



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:25 PM UTC

PDB ID : 6X4T / pdb_00006x4t
Title : Crystal structure of ICOS-L in complex with Prezalumab and VNAR domain
Authors : Rujas, E.; Sicard, T.; Julien, J.P.
Deposited on : 2020-05-23
Resolution : 3.15 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
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

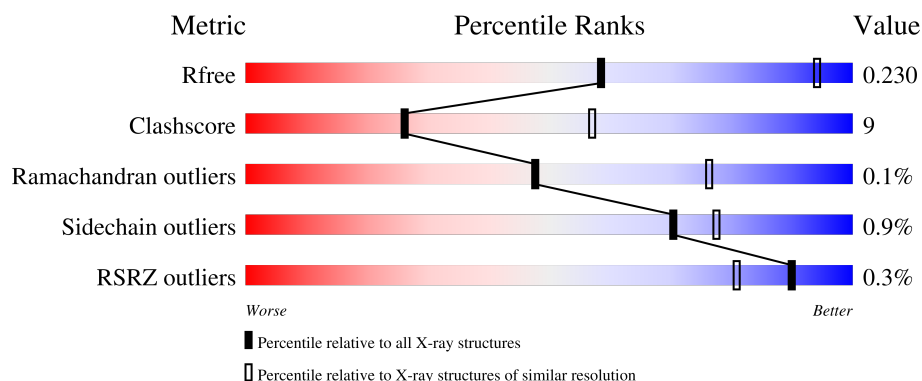
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	240	 62% 24% 12%
1	C	240	 67% 19% 14%
2	B	224	 76% 24%
2	D	224	 75% 24%
3	E	214	 85% 15%

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Mol	Chain	Length	Quality of chain
3	F	214	84% 15%
4	G	130	% 63% 28% 9%
4	N	130	2% 62% 19% 19%
5	H	2	50% 50%
5	I	2	50% 50%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11774 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 ICOS ligand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1642	1028	284	320	10			
1	C	207	Total	C	N	O	S	0	0	0
			1624	1018	281	315	10			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	THR	-	cloning artifact	UNP O75144
A	18	GLY	-	cloning artifact	UNP O75144
A	249	GLY	-	expression tag	UNP O75144
A	250	THR	-	expression tag	UNP O75144
A	251	GLU	-	expression tag	UNP O75144
A	252	ASN	-	expression tag	UNP O75144
A	253	LEU	-	expression tag	UNP O75144
A	254	TYR	-	expression tag	UNP O75144
A	255	PHE	-	expression tag	UNP O75144
A	256	GLN	-	expression tag	UNP O75144
C	17	THR	-	cloning artifact	UNP O75144
C	18	GLY	-	cloning artifact	UNP O75144
C	249	GLY	-	expression tag	UNP O75144
C	250	THR	-	expression tag	UNP O75144
C	251	GLU	-	expression tag	UNP O75144
C	252	ASN	-	expression tag	UNP O75144
C	253	LEU	-	expression tag	UNP O75144
C	254	TYR	-	expression tag	UNP O75144
C	255	PHE	-	expression tag	UNP O75144
C	256	GLN	-	expression tag	UNP O75144

- Molecule 2 is a protein called Prezalumab Fab Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	224	Total	C	N	O	S	0	0	0
			1689	1073	281	328	7			
2	D	223	Total	C	N	O	S	0	0	0
			1683	1070	280	327	6			

- Molecule 3 is a protein called Prezalumab Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	213	Total	C	N	O	S	0	0	0
			1642	1025	276	336	5			
3	F	212	Total	C	N	O	S	0	0	0
			1633	1020	275	333	5			

- Molecule 4 is a protein called VNAR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	118	Total	C	N	O	S	0	0	0
			879	531	160	182	6			
4	N	105	Total	C	N	O	S	0	0	0
			788	478	142	162	6			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).

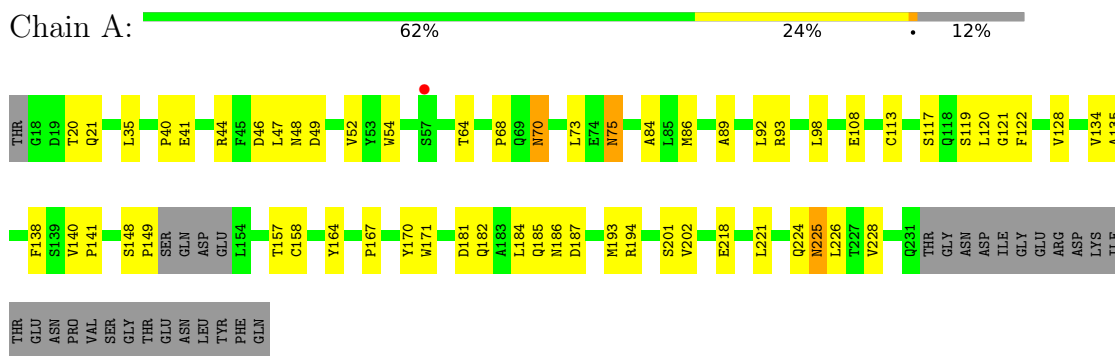


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		

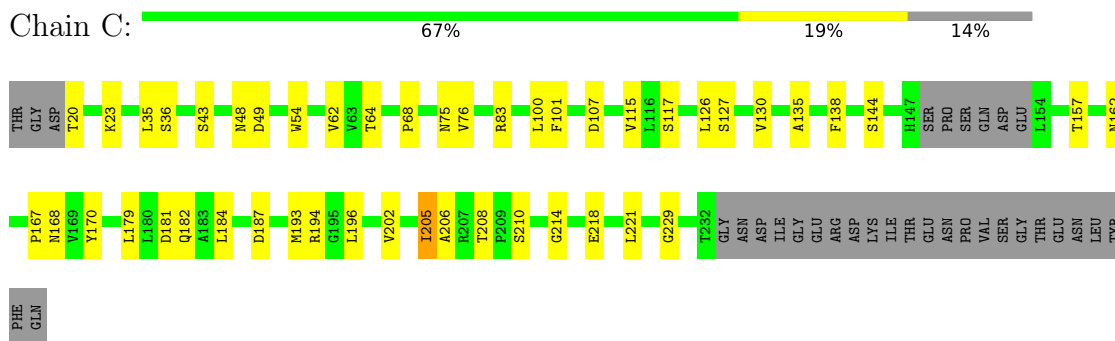
3 Residue-property plots [i](#)

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.

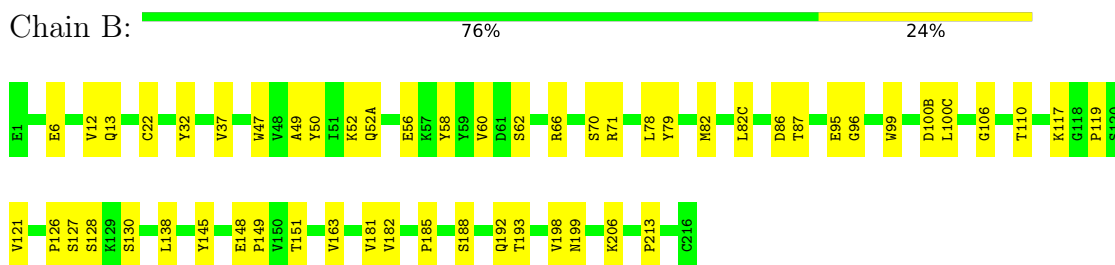
- Molecule 1: ICOS ligand



- Molecule 1: ICOS ligand

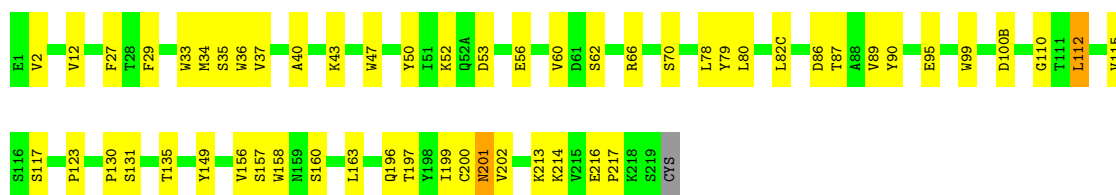


- Molecule 2: Prezalumab Fab Heavy chain



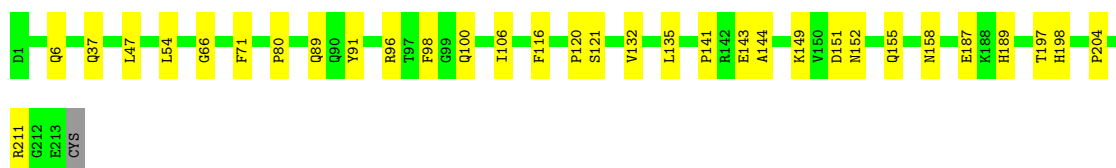
- Molecule 2: Prezalumab Fab Heavy chain

Chain D:  75% 24% .



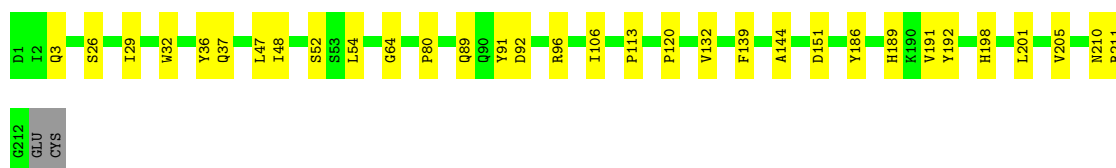
- Molecule 3: Prezalumab Fab Light chain

Chain E:  85% 15%



- Molecule 3: Prezalumab Fab Light chain

Chain F:  84% 15%



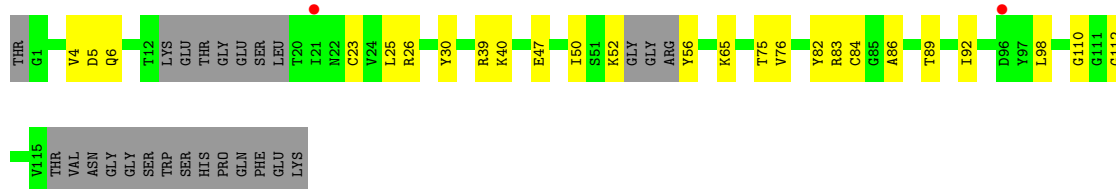
- Molecule 4: VNAR

Chain G:  63% 28% 9%



- Molecule 4: VNAR

Chain N:  62% 19% 19%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  50% 50%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.51Å 151.98Å 86.67Å 90.00° 104.10° 90.00°	Depositor
Resolution (Å)	38.88 – 3.15 38.88 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.88-3.15) 92.9 (38.88-3.15)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.201 , 0.256 (Not available) , 0.230	Depositor DCC
R_{free} test set	1488 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	69.0	Xtriage
Anisotropy	0.698	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.4	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	0.94	EDS
Total number of atoms	11774	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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: NAG, 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	0.20	0/1673	0.52	0/2279
1	C	0.19	0/1654	0.49	0/2253
2	B	0.17	0/1732	0.45	0/2358
2	D	0.19	0/1726	0.48	0/2350
3	E	0.15	0/1678	0.43	0/2278
3	F	0.16	0/1669	0.42	0/2266
4	G	0.16	0/890	0.46	0/1203
4	N	0.17	0/797	0.44	0/1076
All	All	0.18	0/11819	0.46	0/16063

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	1642	0	1596	37	0
1	C	1624	0	1585	26	0
2	B	1689	0	1655	37	0
2	D	1683	0	1650	40	0
3	E	1642	0	1586	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1633	0	1580	20	0
4	G	879	0	844	23	0
4	N	788	0	755	17	0
5	H	28	0	25	1	0
5	I	28	0	25	3	0
6	A	70	0	65	6	0
6	C	56	0	52	2	0
7	A	6	0	8	0	0
7	D	6	0	8	1	0
All	All	11774	0	11434	218	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 9.

The worst 5 of 218 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:C:83:ARG:NH1	1:C:107:ASP:OD2	2.00	0.95
2:D:87:THR:HG22	2:D:115:VAL:H	1.34	0.90
5:I:1:NAG:H4	5:I:2:NAG:HN2	1.47	0.79
1:A:135:ALA:HB2	1:A:221:LEU:HD23	1.62	0.79
2:B:66:ARG:NH2	2:B:86:ASP:OD2	2.15	0.77

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	206/240 (86%)	187 (91%)	18 (9%)	1 (0%)	24 55
1	C	203/240 (85%)	184 (91%)	19 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/224 (99%)	216 (97%)	6 (3%)	0	100	100
2	D	221/224 (99%)	213 (96%)	7 (3%)	1 (0%)	24	55
3	E	211/214 (99%)	203 (96%)	8 (4%)	0	100	100
3	F	210/214 (98%)	205 (98%)	5 (2%)	0	100	100
4	G	116/130 (89%)	113 (97%)	3 (3%)	0	100	100
4	N	99/130 (76%)	95 (96%)	4 (4%)	0	100	100
All	All	1488/1616 (92%)	1416 (95%)	70 (5%)	2 (0%)	48	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	GLY
2	D	112	LEU

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	191/218 (88%)	187 (98%)	4 (2%)	47	67
1	C	189/218 (87%)	185 (98%)	4 (2%)	47	67
2	B	188/188 (100%)	188 (100%)	0	100	100
2	D	187/188 (100%)	186 (100%)	1 (0%)	81	82
3	E	187/188 (100%)	185 (99%)	2 (1%)	65	75
3	F	186/188 (99%)	186 (100%)	0	100	100
4	G	97/108 (90%)	96 (99%)	1 (1%)	68	76
4	N	88/108 (82%)	88 (100%)	0	100	100
All	All	1313/1404 (94%)	1301 (99%)	12 (1%)	70	77

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	205	ILE
2	D	201	ASN
4	G	89	THR
3	E	54	LEU
1	A	225	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	199	GLN
3	F	38	GLN
4	N	6	GLN
3	F	189	HIS
2	D	39	GLN

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 ⓘ

4 monosaccharides 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	$\# Z > 2$
5	NAG	H	1	1,5	14,14,15	0.20	0	17,19,21	0.61	0
5	NAG	H	2	5	14,14,15	1.31	2 (14%)	17,19,21	0.85	1 (5%)
5	NAG	I	1	1,5	14,14,15	0.23	0	17,19,21	0.68	0
5	NAG	I	2	5	14,14,15	1.36	1 (7%)	17,19,21	2.46	3 (17%)

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
5	NAG	H	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	H	2	5	-	2/6/23/26	0/1/1/1
5	NAG	I	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	2	NAG	C1-C2	4.77	1.58	1.52
5	H	2	NAG	C1-C2	3.67	1.57	1.52
5	H	2	NAG	O5-C1	3.20	1.49	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	2	NAG	C2-N2-C7	8.69	134.54	122.90
5	I	2	NAG	O3-C3-C4	-3.68	101.71	110.38
5	H	2	NAG	C1-O5-C5	2.96	116.16	112.19
5	I	2	NAG	C1-C2-N2	-2.47	106.54	110.43

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	2	NAG	O5-C5-C6-O6
5	H	2	NAG	C4-C5-C6-O6
5	I	2	NAG	C8-C7-N2-C2
5	I	2	NAG	O7-C7-N2-C2
5	I	2	NAG	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 4 short contacts:

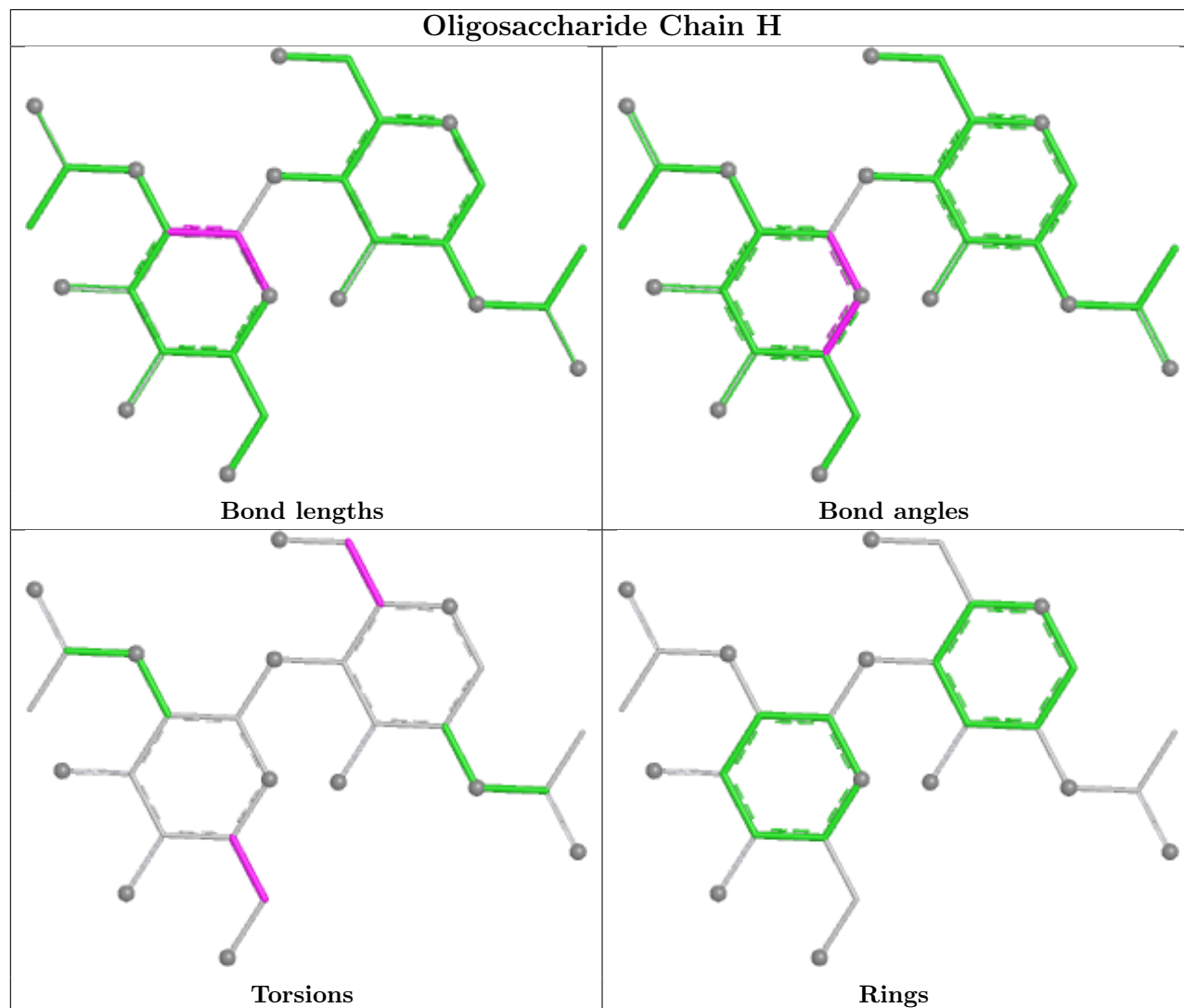
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	2	NAG	1	0
5	I	1	NAG	3	0
5	H	1	NAG	1	0

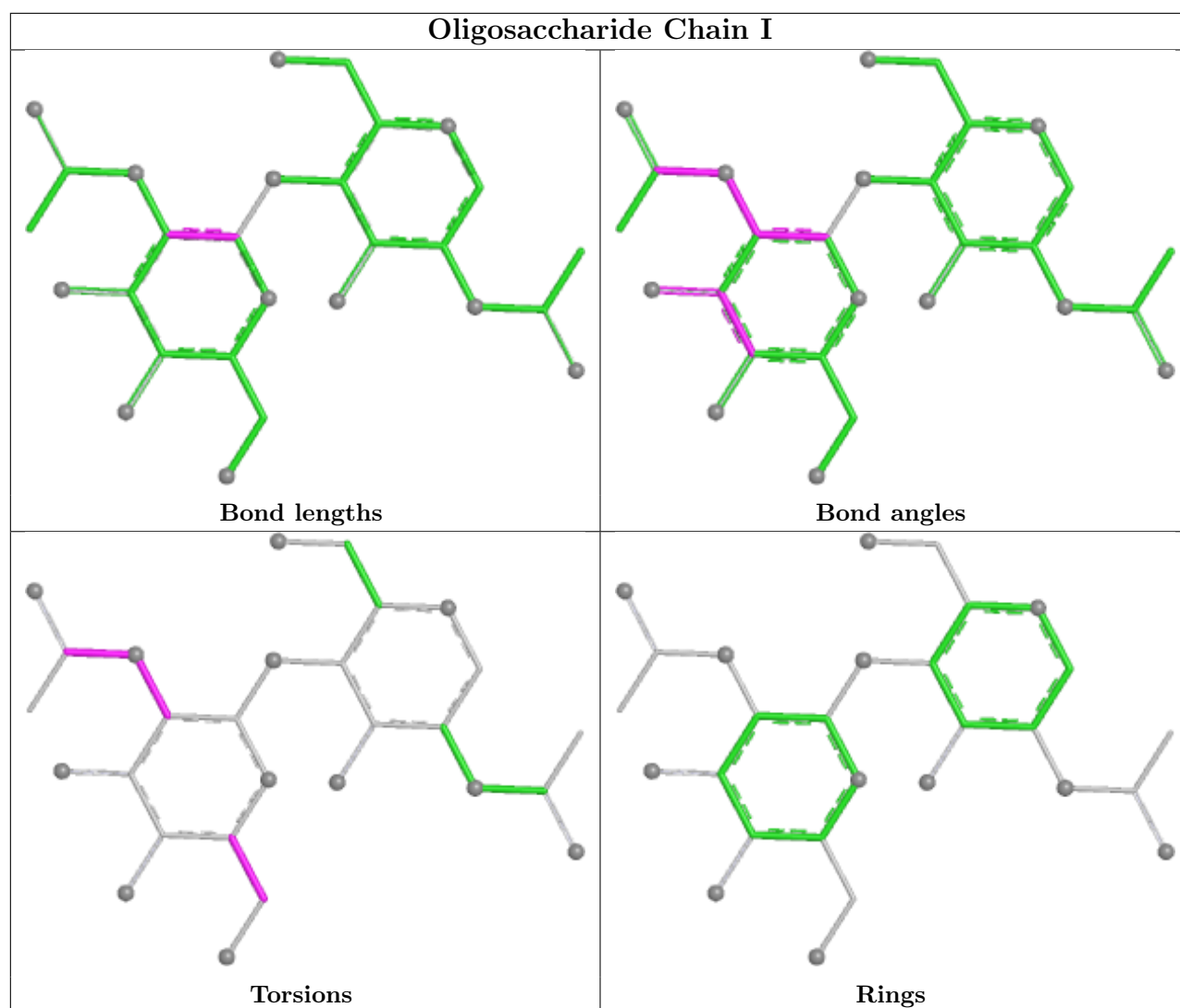
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	2	NAG	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

11 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	$\# Z > 2$
7	GOL	A	306	-	5,5,5	0.86	0	5,5,5	1.08	0
6	NAG	A	302	1	14,14,15	0.35	0	17,19,21	1.54	2 (11%)
6	NAG	C	301	1	14,14,15	0.62	0	17,19,21	0.96	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	A	303	1	14,14,15	0.49	0	17,19,21	0.60	0
7	GOL	D	301	-	5,5,5	0.96	0	5,5,5	1.09	0
6	NAG	C	304	1	14,14,15	0.38	0	17,19,21	0.69	1 (5%)
6	NAG	A	305	1	14,14,15	0.49	0	17,19,21	0.82	1 (5%)
6	NAG	C	302	1	14,14,15	0.37	0	17,19,21	0.82	1 (5%)
6	NAG	C	303	1	14,14,15	0.40	0	17,19,21	0.46	0
6	NAG	A	301	1	14,14,15	0.28	0	17,19,21	0.82	1 (5%)
6	NAG	A	304	1	14,14,15	0.54	0	17,19,21	0.62	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
7	GOL	A	306	-	-	0/4/4/4	-
6	NAG	A	302	1	-	6/6/23/26	0/1/1/1
6	NAG	C	301	1	-	2/6/23/26	0/1/1/1
6	NAG	A	303	1	-	2/6/23/26	0/1/1/1
7	GOL	D	301	-	-	2/4/4/4	-
6	NAG	C	304	1	-	2/6/23/26	0/1/1/1
6	NAG	A	305	1	-	2/6/23/26	0/1/1/1
6	NAG	C	302	1	-	2/6/23/26	0/1/1/1
6	NAG	C	303	1	-	1/6/23/26	0/1/1/1
6	NAG	A	301	1	-	4/6/23/26	0/1/1/1
6	NAG	A	304	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	302	NAG	C2-N2-C7	4.93	129.51	122.90
6	C	301	NAG	C1-O5-C5	3.56	116.96	112.19
6	A	302	NAG	C1-C2-N2	2.97	115.11	110.43
6	A	301	NAG	C1-O5-C5	2.85	116.00	112.19
6	A	305	NAG	C1-O5-C5	2.37	115.37	112.19

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	301	GOL	C1-C2-C3-O3
6	C	304	NAG	O5-C5-C6-O6
6	A	301	NAG	O5-C5-C6-O6
6	A	301	NAG	C4-C5-C6-O6
6	A	304	NAG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	302	NAG	1	0
7	D	301	GOL	1	0
6	A	305	NAG	2	0
6	C	302	NAG	2	0
6	A	304	NAG	3	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	210/240 (87%)	-0.37	1 (0%) 87 75	46, 71, 124, 154	0
1	C	207/240 (86%)	-0.37	0 100 100	58, 79, 124, 138	0
2	B	224/224 (100%)	-0.54	0 100 100	50, 66, 89, 102	0
2	D	223/224 (99%)	-0.45	0 100 100	47, 65, 90, 117	0
3	E	213/214 (99%)	-0.49	0 100 100	55, 75, 94, 112	0
3	F	212/214 (99%)	-0.41	0 100 100	57, 81, 102, 117	0
4	G	118/130 (90%)	-0.07	1 (0%) 82 66	61, 107, 148, 165	0
4	N	105/130 (80%)	-0.00	2 (1%) 66 45	68, 110, 141, 153	0
All	All	1512/1616 (93%)	-0.38	4 (0%) 90 81	46, 76, 124, 165	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	N	96	ASP	2.3
4	G	19	LEU	2.2
1	A	57	SER	2.1
4	N	21	ILE	2.0

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](#)

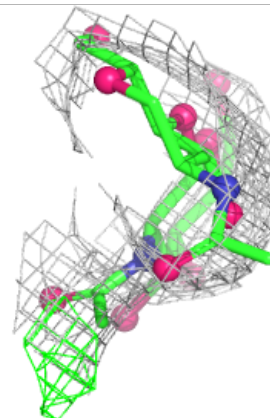
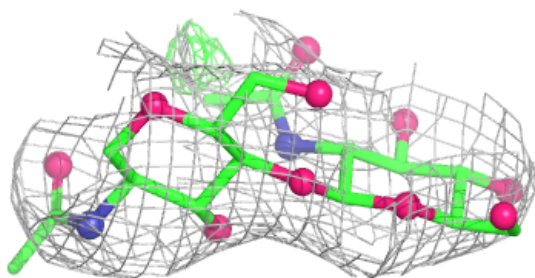
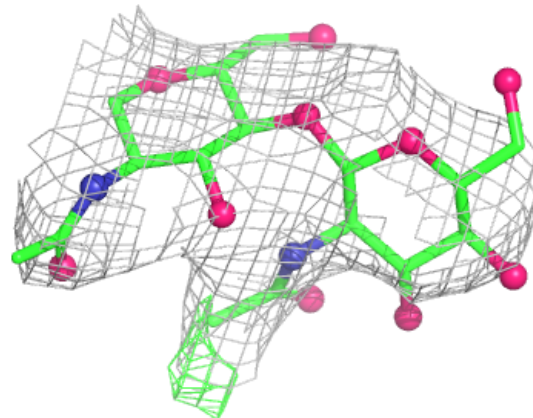
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

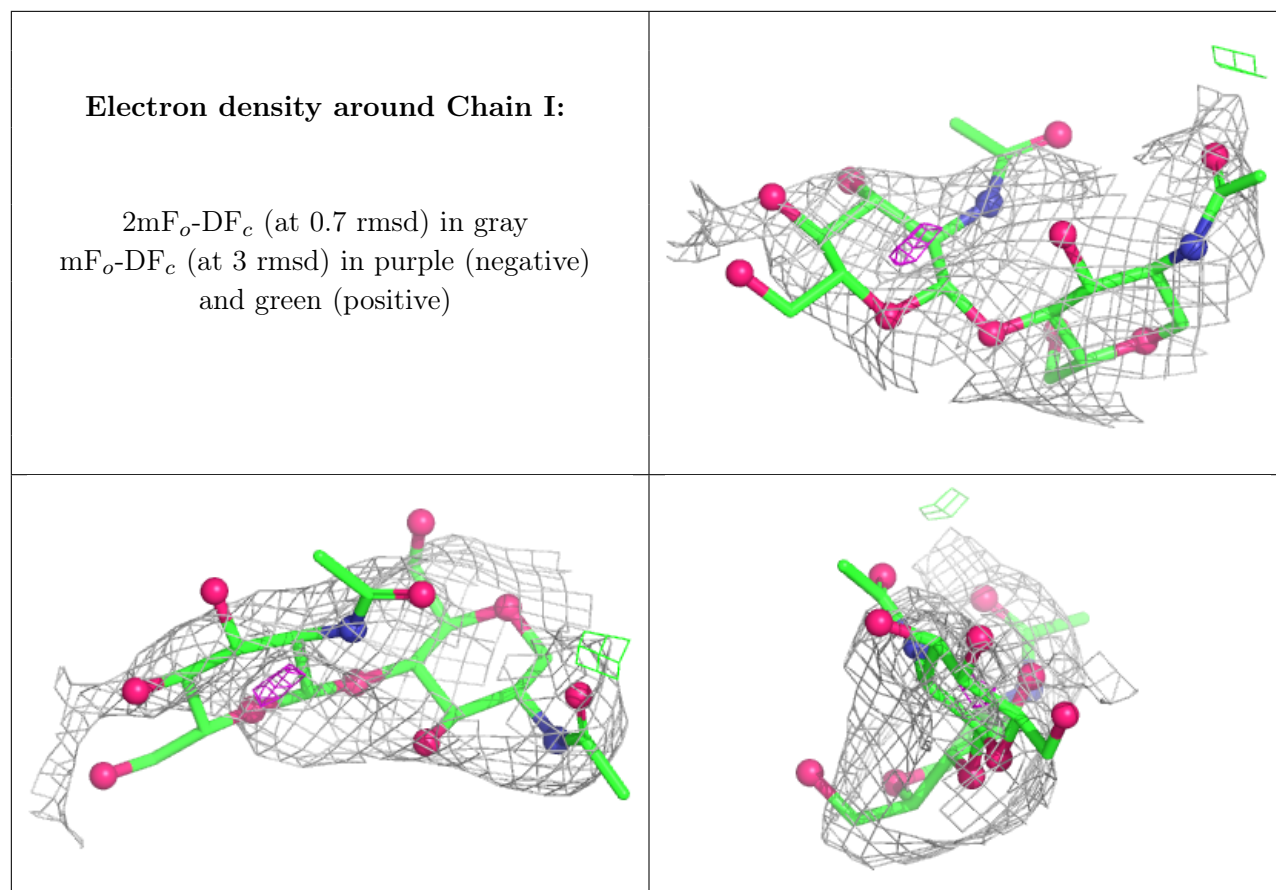
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	H	1	14/15	-	-	101,116,131,146	0
5	NAG	H	2	14/15	-	-	118,138,151,157	0
5	NAG	I	2	14/15	0.44	0.10	116,140,146,148	0
5	NAG	I	1	14/15	0.92	0.09	89,110,122,126	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain H:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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
6	NAG	C	303	14/15	0.35	0.11	105,118,124,128	0
6	NAG	A	305	14/15	0.41	0.11	105,136,154,155	0
6	NAG	C	302	14/15	0.47	0.12	104,109,120,122	0
6	NAG	A	303	14/15	0.57	0.09	117,126,134,137	0
6	NAG	A	301	14/15	0.70	0.10	83,98,123,123	0
7	GOL	A	306	6/6	0.73	0.12	58,75,85,88	0
6	NAG	A	304	14/15	0.81	0.11	77,90,100,101	0
6	NAG	A	302	14/15	0.83	0.12	78,94,109,129	0
6	NAG	C	301	14/15	0.88	0.10	73,91,101,102	0
7	GOL	D	301	6/6	0.89	0.11	63,78,86,87	0
6	NAG	C	304	14/15	0.94	0.07	64,79,88,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.