



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:30 PM UTC

PDB ID : 7SVH / pdb_00007svh
Title : Bile Salt Hydrolase B from *Lactobacillus gasseri*
Authors : Walker, M.E.; Redinbo, M.R.
Deposited on : 2021-11-19
Resolution : 1.56 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

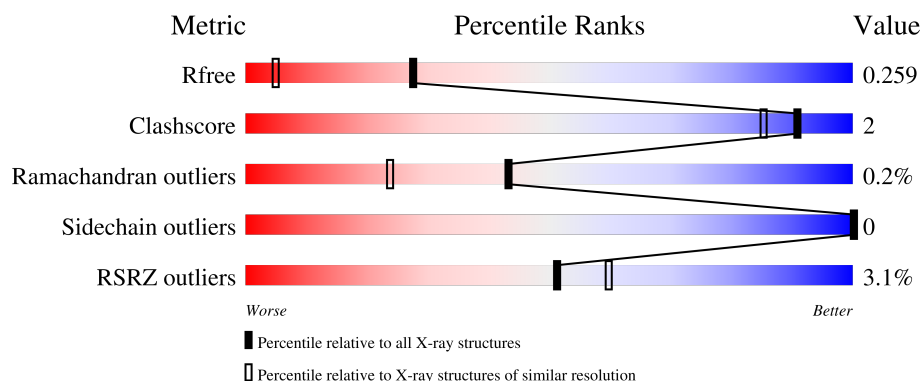
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.56 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	331	2% 94% 5% • •
1	B	331	2% 93% 5% •
1	C	331	2% 96% 5% • •
1	D	331	2% 93% 5% • •
1	E	331	5% 92% 6% •

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Mol	Chain	Length	Quality of chain
1	F	331	3% 94% 5% • •
1	G	331	5% 92% 5% •
1	H	331	5% 92% 5% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22086 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 Choloylglycine hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2515	1606	403	494	12			
1	B	324	Total	C	N	O	S	0	0	0
			2520	1609	405	494	12			
1	C	329	Total	C	N	O	S	0	0	0
			2553	1633	418	490	12			
1	D	321	Total	C	N	O	S	0	0	0
			2497	1598	401	486	12			
1	E	324	Total	C	N	O	S	0	0	0
			2521	1610	407	492	12			
1	F	326	Total	C	N	O	S	0	0	0
			2531	1615	409	495	12			
1	G	321	Total	C	N	O	S	0	0	0
			2494	1594	401	487	12			
1	H	321	Total	C	N	O	S	0	0	0
			2481	1589	399	481	12			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	326	HIS	-	expression tag	UNP A0A833FHE1
A	327	HIS	-	expression tag	UNP A0A833FHE1
A	328	HIS	-	expression tag	UNP A0A833FHE1
A	329	HIS	-	expression tag	UNP A0A833FHE1
A	330	HIS	-	expression tag	UNP A0A833FHE1
A	331	HIS	-	expression tag	UNP A0A833FHE1
B	326	HIS	-	expression tag	UNP A0A833FHE1
B	327	HIS	-	expression tag	UNP A0A833FHE1
B	328	HIS	-	expression tag	UNP A0A833FHE1
B	329	HIS	-	expression tag	UNP A0A833FHE1
B	330	HIS	-	expression tag	UNP A0A833FHE1
B	331	HIS	-	expression tag	UNP A0A833FHE1
C	326	HIS	-	expression tag	UNP A0A833FHE1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	327	HIS	-	expression tag	UNP A0A833FHE1
C	328	HIS	-	expression tag	UNP A0A833FHE1
C	329	HIS	-	expression tag	UNP A0A833FHE1
C	330	HIS	-	expression tag	UNP A0A833FHE1
C	331	HIS	-	expression tag	UNP A0A833FHE1
D	326	HIS	-	expression tag	UNP A0A833FHE1
D	327	HIS	-	expression tag	UNP A0A833FHE1
D	328	HIS	-	expression tag	UNP A0A833FHE1
D	329	HIS	-	expression tag	UNP A0A833FHE1
D	330	HIS	-	expression tag	UNP A0A833FHE1
D	331	HIS	-	expression tag	UNP A0A833FHE1
E	326	HIS	-	expression tag	UNP A0A833FHE1
E	327	HIS	-	expression tag	UNP A0A833FHE1
E	328	HIS	-	expression tag	UNP A0A833FHE1
E	329	HIS	-	expression tag	UNP A0A833FHE1
E	330	HIS	-	expression tag	UNP A0A833FHE1
E	331	HIS	-	expression tag	UNP A0A833FHE1
F	326	HIS	-	expression tag	UNP A0A833FHE1
F	327	HIS	-	expression tag	UNP A0A833FHE1
F	328	HIS	-	expression tag	UNP A0A833FHE1
F	329	HIS	-	expression tag	UNP A0A833FHE1
F	330	HIS	-	expression tag	UNP A0A833FHE1
F	331	HIS	-	expression tag	UNP A0A833FHE1
G	326	HIS	-	expression tag	UNP A0A833FHE1
G	327	HIS	-	expression tag	UNP A0A833FHE1
G	328	HIS	-	expression tag	UNP A0A833FHE1
G	329	HIS	-	expression tag	UNP A0A833FHE1
G	330	HIS	-	expression tag	UNP A0A833FHE1
G	331	HIS	-	expression tag	UNP A0A833FHE1
H	326	HIS	-	expression tag	UNP A0A833FHE1
H	327	HIS	-	expression tag	UNP A0A833FHE1
H	328	HIS	-	expression tag	UNP A0A833FHE1
H	329	HIS	-	expression tag	UNP A0A833FHE1
H	330	HIS	-	expression tag	UNP A0A833FHE1
H	331	HIS	-	expression tag	UNP A0A833FHE1

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total 1	Mg 1	0	0
2	H	1	Total 1	Mg 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	277	Total 277	O 277	0	0
3	B	269	Total 269	O 269	0	0
3	C	280	Total 280	O 280	0	0
3	D	256	Total 256	O 256	0	0
3	E	243	Total 243	O 243	0	0
3	F	255	Total 255	O 255	0	0
3	G	194	Total 194	O 194	0	0
3	H	196	Total 196	O 196	0	0

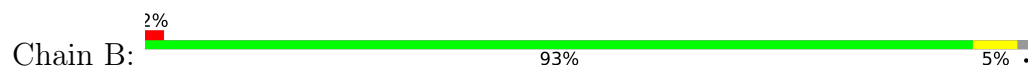
3 Residue-property plots [i](#)

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: Choloylglycine hydrolase



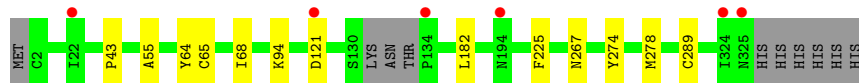
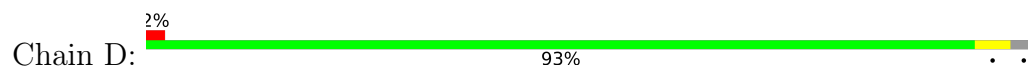
- Molecule 1: Choloylglycine hydrolase



- Molecule 1: Choloylglycine hydrolase



- Molecule 1: Choloylglycine hydrolase

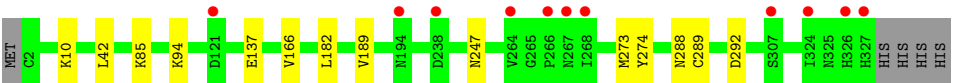
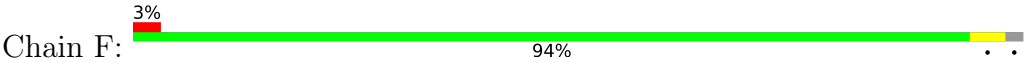


- Molecule 1: Choloylglycine hydrolase

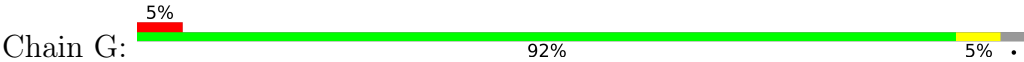




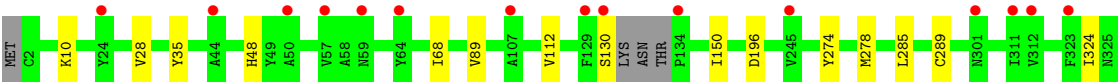
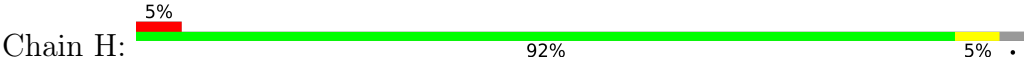
● Molecule 1: Choloylglycine hydrolase



● Molecule 1: Choloylglycine hydrolase



● Molecule 1: Choloylglycine hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.35Å 167.38Å 88.15Å 90.00° 98.98° 90.00°	Depositor
Resolution (Å)	29.02 – 1.56 29.02 – 1.56	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.02-1.56) 97.0 (29.02-1.56)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 1.56Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.221 , 0.260 0.221 , 0.259	Depositor DCC
R_{free} test set	1996 reflections (0.56%)	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	22086	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 83.38 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2014e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MG

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	0.28	0/2575	0.51	0/3505
1	B	0.28	0/2580	0.49	0/3510
1	C	0.29	0/2617	0.51	0/3560
1	D	0.28	0/2556	0.51	0/3473
1	E	0.28	0/2582	0.49	0/3511
1	F	0.26	0/2593	0.48	0/3530
1	G	0.26	0/2553	0.48	0/3471
1	H	0.26	0/2540	0.46	0/3454
All	All	0.28	0/20596	0.49	0/28014

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 [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	2515	0	2384	8	0
1	B	2520	0	2400	12	0
1	C	2553	0	2427	6	0
1	D	2497	0	2388	9	0
1	E	2521	0	2390	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2531	0	2395	9	0
1	G	2494	0	2377	9	0
1	H	2481	0	2363	10	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	F	1	0	0	0	0
2	H	1	0	0	0	0
3	A	277	0	0	2	1
3	B	269	0	0	5	0
3	C	280	0	0	1	1
3	D	256	0	0	4	0
3	E	243	0	0	0	0
3	F	255	0	0	3	0
3	G	194	0	0	1	0
3	H	196	0	0	3	0
All	All	22086	0	19124	68	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 2.

The worst 5 of 68 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:282:LYS:NZ	3:B:402:HOH:O	2.15	0.80
1:D:65:CYS:SG	3:D:742:HOH:O	2.40	0.78
1:E:21:GLU:HG2	1:E:22:ILE:HG13	1.70	0.73
1:G:2:CYS:O	1:G:224:ARG:NH2	2.23	0.72
1:F:247:ASN:OD1	3:F:502:HOH:O	2.15	0.64

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:634:HOH:O	3:C:747:HOH:O[1_556]	2.16	0.04

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	322/331 (97%)	314 (98%)	7 (2%)	1 (0%)	36	18
1	B	322/331 (97%)	314 (98%)	8 (2%)	0	100	100
1	C	327/331 (99%)	321 (98%)	6 (2%)	0	100	100
1	D	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
1	E	320/331 (97%)	310 (97%)	9 (3%)	1 (0%)	36	18
1	F	324/331 (98%)	317 (98%)	6 (2%)	1 (0%)	36	18
1	G	317/331 (96%)	308 (97%)	7 (2%)	2 (1%)	21	6
1	H	317/331 (96%)	305 (96%)	11 (4%)	1 (0%)	36	18
All	All	2566/2648 (97%)	2499 (97%)	61 (2%)	6 (0%)	43	24

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	10	LYS
1	F	10	LYS
1	G	10	LYS
1	G	307	SER
1	H	10	LYS

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	275/291 (94%)	275 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	277/291 (95%)	277 (100%)	0	100	100
1	C	277/291 (95%)	277 (100%)	0	100	100
1	D	274/291 (94%)	274 (100%)	0	100	100
1	E	276/291 (95%)	276 (100%)	0	100	100
1	F	277/291 (95%)	277 (100%)	0	100	100
1	G	274/291 (94%)	274 (100%)	0	100	100
1	H	270/291 (93%)	270 (100%)	0	100	100
All	All	2200/2328 (94%)	2200 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	267	ASN
1	G	59	ASN
1	F	301	ASN
1	G	83	GLN
1	C	214	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	324/331 (97%)	0.21	5 (1%) 72 79	21, 28, 40, 49	0
1	B	324/331 (97%)	0.28	6 (1%) 66 75	22, 29, 41, 52	0
1	C	329/331 (99%)	0.41	7 (2%) 63 72	22, 30, 41, 48	0
1	D	321/331 (96%)	0.42	6 (1%) 66 75	24, 31, 41, 55	0
1	E	324/331 (97%)	0.64	15 (4%) 37 45	24, 33, 47, 67	0
1	F	326/331 (98%)	0.49	11 (3%) 48 56	24, 32, 43, 55	0
1	G	321/331 (96%)	0.62	15 (4%) 36 44	24, 33, 46, 57	0
1	H	321/331 (96%)	0.73	15 (4%) 36 44	26, 34, 45, 56	0
All	All	2590/2648 (97%)	0.47	80 (3%) 51 60	21, 31, 44, 67	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	311	ILE	3.5
1	E	134	PRO	3.3
1	E	312	VAL	3.3
1	B	264	VAL	3.2
1	G	22	ILE	3.1

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(Å ²)	Q<0.9
2	MG	F	401	1/1	0.96	0.04	34,34,34,34	0
2	MG	H	401	1/1	0.96	0.05	37,37,37,37	0
2	MG	C	401	1/1	0.98	0.04	34,34,34,34	0
2	MG	D	401	1/1	0.98	0.06	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.