:17 am GMT

PDB ID : 5O5Y
Title : Crystal structure of *Thermococcus litoralis* ADP-dependent glucokinase (GK)
Authors : Herrera-Morande, A.; Castro-Fernandez, V.; Merino, F.; Ramirez-Sarmiento, C.A.; Fernandez, F.J.; Guixe, V.; Vega, M.C.
Deposited on : 2017-06-02
Resolution : 1.92 Å (reported)

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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 : 1.8.4, 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

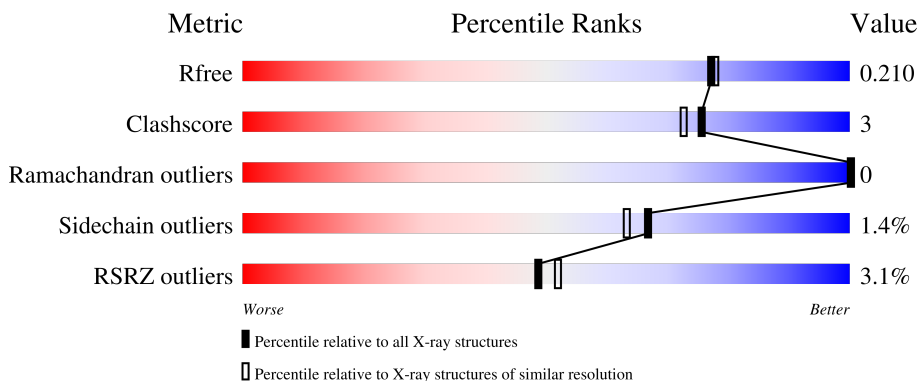
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

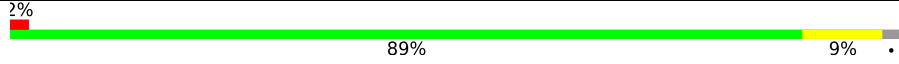
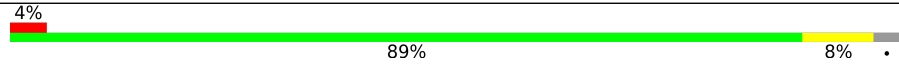
The reported resolution of this entry is 1.92 Å.

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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	464	
1	B	464	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8059 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 ADP-dependent glucokinase,ADP-dependent glucokinase,AD P-dependent glucokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	454	Total	C	N	O	S	0	5	0
			3666	2346	626	686	8			
1	B	449	Total	C	N	O	S	0	2	0
			3606	2306	614	679	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	ALA	LYS	conflict	UNP Q7M537
A	59	LYS	ILE	conflict	UNP Q7M537
A	256	LYS	ARG	conflict	UNP Q7M537
A	363	GLY	-	linker	UNP Q7M537
A	364	GLY	-	linker	UNP Q7M537
A	365	GLY	-	linker	UNP Q7M537
A	399	GLY	-	linker	UNP Q7M537
A	400	GLY	-	linker	UNP Q7M537
A	401	GLY	-	linker	UNP Q7M537
A	402	GLY	-	linker	UNP Q7M537
A	403	GLY	-	linker	UNP Q7M537
B	49	ALA	LYS	conflict	UNP Q7M537
B	59	LYS	ILE	conflict	UNP Q7M537
B	256	LYS	ARG	conflict	UNP Q7M537
B	363	GLY	-	linker	UNP Q7M537
B	364	GLY	-	linker	UNP Q7M537
B	365	GLY	-	linker	UNP Q7M537
B	399	GLY	-	linker	UNP Q7M537
B	400	GLY	-	linker	UNP Q7M537
B	401	GLY	-	linker	UNP Q7M537
B	402	GLY	-	linker	UNP Q7M537
B	403	GLY	-	linker	UNP Q7M537

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



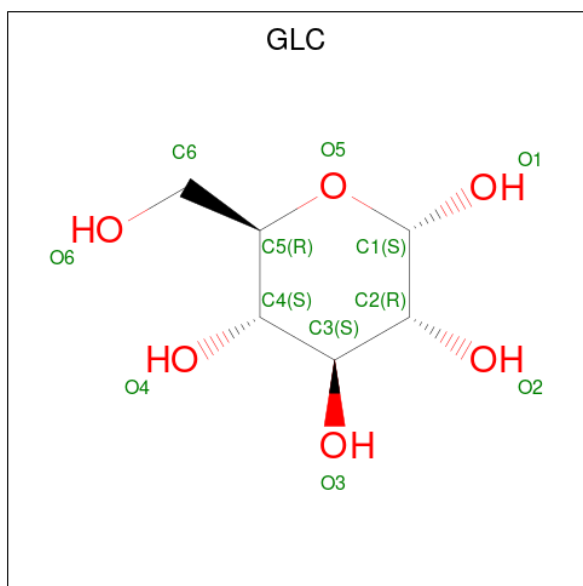
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	10	6	4	0	0

- Molecule 4 is alpha-D-glucopyranose (three-letter code: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	B	1	12	6	6	0	0

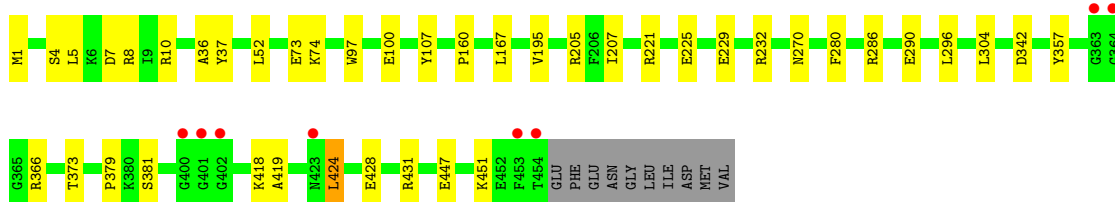
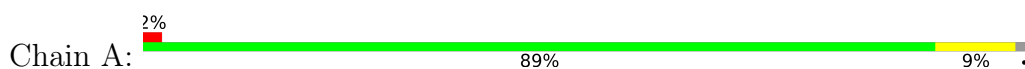
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	390	Total 390	O 390	0	0
5	B	315	Total 315	O 315	0	0

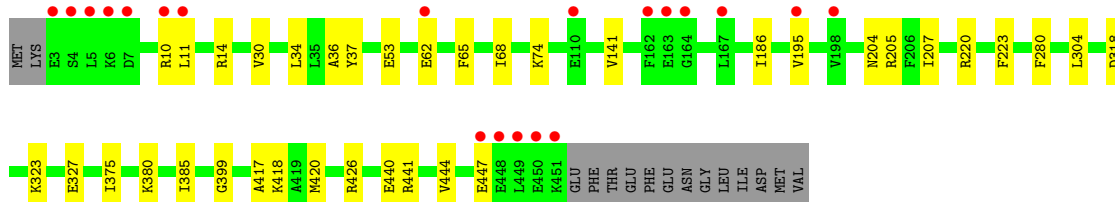
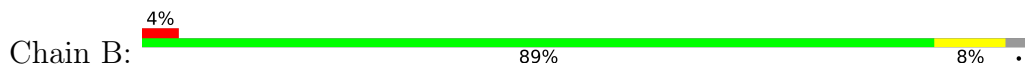
3 Residue-property plots [i](#)

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: ADP-dependent glucokinase,ADP-dependent glucokinase,ADP-dependent glucokinase



- Molecule 1: ADP-dependent glucokinase,ADP-dependent glucokinase,ADP-dependent glucokinase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.64Å 97.61Å 113.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.12 – 1.92 49.12 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.12-1.92) 99.5 (49.12-1.91)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 1.91Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.171 , 0.209 0.171 , 0.210	Depositor DCC
R_{free} test set	4141 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtrriage
Anisotropy	0.763	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.018 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8059	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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: GOL, GLC, PGE

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	0.41	0/3748	0.54	0/5063
1	B	0.39	0/3675	0.53	0/4968
All	All	0.40	0/7423	0.53	0/10031

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3666	0	3688	22	0
1	B	3606	0	3607	23	0
2	A	42	0	56	3	0
2	B	18	0	24	1	0
3	A	10	0	14	1	0
4	B	12	0	12	0	0
5	A	390	0	0	0	0
5	B	315	0	0	4	0
All	All	8059	0	7401	46	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 3.

The worst 5 of 46 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:186:ILE:HG13	1:B:207:ILE:HG12	1.70	0.73
1:A:7:ASP:OD1	1:A:10:ARG:NH2	2.26	0.68
1:A:160:PRO:HB2	1:A:167:LEU:HD11	1.76	0.68
1:B:10:ARG:NH2	1:B:14:ARG:HH12	1.96	0.64
1:B:10:ARG:HH21	1:B:14:ARG:HH12	1.46	0.62

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	457/464 (98%)	445 (97%)	12 (3%)	0	100	100
1	B	449/464 (97%)	440 (98%)	9 (2%)	0	100	100
All	All	906/928 (98%)	885 (98%)	21 (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	390/394 (99%)	385 (99%)	5 (1%)	69	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	382/394 (97%)	376 (98%)	6 (2%)	62	58
All	All	772/788 (98%)	761 (99%)	11 (1%)	67	63

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	280	PHE
1	B	304	LEU
1	B	380	LYS
1	B	318	ASP
1	A	424	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	423	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	506	-	5,5,5	0.24	0	5,5,5	0.89	0
2	GOL	A	507	-	5,5,5	0.34	0	5,5,5	0.78	0
2	GOL	B	503	-	5,5,5	0.34	0	5,5,5	0.49	0
2	GOL	A	501	-	5,5,5	0.42	0	5,5,5	0.38	0
2	GOL	A	505	-	5,5,5	0.38	0	5,5,5	0.30	0
2	GOL	B	501	-	5,5,5	0.34	0	5,5,5	0.36	0
3	PGE	A	508	-	9,9,9	0.32	0	8,8,8	0.41	0
2	GOL	A	503	-	5,5,5	0.45	0	5,5,5	0.48	0
2	GOL	B	502	-	5,5,5	0.35	0	5,5,5	0.59	0
4	GLC	B	504	-	12,12,12	0.94	1 (8%)	17,17,17	1.08	0
2	GOL	A	502	-	5,5,5	0.43	0	5,5,5	0.33	0
2	GOL	A	504	-	5,5,5	0.41	0	5,5,5	0.65	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	506	-	-	2/4/4/4	-
2	GOL	A	507	-	-	2/4/4/4	-
2	GOL	B	503	-	-	4/4/4/4	-
2	GOL	A	501	-	-	0/4/4/4	-
2	GOL	A	505	-	-	2/4/4/4	-
2	GOL	B	501	-	-	2/4/4/4	-
3	PGE	A	508	-	-	4/7/7/7	-
2	GOL	A	503	-	-	2/4/4/4	-
2	GOL	B	502	-	-	2/4/4/4	-
4	GLC	B	504	-	-	0/2/22/22	0/1/1/1
2	GOL	A	502	-	-	4/4/4/4	-
2	GOL	A	504	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	504	GLC	O5-C1	2.03	1.48	1.42

There are no bond angle outliers.

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	502	GOL	O1-C1-C2-C3
2	A	502	GOL	C1-C2-C3-O3
2	A	502	GOL	O2-C2-C3-O3
2	A	503	GOL	O1-C1-C2-C3
2	A	504	GOL	O1-C1-C2-C3

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	506	GOL	1	0
3	A	508	PGE	1	0
2	A	503	GOL	1	0
2	B	502	GOL	1	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	454/464 (97%)	-0.17	8 (1%) 68 71	20, 31, 51, 87	0
1	B	449/464 (96%)	0.26	20 (4%) 33 36	21, 35, 58, 86	0
All	All	903/928 (97%)	0.05	28 (3%) 49 52	20, 33, 56, 87	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	401	GLY	6.1
1	A	453	PHE	5.5
1	A	402	GLY	5.2
1	B	164	GLY	4.8
1	B	10	ARG	4.6

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, 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(\AA^2)	Q<0.9
3	PGE	A	508	10/10	0.70	0.37	57,62,64,67	0
2	GOL	B	501	6/6	0.77	0.20	42,50,55,56	0
2	GOL	B	503	6/6	0.80	0.26	44,50,53,54	0
2	GOL	A	503	6/6	0.80	0.37	35,41,50,51	0
2	GOL	A	506	6/6	0.82	0.23	41,43,47,49	0
2	GOL	A	501	6/6	0.83	0.15	32,34,35,42	0
2	GOL	B	502	6/6	0.83	0.20	48,50,55,59	0
2	GOL	A	504	6/6	0.84	0.15	39,52,54,54	0
2	GOL	A	502	6/6	0.89	0.15	40,42,45,50	0
2	GOL	A	505	6/6	0.90	0.14	36,44,48,62	0
2	GOL	A	507	6/6	0.91	0.31	34,38,55,66	0
4	GLC	B	504	12/12	0.97	0.07	28,32,37,42	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.