



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 28, 2018 – 11:20 AM EST

PDB ID : 5O2X
Title : Extended catalytic domain of H. jecorina LPMO9A a.k.a EG4
Authors : Hansson, H.; Karkehabadi, S.; Mikkelsen, N.E.; Sandgren, M.; Kelemen, B.; Kaper, T.
Deposited on : 2017-05-23
Resolution : 0.95 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

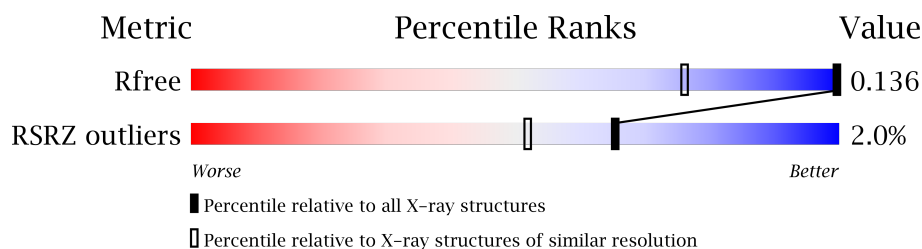
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 0.95 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}	100719	1062 (1.08-0.84)
RSRZ outliers	101464	1070 (1.08-0.84)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

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	NAG	A	301[A]	-	-	-	X
2	NAG	A	301[B]	-	-	-	X
3	MAN	A	308[A]	-	-	-	X
3	MAN	A	313[A]	-	-	-	X
3	MAN	A	313[B]	-	-	-	X
3	MAN	A	316	-	-	-	X
5	SO4	A	320	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2655 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.

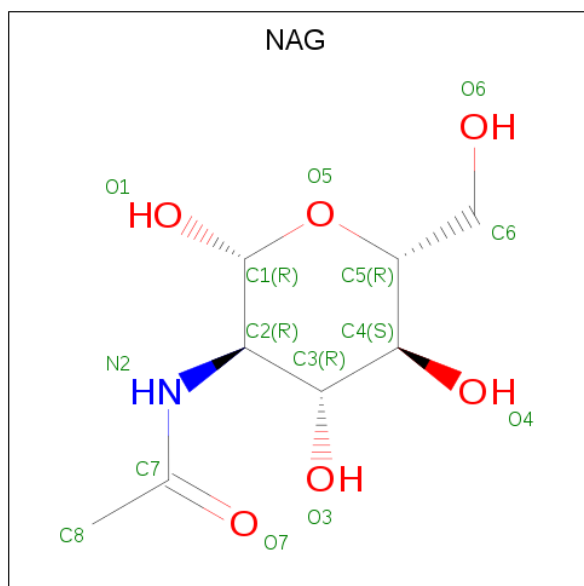
- Molecule 1 is a protein called Glycoside hydrolase family 61.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	28	0
			1994	1279	324	387	4			

There is a discrepancy between the modelled and reference sequences:

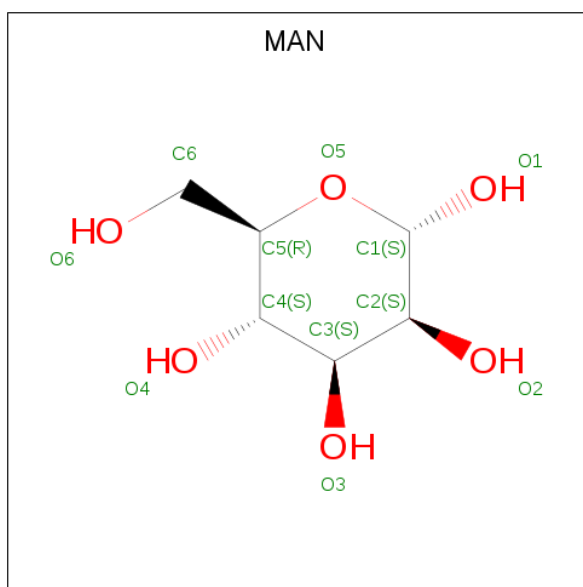
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIC	-	expression tag	UNP G0R6T8

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	1
			15	8	1	6		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	1
			22	12	10		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	1
			22	12	10		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	1
			22	12	10		
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		

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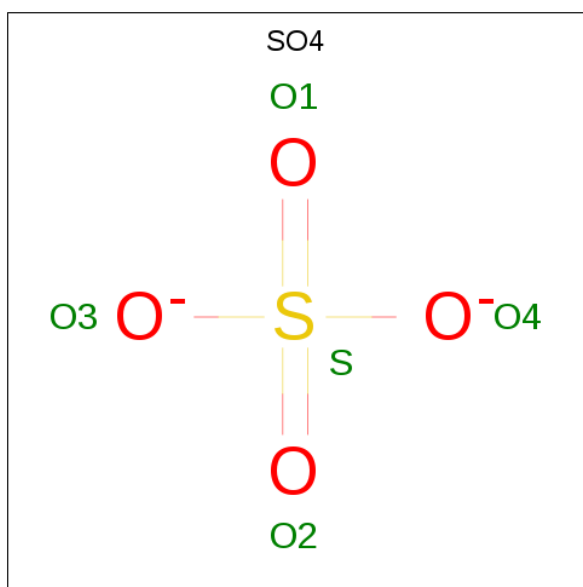
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cu	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	372	Total	O	0	46
			407	407		

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3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.82Å 61.55Å 47.78Å 90.00° 112.03° 90.00°	Depositor
Resolution (Å)	44.29 – 0.95 23.75 – 0.95	Depositor EDS
% Data completeness (in resolution range)	89.0 (44.29-0.95) 89.0 (23.75-0.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 0.95Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.115 , 0.127 0.125 , 0.136	Depositor DCC
R_{free} test set	6451 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	5.6	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2655	wwPDB-VP
Average B, all atoms (Å ²)	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.67% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	HIC	A	1	1,4	9,11,12	1.22	1 (11%)	7,14,16	0.67	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
1	HIC	A	1	1,4	-	0/4/6/8	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	HIC	CD2-NE2	-3.06	1.33	1.38

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.

4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

4.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 1 is monoatomic - leaving 25 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	$\# Z > 2$
2	NAG	A	301[A]	-	14,14,15	0.62	0	15,19,21	0.83	1 (6%)
2	NAG	A	301[B]	-	14,14,15	0.63	0	15,19,21	1.04	2 (13%)
2	NAG	A	302	1	14,14,15	0.74	0	15,19,21	0.78	1 (6%)
3	MAN	A	303	1	11,11,12	0.54	0	13,15,17	0.88	0
3	MAN	A	304	1	11,11,12	0.94	1 (9%)	13,15,17	0.83	0
3	MAN	A	305	1	11,11,12	0.59	0	13,15,17	1.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	A	306	1	11,11,12	0.70	0	13,15,17	0.85	1 (7%)
3	MAN	A	307	1	11,11,12	0.68	0	13,15,17	1.13	1 (7%)
3	MAN	A	308[A]	1	11,11,12	0.68	0	13,15,17	0.99	1 (7%)
3	MAN	A	308[B]	1	11,11,12	0.88	0	13,15,17	1.49	2 (15%)
3	MAN	A	309	1	11,11,12	0.64	0	13,15,17	1.24	2 (15%)
3	MAN	A	310[A]	1	11,11,12	0.70	0	13,15,17	1.25	1 (7%)
3	MAN	A	310[B]	1	11,11,12	0.66	0	13,15,17	1.75	2 (15%)
3	MAN	A	311	1	11,11,12	0.37	0	13,15,17	0.99	1 (7%)
3	MAN	A	312	1	11,11,12	0.60	0	13,15,17	0.79	0
3	MAN	A	313[A]	1	11,11,12	0.79	0	13,15,17	0.88	1 (7%)
3	MAN	A	313[B]	1	11,11,12	0.33	0	13,15,17	1.45	1 (7%)
3	MAN	A	314[A]	1	11,11,12	0.90	1 (9%)	13,15,17	1.69	3 (23%)
3	MAN	A	314[B]	1	11,11,12	0.52	0	13,15,17	1.17	1 (7%)
3	MAN	A	315	1	11,11,12	0.78	0	13,15,17	1.65	3 (23%)
3	MAN	A	316	1	11,11,12	0.49	0	13,15,17	1.63	1 (7%)
3	MAN	A	317	1	11,11,12	0.50	0	13,15,17	0.86	0
5	SO4	A	319	-	4,4,4	0.43	0	6,6,6	0.64	0
5	SO4	A	320	-	4,4,4	0.46	0	6,6,6	0.65	0
5	SO4	A	321	-	4,4,4	0.63	0	6,6,6	0.70	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	NAG	A	301[A]	-	-	0/6/23/26	0/1/1/1
2	NAG	A	301[B]	-	-	0/6/23/26	0/1/1/1
2	NAG	A	302	1	-	0/6/23/26	0/1/1/1
3	MAN	A	303	1	-	0/2/19/22	0/1/1/1
3	MAN	A	304	1	-	0/2/19/22	0/1/1/1
3	MAN	A	305	1	-	0/2/19/22	0/1/1/1
3	MAN	A	306	1	-	0/2/19/22	0/1/1/1
3	MAN	A	307	1	-	0/2/19/22	0/1/1/1
3	MAN	A	308[A]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	308[B]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	309	1	-	0/2/19/22	0/1/1/1
3	MAN	A	310[A]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	310[B]	1	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	A	311	1	-	0/2/19/22	0/1/1/1
3	MAN	A	312	1	-	0/2/19/22	0/1/1/1
3	MAN	A	313[A]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	313[B]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	314[A]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	314[B]	1	-	0/2/19/22	0/1/1/1
3	MAN	A	315	1	-	0/2/19/22	0/1/1/1
3	MAN	A	316	1	-	0/2/19/22	0/1/1/1
3	MAN	A	317	1	-	0/2/19/22	0/1/1/1
5	SO4	A	319	-	-	0/0/0/0	0/0/0/0
5	SO4	A	320	-	-	0/0/0/0	0/0/0/0
5	SO4	A	321	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	314[A]	MAN	O5-C1	-2.45	1.39	1.43
3	A	304	MAN	C2-C3	2.31	1.55	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	310[B]	MAN	C2-C3-C4	-4.56	102.92	110.88
3	A	315	MAN	C1-C2-C3	-3.73	104.92	109.65
3	A	314[A]	MAN	O2-C2-C1	-3.10	102.87	109.18
3	A	314[A]	MAN	O3-C3-C4	-3.07	103.68	110.36
2	A	302	NAG	O5-C1-C2	-2.62	107.83	111.47
2	A	301[B]	NAG	O6-C6-C5	-2.42	103.21	111.34
3	A	308[B]	MAN	C2-C3-C4	-2.42	106.66	110.88
3	A	309	MAN	O4-C4-C3	-2.41	105.11	110.36
3	A	309	MAN	C6-C5-C4	-2.32	107.58	113.00
3	A	308[A]	MAN	C6-C5-C4	-2.20	107.85	113.00
2	A	301[A]	NAG	O5-C1-C2	-2.17	108.45	111.47
2	A	301[B]	NAG	O5-C1-C2	-2.17	108.45	111.47
3	A	306	MAN	C1-O5-C5	2.00	114.92	112.17
3	A	307	MAN	O3-C3-C2	2.05	113.76	110.02
3	A	315	MAN	O4-C4-C3	2.05	114.82	110.36
3	A	313[A]	MAN	C1-O5-C5	2.08	115.04	112.17
3	A	310[B]	MAN	C1-O5-C5	2.11	115.07	112.17
3	A	315	MAN	O2-C2-C3	2.25	114.59	110.17
3	A	310[A]	MAN	O2-C2-C3	2.52	115.13	110.17
3	A	311	MAN	C1-O5-C5	2.56	115.69	112.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	314[A]	MAN	C1-O5-C5	2.86	116.11	112.17
3	A	314[B]	MAN	C1-O5-C5	3.21	116.59	112.17
3	A	308[B]	MAN	C1-O5-C5	3.80	117.41	112.17
3	A	313[B]	MAN	C1-O5-C5	3.99	117.66	112.17
3	A	316	MAN	C1-O5-C5	4.69	118.64	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 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	247/248 (99%)	0.47	5 (2%) 65 52	4, 6, 13, 22	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	PRO	3.1
1	A	26	SER	2.6
1	A	216	ASN	2.1
1	A	4[A]	ILE	2.1
1	A	213	SER	2.0

5.2 Non-standard residues in protein, DNA, RNA chains

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	HIC	A	1	11/12	0.99	0.07	-	5,6,7,9	0

5.3 Carbohydrates

There are no carbohydrates in this entry.

5.4 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	A	301[A]	14/15	0.97	0.15	19.12	8,9,11,12	1
2	NAG	A	301[B]	14/15	0.97	0.15	19.12	8,9,12,14	1
3	MAN	A	316	11/12	0.84	0.15	10.23	15,17,25,26	11
5	SO4	A	320	5/5	0.91	0.30	5.89	20,29,33,34	5
3	MAN	A	308[A]	11/12	0.96	0.12	3.54	7,9,12,15	11
3	MAN	A	313[A]	11/12	0.96	0.14	3.00	5,6,8,10	11
3	MAN	A	313[B]	11/12	0.96	0.14	3.00	7,8,9,11	11
3	MAN	A	314[B]	11/12	0.92	0.13	1.07	9,11,16,20	11
3	MAN	A	310[A]	11/12	0.95	0.11	1.03	7,9,12,16	11
3	MAN	A	310[B]	11/12	0.95	0.11	0.92	7,9,12,13	11
3	MAN	A	317	11/12	0.98	0.09	0.72	5,5,7,7	0
3	MAN	A	314[A]	11/12	0.92	0.13	0.48	8,10,13,14	11
2	NAG	A	302	14/15	0.98	0.09	0.24	5,6,8,8	14
3	MAN	A	309	11/12	0.96	0.09	-0.22	8,9,14,20	11
3	MAN	A	311	11/12	0.99	0.08	-0.41	4,4,5,6	0
3	MAN	A	306	11/12	0.95	0.09	-0.78	6,8,12,14	11
3	MAN	A	304	11/12	0.98	0.08	-0.88	5,6,8,9	11
3	MAN	A	312	11/12	0.99	0.07	-1.47	5,5,6,9	0
5	SO4	A	321	5/5	0.72	0.29	-	17,50,56,61	0
3	MAN	A	303	11/12	0.86	0.17	-	14,16,20,21	11
4	CU	A	318	1/1	1.00	0.07	-	5,5,5,5	1
3	MAN	A	305	11/12	0.89	0.09	-	13,16,20,20	11
5	SO4	A	319	5/5	0.94	0.18	-	17,18,21,22	5
3	MAN	A	308[B]	11/12	0.96	0.12	-	7,9,12,18	11
3	MAN	A	315	11/12	0.88	0.15	-	15,19,27,31	11
3	MAN	A	307	11/12	0.83	0.14	-	14,18,27,28	11

5.5 Other polymers ⓘ

There are no such residues in this entry.