



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 19, 2024 – 11:10 AM EDT

PDB ID : 4Z7O
Title : Integrin alphaIIb beta3 in complex with AGDV peptide
Authors : Lin, F.Y.; Zhu, J.; Springer, T.A.
Deposited on : 2015-04-07
Resolution : 2.85 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

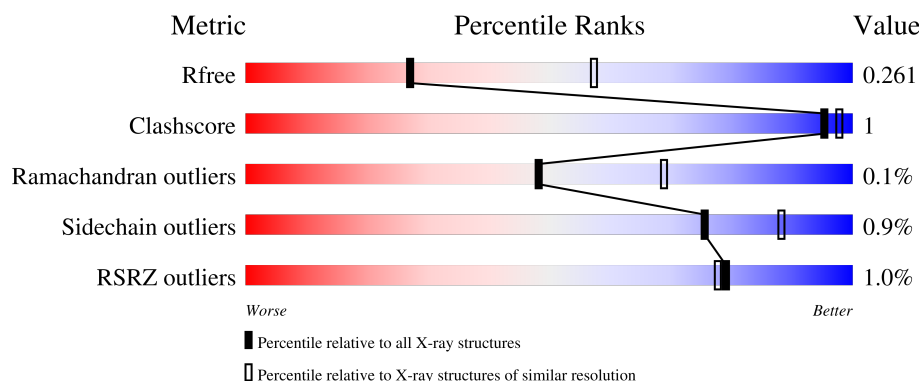
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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.





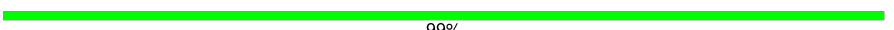
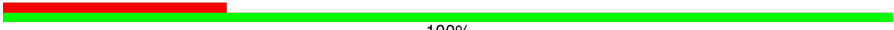


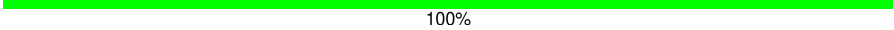


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1268 (2.88-2.84)
Clashscore	180529	1351 (2.88-2.84)
Ramachandran outliers	177936	1318 (2.88-2.84)
Sidechain outliers	177891	1319 (2.88-2.84)
RSRZ outliers	164620	1269 (2.88-2.84)

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	455	<div> <div>%</div> <div>96%</div> <div>.</div> </div>
1	C	455	<div> <div>%</div> <div>96%</div> <div>.</div> </div>
2	B	469	<div> <div>%</div> <div>94%</div> <div>5%</div> <div>.</div> </div>
2	D	469	<div> <div>2%</div> <div>97%</div> <div>.</div> </div>
3	E	221	<div> <div>95%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	221	 94%
4	F	214	 99%
4	L	214	 99%
5	G	4	 25% 100%
5	I	4	 25% 100%
6	J	5	 40% 40% 20%
7	K	2	 100%
7	N	2	 100%
8	M	4	 75% 25%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 41839 atoms, of which 20230 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 Integrin alpha-IIb.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	455	Total	C	H	N	O	S	0	5	0
			6886	2237	3369	607	665	8			
1	C	453	Total	C	H	N	O	S	0	1	0
			6796	2212	3315	600	661	8			

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	464	Total	C	H	N	O	S	0	1	0
			7066	2230	3484	612	707	33			
2	D	469	Total	C	H	N	O	S	0	0	0
			7140	2248	3528	617	713	34			

- Molecule 3 is a protein called Monoclonal antibody 10E5 Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	E	216	Total	C	H	N	O	S	0	0	0
			3242	1041	1600	266	329	6			
3	H	216	Total	C	H	N	O	S	0	0	0
			3243	1041	1601	266	329	6			

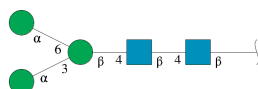
- Molecule 4 is a protein called Monoclonal antibody 10E5 Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	F	214	Total	C	H	N	O	S	0	0	0
			3190	1019	1553	268	341	9			
4	L	214	Total	C	H	N	O	S	0	0	0
			3191	1019	1554	268	341	9			

- Molecule 5 is a protein called Tetrapeptide ALA-GLY-ASP-VAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	4	Total	C	H	N	O	0	0	0
			45	14	20	4	7			
5	I	4	Total	C	H	N	O	0	0	0
			45	14	20	4	7			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	5	Total	C	H	N	O	0	0	0
			118	34	57	2	25			

- Molecule 7 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
7	K	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
7	N	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	M	4	Total	C	H	N	O	0	0	0
			97	28	47	2	20			

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 10 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	4	Total	Ca	0	0
			4	4		
10	C	4	Total	Ca	0	0
			4	4		

- Molecule 11 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	3	Total	Mn	0	0
			3	3		
11	D	3	Total	Mn	0	0
			3	3		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
12	D	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 13 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	1	Total	Cl	0	0
			1	1		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	265	Total	O	0	0
			265	265		
14	B	117	Total	O	0	0
			117	117		
14	C	84	Total	O	0	0
			84	84		
14	D	64	Total	O	0	0
			64	64		
14	E	5	Total	O	0	0
			5	5		
14	F	9	Total	O	0	0
			9	9		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	H	22	Total 22	O 22	0	0
14	L	16	Total 16	O 16	0	0
14	G	2	Total 2	O 2	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: Integrin alpha-IIb



- Molecule 1: Integrin alpha-IIb



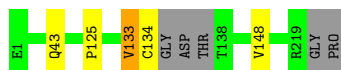
- Molecule 2: Integrin beta-3



- Molecule 2: Integrin beta-3

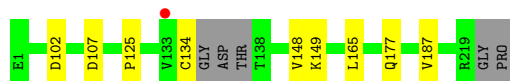


- Molecule 3: Monoclonal antibody 10E5 Fab heavy chain



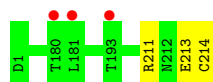
- Molecule 3: Monoclonal antibody 10E5 Fab heavy chain

Chain H:  94%



- Molecule 4: Monoclonal antibody 10E5 Fab light chain

Chain F:  99%



- Molecule 4: Monoclonal antibody 10E5 Fab light chain

Chain L:  99%



- Molecule 5: Tetrapeptide ALA-GLY-ASP-VAL

Chain G:  100%



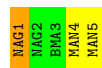
- Molecule 5: Tetrapeptide ALA-GLY-ASP-VAL

Chain I:  100%



- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  40% 40% 20%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%




- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

NAG1
NAG2

- Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  75% 25%

NAG1
NAG2
BMA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	259.92Å 144.52Å 104.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.03 – 2.85 49.03 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.8 (49.03-2.85) 84.1 (49.03-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.28 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.10_2142: ???)	Depositor
R, R_{free}	0.223 , 0.257 0.236 , 0.261	Depositor DCC
R_{free} test set	2000 reflections (2.18%)	wwPDB-VP
Wilson B-factor (Å ²)	59.4	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 74.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	41839	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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: SO4, NAG, CA, MN, BMA, MAN, CL

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	0.29	0/3629	0.44	0/4944
1	C	0.26	0/3581	0.42	0/4880
2	B	0.26	0/3651	0.43	0/4950
2	D	0.26	0/3678	0.41	0/4986
3	E	0.25	0/1684	0.42	0/2305
3	H	0.24	0/1684	0.43	0/2305
4	F	0.25	0/1673	0.41	0/2269
4	L	0.25	0/1673	0.42	0/2269
5	G	0.19	0/24	0.45	0/30
5	I	0.25	0/24	0.48	0/30
All	All	0.26	0/21301	0.42	0/28968

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	3517	3369	3370	10	0
1	C	3481	3315	3315	8	0
2	B	3582	3484	3495	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3612	3528	3526	6	0
3	E	1642	1600	1600	3	0
3	H	1642	1601	1600	6	0
4	F	1637	1553	1553	1	0
4	L	1637	1554	1553	2	0
5	G	25	20	20	0	0
5	I	25	20	20	0	0
6	J	61	57	52	1	0
7	K	28	27	25	0	0
7	N	28	27	25	0	0
8	M	50	47	43	0	0
9	A	5	0	0	0	0
9	C	5	0	0	0	0
9	L	5	0	0	0	0
10	A	4	0	0	0	0
10	C	4	0	0	0	0
11	B	3	0	0	0	0
11	D	3	0	0	0	0
12	B	14	14	13	0	0
12	D	14	14	13	0	0
13	C	1	0	0	0	0
14	A	265	0	0	5	1
14	B	117	0	0	1	0
14	C	84	0	0	4	1
14	D	64	0	0	1	0
14	E	5	0	0	0	0
14	F	9	0	0	0	0
14	G	2	0	0	0	0
14	H	22	0	0	1	0
14	L	16	0	0	1	0
All	All	21609	20230	20223	44	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 1.

The worst 5 of 44 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:A:351:GLN:OE1	14:A:601:HOH:O	2.13	0.67
1:A:15[B]:ASN:OD1	14:A:602:HOH:O	2.15	0.65
4:L:157:ASN:OD1	14:L:401:HOH:O	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:320:ASN:ND2	6:J:1:NAG:O7	2.37	0.56
1:A:142:GLU:OE1	14:A:603:HOH:O	2.18	0.56

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)
14:A:833:HOH:O	14:C:650:HOH:O[1_554]	2.14	0.06

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	458/455 (101%)	432 (94%)	26 (6%)	0	100	100
1	C	452/455 (99%)	429 (95%)	23 (5%)	0	100	100
2	B	463/469 (99%)	435 (94%)	26 (6%)	2 (0%)	30	49
2	D	467/469 (100%)	438 (94%)	28 (6%)	1 (0%)	44	63
3	E	212/221 (96%)	198 (93%)	13 (6%)	1 (0%)	25	43
3	H	212/221 (96%)	202 (95%)	10 (5%)	0	100	100
4	F	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
4	L	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
5	G	2/4 (50%)	2 (100%)	0	0	100	100
5	I	2/4 (50%)	2 (100%)	0	0	100	100
All	All	2692/2726 (99%)	2545 (94%)	143 (5%)	4 (0%)	48	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	133	VAL
2	B	139	ALA
2	D	374	CYS
2	B	157	VAL

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	368/363 (101%)	362 (98%)	6 (2%)	58	79
1	C	362/363 (100%)	359 (99%)	3 (1%)	79	90
2	B	411/415 (99%)	405 (98%)	6 (2%)	60	81
2	D	415/415 (100%)	411 (99%)	4 (1%)	73	87
3	E	187/190 (98%)	187 (100%)	0	100	100
3	H	187/190 (98%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	86	94
4	L	188/188 (100%)	187 (100%)	1 (0%)	86	94
5	G	2/2 (100%)	2 (100%)	0	100	100
5	I	2/2 (100%)	2 (100%)	0	100	100
All	All	2310/2316 (100%)	2289 (99%)	21 (1%)	75	88

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	288	TYR
2	D	215	ASN
4	L	214	CYS
2	D	365	GLU
2	D	158	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	132	GLN
2	D	280	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 ⓘ

13 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$
6	NAG	J	1	2,6	14,14,15	0.40	0	17,19,21	0.67	1 (5%)
6	NAG	J	2	6	14,14,15	0.23	0	17,19,21	0.49	0
6	BMA	J	3	6	11,11,12	0.64	0	15,15,17	0.96	0
6	MAN	J	4	6	11,11,12	0.48	0	15,15,17	0.89	1 (6%)
6	MAN	J	5	6	11,11,12	0.64	0	15,15,17	1.26	2 (13%)
7	NAG	K	1	7,2	14,14,15	0.48	0	17,19,21	0.47	0
7	NAG	K	2	7	14,14,15	0.17	0	17,19,21	0.46	0
8	NAG	M	1	2,8	14,14,15	0.55	0	17,19,21	0.51	0
8	NAG	M	2	8	14,14,15	0.34	0	17,19,21	0.54	0
8	BMA	M	3	8	11,11,12	0.71	0	15,15,17	0.78	0
8	MAN	M	4	8	11,11,12	0.53	0	15,15,17	1.04	2 (13%)
7	NAG	N	1	7,2	14,14,15	0.41	0	17,19,21	0.48	0
7	NAG	N	2	7	14,14,15	0.28	0	17,19,21	0.44	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
6	NAG	J	1	2,6	-	4/6/23/26	0/1/1/1
6	NAG	J	2	6	-	0/6/23/26	0/1/1/1
6	BMA	J	3	6	-	2/2/19/22	0/1/1/1
6	MAN	J	4	6	-	0/2/19/22	0/1/1/1
6	MAN	J	5	6	-	2/2/19/22	0/1/1/1
7	NAG	K	1	7,2	-	0/6/23/26	0/1/1/1
7	NAG	K	2	7	-	2/6/23/26	0/1/1/1
8	NAG	M	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	M	2	8	-	0/6/23/26	0/1/1/1
8	BMA	M	3	8	-	0/2/19/22	0/1/1/1
8	MAN	M	4	8	-	0/2/19/22	0/1/1/1
7	NAG	N	1	7,2	-	0/6/23/26	0/1/1/1
7	NAG	N	2	7	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	5	MAN	C1-O5-C5	3.85	117.35	112.19
8	M	4	MAN	C1-O5-C5	2.88	116.05	112.19
6	J	5	MAN	O2-C2-C3	-2.18	105.63	110.15
6	J	4	MAN	C1-O5-C5	2.13	115.04	112.19
8	M	4	MAN	O2-C2-C3	-2.10	105.79	110.15

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

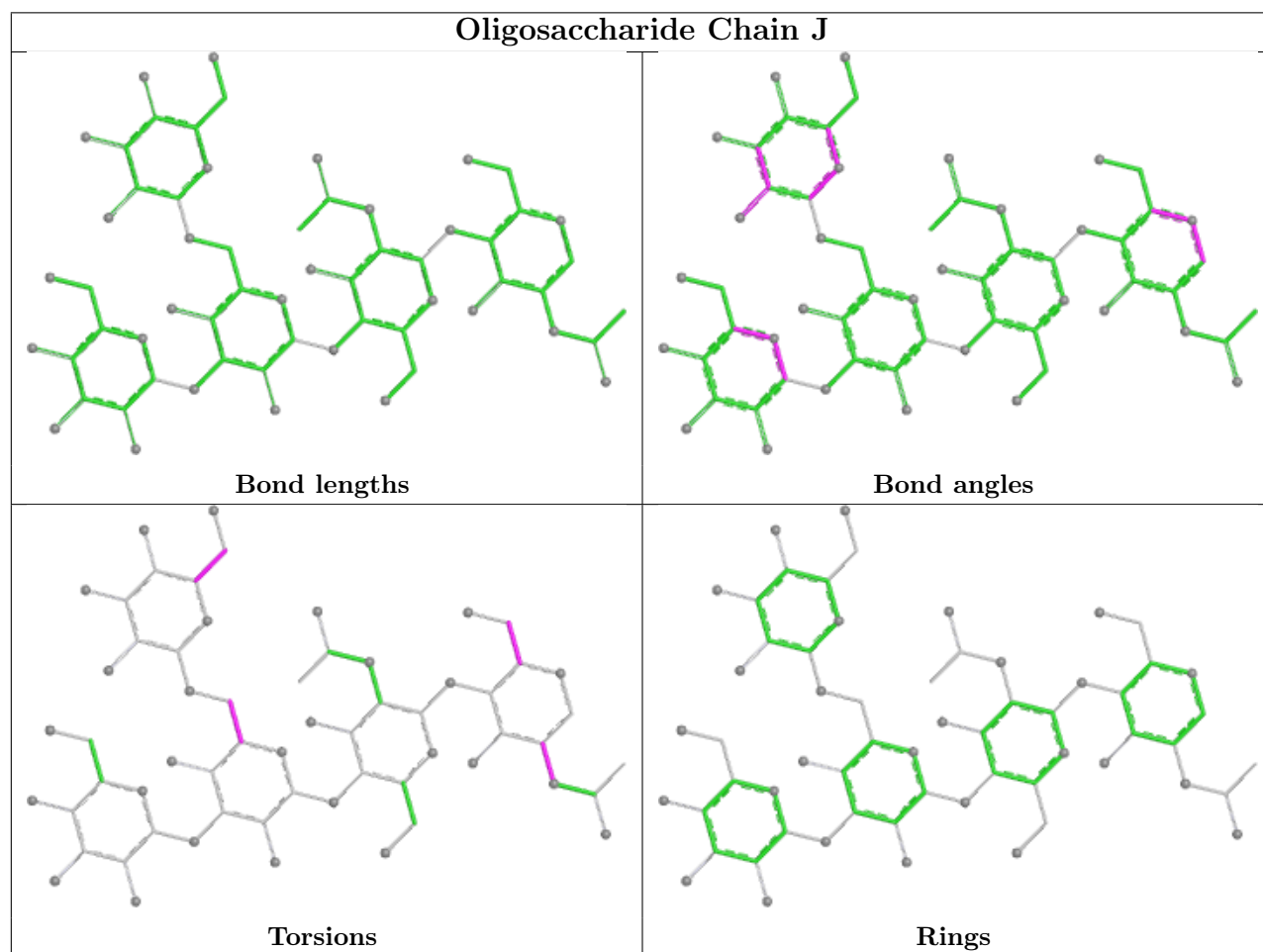
Mol	Chain	Res	Type	Atoms
7	K	2	NAG	O5-C5-C6-O6
6	J	3	BMA	O5-C5-C6-O6
6	J	5	MAN	O5-C5-C6-O6
7	K	2	NAG	C4-C5-C6-O6
6	J	5	MAN	C4-C5-C6-O6

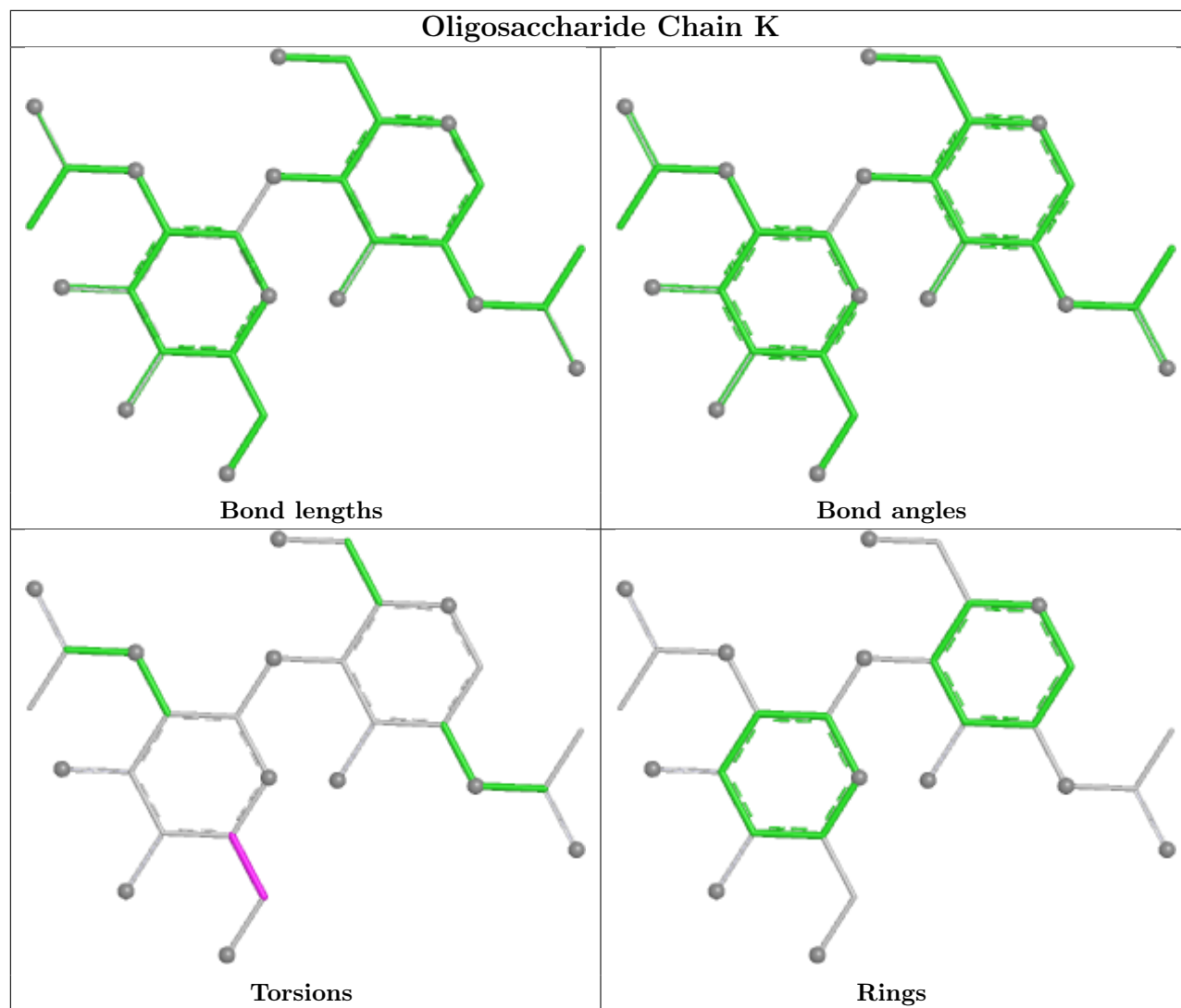
There are no ring outliers.

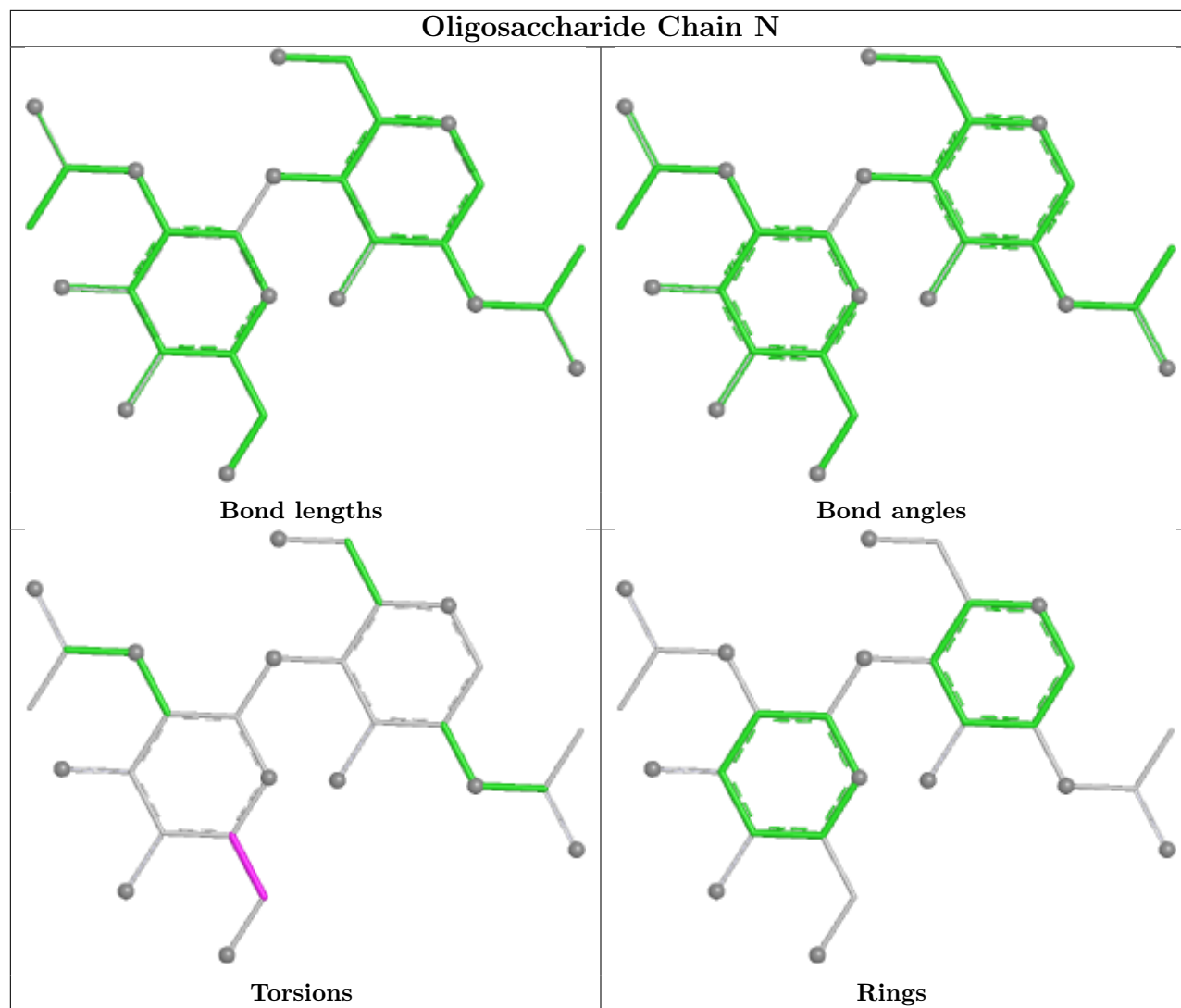
1 monomer is involved in 1 short contact:

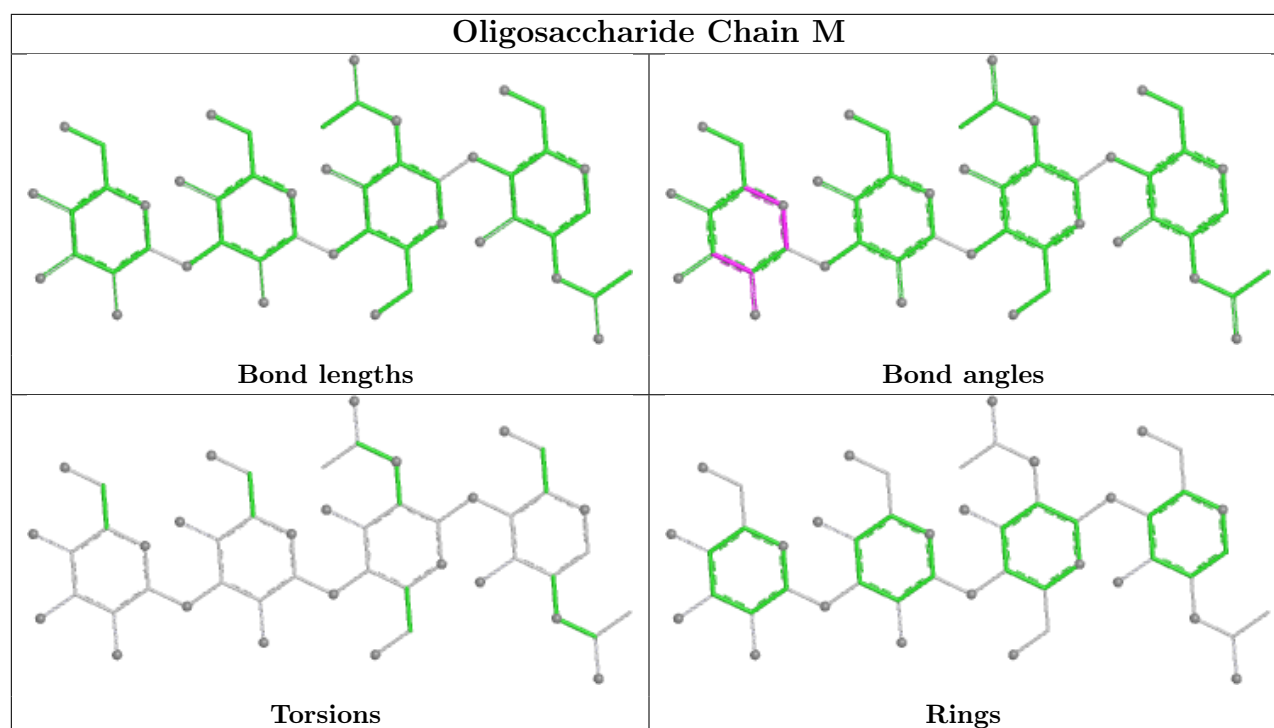
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	1	NAG	1	0

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](#)

Of 20 ligands modelled in this entry, 15 are monoatomic - leaving 5 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	$\# Z > 2$
12	NAG	B	2004	2	14,14,15	0.55	0	17,19,21	0.75	1 (5%)
12	NAG	D	2004	2	14,14,15	0.38	0	17,19,21	0.60	0
9	SO4	A	501	-	4,4,4	0.24	0	6,6,6	0.04	0
9	SO4	C	501	-	4,4,4	0.24	0	6,6,6	0.05	0
9	SO4	L	301	-	4,4,4	0.23	0	6,6,6	0.06	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
12	NAG	D	2004	2	-	2/6/23/26	0/1/1/1
12	NAG	B	2004	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	2004	NAG	C1-O5-C5	2.55	115.60	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	B	2004	NAG	O5-C5-C6-O6
12	D	2004	NAG	O5-C5-C6-O6
12	D	2004	NAG	C4-C5-C6-O6
12	B	2004	NAG	C4-C5-C6-O6

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	455/455 (100%)	-0.33	4 (0%) 81 79	34, 74, 108, 207	5 (1%)
1	C	453/455 (99%)	0.00	3 (0%) 84 83	65, 105, 149, 194	1 (0%)
2	B	464/469 (98%)	-0.16	3 (0%) 85 84	52, 114, 200, 267	1 (0%)
2	D	469/469 (100%)	0.22	10 (2%) 63 60	80, 141, 201, 282	0
3	E	216/221 (97%)	0.31	0 100 100	121, 195, 279, 303	0
3	H	216/221 (97%)	0.07	1 (0%) 87 86	80, 145, 210, 243	0
4	F	214/214 (100%)	0.28	3 (1%) 73 70	125, 187, 277, 329	0
4	L	214/214 (100%)	-0.11	0 100 100	85, 130, 165, 251	0
5	G	4/4 (100%)	0.78	1 (25%) 2 2	66, 89, 101, 102	0
5	I	4/4 (100%)	1.33	1 (25%) 2 2	101, 112, 116, 138	0
All	All	2709/2726 (99%)	0.00	26 (0%) 79 78	34, 123, 227, 329	7 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	454	VAL	5.4
2	D	151	ILE	3.8
1	A	455	LYS	3.6
2	D	375	LEU	3.3
1	C	1	LEU	3.3

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](#)

SUGAR-RSR INFOmissingINFO

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
12	NAG	D	2004	14/15	0.64	0.11	114,142,170,175	0
11	MN	D	2002	1/1	0.65	0.23	431,431,431,431	0
12	NAG	B	2004	14/15	0.73	0.10	118,139,166,167	0
11	MN	B	2002	1/1	0.73	0.19	361,361,361,361	0
9	SO4	L	301	5/5	0.80	0.09	151,154,159,161	0
9	SO4	C	501	5/5	0.86	0.20	184,193,196,198	0
9	SO4	A	501	5/5	0.90	0.14	118,124,133,142	0
13	CL	C	502	1/1	0.91	0.11	85,85,85,85	0
11	MN	D	2003	1/1	0.95	0.10	216,216,216,216	0
10	CA	C	504	1/1	0.95	0.07	168,168,168,168	0
10	CA	C	506	1/1	0.98	0.06	108,108,108,108	0
10	CA	C	503	1/1	0.98	0.08	197,197,197,197	0
11	MN	D	2001	1/1	0.98	0.05	121,121,121,121	0
10	CA	A	504	1/1	0.98	0.04	57,57,57,57	0
10	CA	A	503	1/1	0.99	0.05	80,80,80,80	0
11	MN	B	2001	1/1	0.99	0.04	57,57,57,57	0
10	CA	A	502	1/1	0.99	0.03	77,77,77,77	0
11	MN	B	2003	1/1	0.99	0.03	90,90,90,90	0
10	CA	C	505	1/1	0.99	0.03	99,99,99,99	0
10	CA	A	505	1/1	1.00	0.02	66,66,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.