



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:57 PM UTC

PDB ID : 7U9V / pdb_00007u9v
Title : Integrin alpha IIB beta3 complex with BMS4-1
Authors : Zhu, J.; Lin, F.-Y.; Zhu, J.; Springer, T.A.
Deposited on : 2022-03-11
Resolution : 2.25 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

<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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

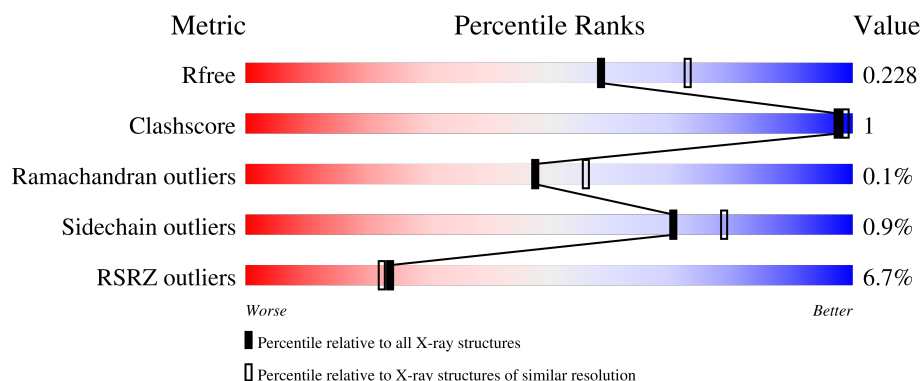
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	454	96% .
1	C	454	96% .
2	B	471	6% 95% ..
2	D	471	5% 95% 5%
3	E	216	25% 98% ..

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Mol	Chain	Length	Quality of chain
3	H	216	9% 98%
4	F	214	20% 97%
4	L	214	% 99%
5	G	5	60% 40%
6	I	2	100%
6	K	2	50% 50%
7	J	4	50% 50%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 22257 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 Integrin alpha-IIb.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	4	0
			3499	2226	601	664	8			
1	C	453	Total	C	N	O	S	0	4	0
			3502	2224	604	666	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	466	Total	C	N	O	S	4	7	0
			3643	2267	621	721	34			
2	D	471	Total	C	N	O	S	3	1	0
			3634	2265	620	715	34			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	214	Total	C	N	O	S	0	0	0
			1631	1035	264	326	6			
3	H	216	Total	C	N	O	S	0	0	0
			1642	1041	266	329	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			
4	L	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			

- Molecule 5 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
5	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 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
6	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
6	K	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 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
7	J	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 9 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 10 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

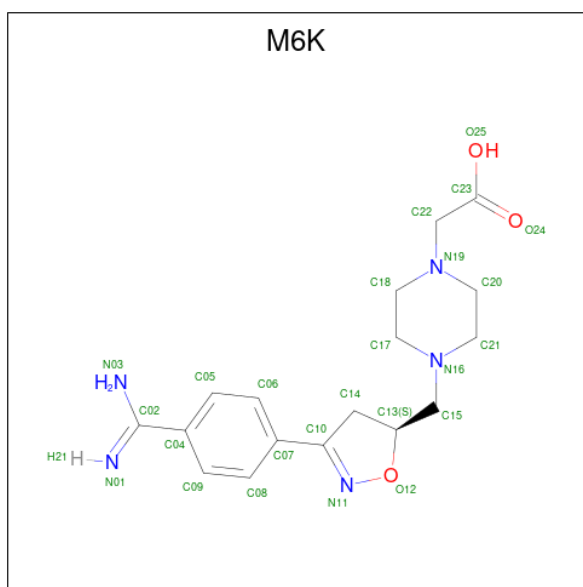
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	3	Total	Mn	0	0
			3	3		
10	D	3	Total	Mn	0	0
			3	3		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 12 is (4-[(5S)-3-(4-carbamimidoylphenyl)-4,5-dihydro-1,2-oxazol-5-yl]methyl} piperazin-1-yl)acetic acid (CCD ID: M6K) (formula: $C_{17}H_{23}N_5O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	C	N	O	0	0
			25	17	5	3		
12	D	1	Total	C	N	O	0	0
			25	17	5	3		

- Molecule 13 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	410	Total	O	0	0
			410	410		
14	B	236	Total	O	0	0
			236	236		
14	C	186	Total	O	0	0
			186	186		
14	D	156	Total	O	0	0
			156	156		
14	E	19	Total	O	0	0
			19	19		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	F	20	Total 20	O 20	0	0
14	H	33	Total 33	O 33	0	0
14	L	65	Total 65	O 65	0	0

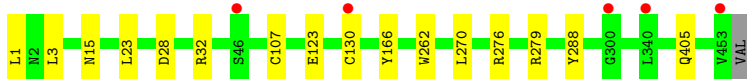
3 Residue-property plots [i](#)

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.

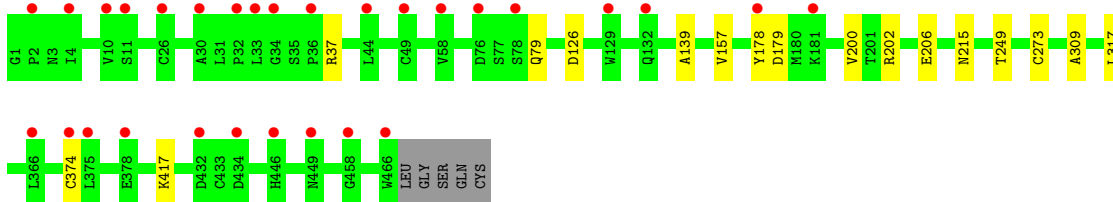
- Molecule 1: Integrin alpha-IIb



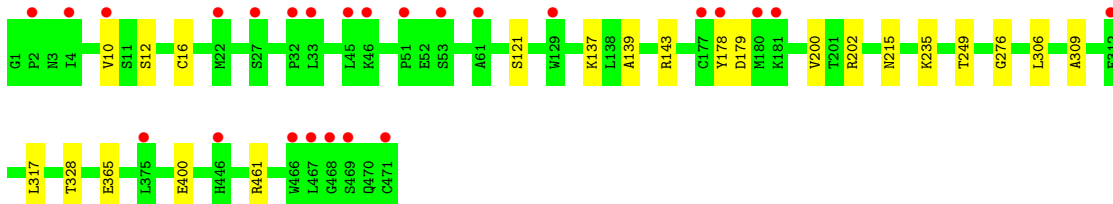
- Molecule 1: Integrin alpha-IIb



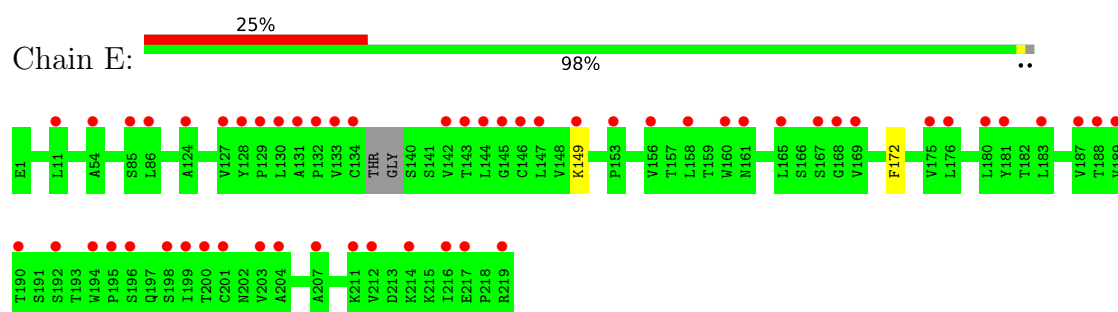
- Molecule 2: Integrin beta-3



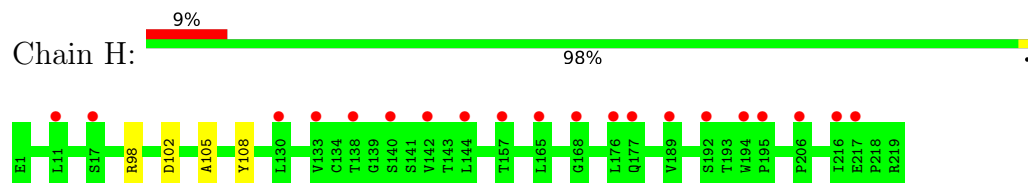
- Molecule 2: Integrin beta-3



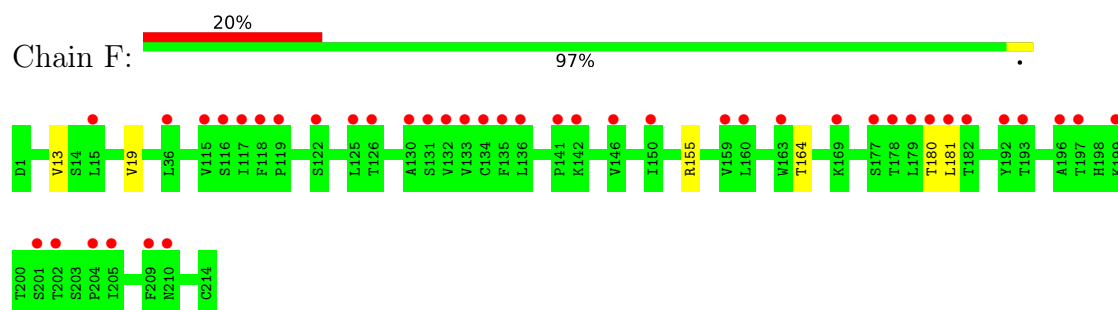
- Molecule 3: 10E5 Fab heavy chain



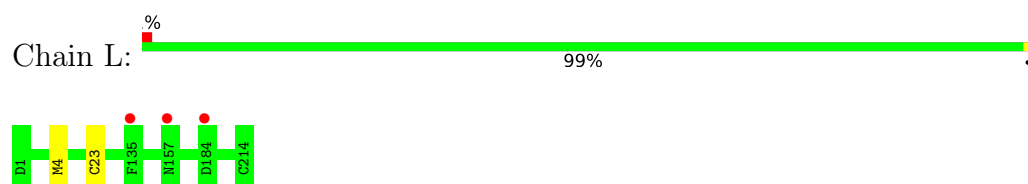
- Molecule 3: 10E5 Fab heavy chain



- Molecule 4: 10E5 light chain



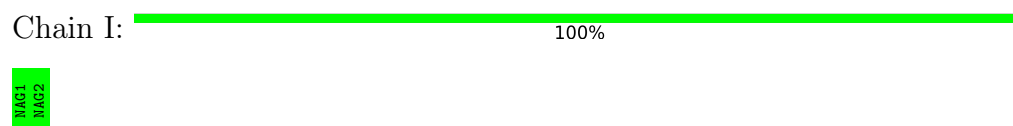
- Molecule 4: 10E5 light chain



- Molecule 5: 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



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%


MAG1
MAG2

- Molecule 7: 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 J:  50% 50%


MAG1
MAG2
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	257.80Å 143.89Å 104.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.95 – 2.25 44.95 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.2 (44.95-2.25) 86.6 (44.95-2.25)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.203 , 0.226 0.205 , 0.228	Depositor DCC
R_{free} test set	1999 reflections (1.09%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.5	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	0.95	EDS
Total number of atoms	22257	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: CA, NAG, BMA, MN, MAN, SO4, CL, M6K

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	0.11	0/3608	0.35	0/4918
1	C	0.10	0/3605	0.33	0/4912
2	B	0.11	0/3713	0.31	0/5034
2	D	0.10	0/3706	0.30	0/5026
3	E	0.11	0/1673	0.28	0/2290
3	H	0.09	0/1684	0.29	0/2305
4	F	0.11	0/1673	0.28	0/2269
4	L	0.10	0/1673	0.28	0/2269
All	All	0.11	0/21335	0.31	0/29023

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	3499	0	3345	7	0
1	C	3502	0	3334	5	0
2	B	3643	0	3553	7	0
2	D	3634	0	3550	11	0
3	E	1631	0	1590	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	0	1600	2	0
4	F	1637	0	1553	4	0
4	L	1637	0	1553	1	0
5	G	61	0	52	0	0
6	I	28	0	25	0	0
6	K	28	0	25	1	0
7	J	50	0	43	0	0
8	A	20	0	0	0	0
8	C	20	0	0	0	0
8	L	5	0	0	0	0
9	A	4	0	0	0	0
9	C	4	0	0	0	0
10	B	3	0	0	0	0
10	D	3	0	0	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	B	25	0	0	0	0
12	D	25	0	0	1	0
13	C	2	0	0	0	0
13	D	1	0	0	0	0
14	A	410	0	0	1	0
14	B	236	0	0	1	0
14	C	186	0	0	0	0
14	D	156	0	0	0	0
14	E	19	0	0	0	0
14	F	20	0	0	1	0
14	H	33	0	0	0	0
14	L	65	0	0	0	0
All	All	22257	0	20249	34	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 1.

All (34) 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)
2:B:273:CYS:SG	14:B:2290:HOH:O	2.55	0.64
2:B:126[A]:ASP:OD1	2:B:126[A]:ASP:N	2.39	0.55
4:F:155:ARG:NH1	14:F:302:HOH:O	2.40	0.54
1:C:3:LEU:O	1:C:405:GLN:NE2	2.32	0.52
2:B:202:ARG:NH2	2:B:206:GLU:OE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:THR:HB	1:A:447:VAL:HB	1.92	0.50
1:A:262:TRP:HB3	2:B:317:LEU:HD13	1.94	0.49
1:C:107:CYS:HA	1:C:130:CYS:HA	1.94	0.48
2:B:139:ALA:HB2	2:B:200:VAL:HG11	1.94	0.48
1:A:422:ARG:NH1	14:A:613:HOH:O	2.46	0.46
2:D:139:ALA:HB2	2:D:200:VAL:HG11	1.99	0.44
1:A:159:ASP:CG	2:D:137:LYS:HE2	2.43	0.44
2:D:10:VAL:HG21	2:D:16:CYS:HB2	2.00	0.44
2:D:400:GLU:HB2	6:K:1:NAG:H83	2.00	0.43
1:A:107:CYS:HA	1:A:130:CYS:HA	1.99	0.43
3:H:98:ARG:HG3	3:H:108:TYR:HB2	2.01	0.43
1:C:262:TRP:HB3	2:D:317:LEU:HD13	2.01	0.42
2:B:249:THR:HA	2:B:309:ALA:O	2.19	0.42
2:D:178:TYR:CG	2:D:179:ASP:N	2.87	0.42
2:D:235:LYS:HE3	2:D:276:GLY:O	2.20	0.42
2:D:306:LEU:HB3	2:D:328:THR:HG22	2.01	0.42
4:L:4:MET:HE3	4:L:23:CYS:SG	2.60	0.42
1:A:192:LEU:HD11	1:A:231:PHE:CD1	2.55	0.42
2:D:121:SER:HB2	12:D:2006:M6K:O24	2.19	0.41
1:C:276:ARG:HD2	1:C:279:ARG:HB2	2.03	0.41
4:F:13:VAL:HG11	4:F:19:VAL:HG11	2.02	0.41
3:E:172:PHE:CD2	4:F:164:THR:HG23	2.56	0.41
1:A:3:LEU:O	1:A:5:PRO:HD3	2.21	0.41
3:H:102:ASP:HB3	3:H:105:ALA:HB2	2.03	0.41
2:B:178:TYR:CG	2:B:179:ASP:N	2.89	0.41
1:C:28:ASP:OD1	1:C:32:ARG:N	2.54	0.40
2:D:249:THR:HA	2:D:309:ALA:O	2.21	0.40
2:D:12:SER:HB3	2:D:461:ARG:HD3	2.03	0.40
3:E:149:LYS:NZ	4:F:180:THR:HG21	2.36	0.40

There are no symmetry-related clashes.

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	456/454 (100%)	444 (97%)	11 (2%)	1 (0%)	43	50
1	C	455/454 (100%)	440 (97%)	14 (3%)	1 (0%)	43	50
2	B	471/471 (100%)	458 (97%)	12 (2%)	1 (0%)	43	50
2	D	470/471 (100%)	453 (96%)	17 (4%)	0	100	100
3	E	210/216 (97%)	194 (92%)	16 (8%)	0	100	100
3	H	212/216 (98%)	199 (94%)	13 (6%)	0	100	100
4	F	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
4	L	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
All	All	2698/2710 (100%)	2594 (96%)	101 (4%)	3 (0%)	48	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
1	C	123	GLU
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	366/362 (101%)	362 (99%)	4 (1%)	65	75
1	C	365/362 (101%)	359 (98%)	6 (2%)	55	66
2	B	419/416 (101%)	414 (99%)	5 (1%)	63	74
2	D	417/416 (100%)	413 (99%)	4 (1%)	68	77
3	E	186/187 (100%)	186 (100%)	0	100	100
3	H	187/187 (100%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	81	87
4	L	188/188 (100%)	188 (100%)	0	100	100
All	All	2316/2306 (100%)	2296 (99%)	20 (1%)	70	79

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	166	TYR
1	A	270	LEU
1	A	288	TYR
2	B	37	ARG
2	B	79	GLN
2	B	215	ASN
2	B	374	CYS
2	B	417	LYS
1	C	1	LEU
1	C	15	ASN
1	C	23	LEU
1	C	166	TYR
1	C	270	LEU
1	C	288	TYR
2	D	143	ARG
2	D	202	ARG
2	D	215	ASN
2	D	365	GLU
4	F	181	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	197	GLN
1	A	215	HIS
1	A	372	ASN
1	A	444	GLN
1	C	30	HIS
1	C	158	ASN
1	C	197	GLN
1	C	215	HIS
2	D	15	GLN
2	D	133	ASN
2	D	319	GLN
4	F	137	ASN
4	L	137	ASN

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$
5	NAG	G	1	2,5	14,14,15	0.34	0	17,19,21	0.54	0
5	NAG	G	2	5	14,14,15	0.15	0	17,19,21	0.47	0
5	BMA	G	3	5	11,11,12	0.82	0	15,15,17	0.76	0
5	MAN	G	4	5	11,11,12	0.62	0	15,15,17	1.05	2 (13%)
5	MAN	G	5	5	11,11,12	0.65	0	15,15,17	1.04	2 (13%)
6	NAG	I	1	2,6	14,14,15	0.32	0	17,19,21	0.38	0
6	NAG	I	2	6	14,14,15	0.35	0	17,19,21	0.41	0
7	NAG	J	1	2,7	14,14,15	0.36	0	17,19,21	0.56	0
7	NAG	J	2	7	14,14,15	0.27	0	17,19,21	0.42	0
7	BMA	J	3	7	11,11,12	1.06	1 (9%)	15,15,17	1.11	1 (6%)
7	MAN	J	4	7	11,11,12	0.75	0	15,15,17	1.10	2 (13%)
6	NAG	K	1	2,6	14,14,15	0.26	0	17,19,21	0.45	0
6	NAG	K	2	6	14,14,15	0.22	0	17,19,21	0.49	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
5	NAG	G	1	2,5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	2/2/19/22	0/1/1/1
5	MAN	G	5	5	-	1/2/19/22	0/1/1/1
6	NAG	I	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	I	2	6	-	3/6/23/26	0/1/1/1
7	NAG	J	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	2/2/19/22	0/1/1/1
6	NAG	K	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	3	BMA	C4-C5	2.05	1.57	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	4	MAN	C1-O5-C5	3.01	116.22	112.19
5	G	5	MAN	C1-O5-C5	2.92	116.10	112.19
7	J	4	MAN	C1-O5-C5	2.89	116.06	112.19
7	J	3	BMA	C3-C4-C5	2.72	115.17	110.23
7	J	4	MAN	O2-C2-C3	-2.26	105.47	110.15
5	G	4	MAN	O2-C2-C3	-2.16	105.69	110.15
5	G	5	MAN	O2-C2-C3	-2.12	105.75	110.15

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	J	3	BMA	O5-C5-C6-O6
7	J	3	BMA	C4-C5-C6-O6
7	J	4	MAN	O5-C5-C6-O6
5	G	4	MAN	O5-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	K	2	NAG	C8-C7-N2-C2

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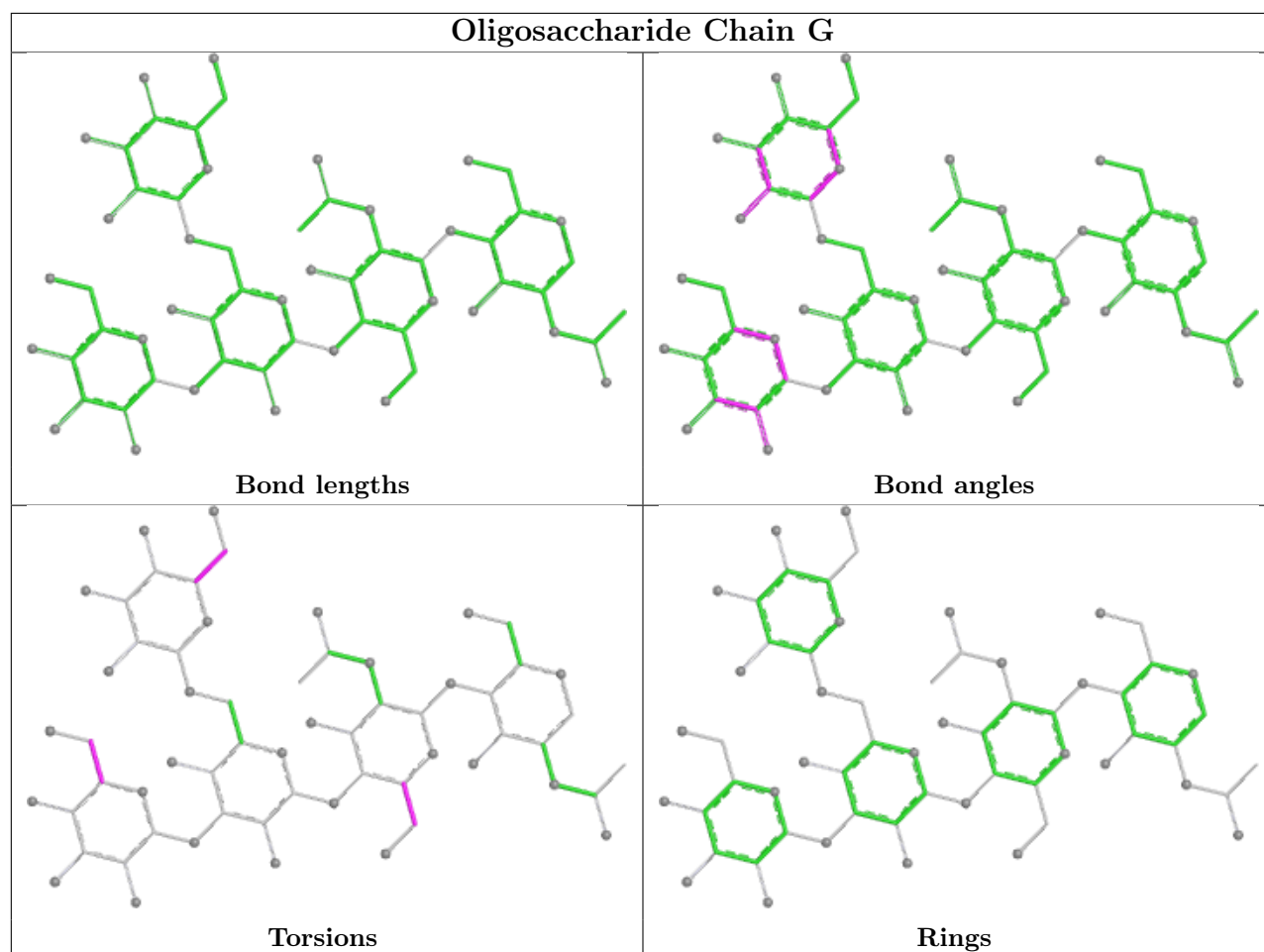
Mol	Chain	Res	Type	Atoms
6	K	2	NAG	O7-C7-N2-C2
6	I	1	NAG	C4-C5-C6-O6
7	J	4	MAN	C4-C5-C6-O6
5	G	4	MAN	C4-C5-C6-O6
5	G	2	NAG	C4-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
6	I	1	NAG	O5-C5-C6-O6
5	G	5	MAN	O5-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6

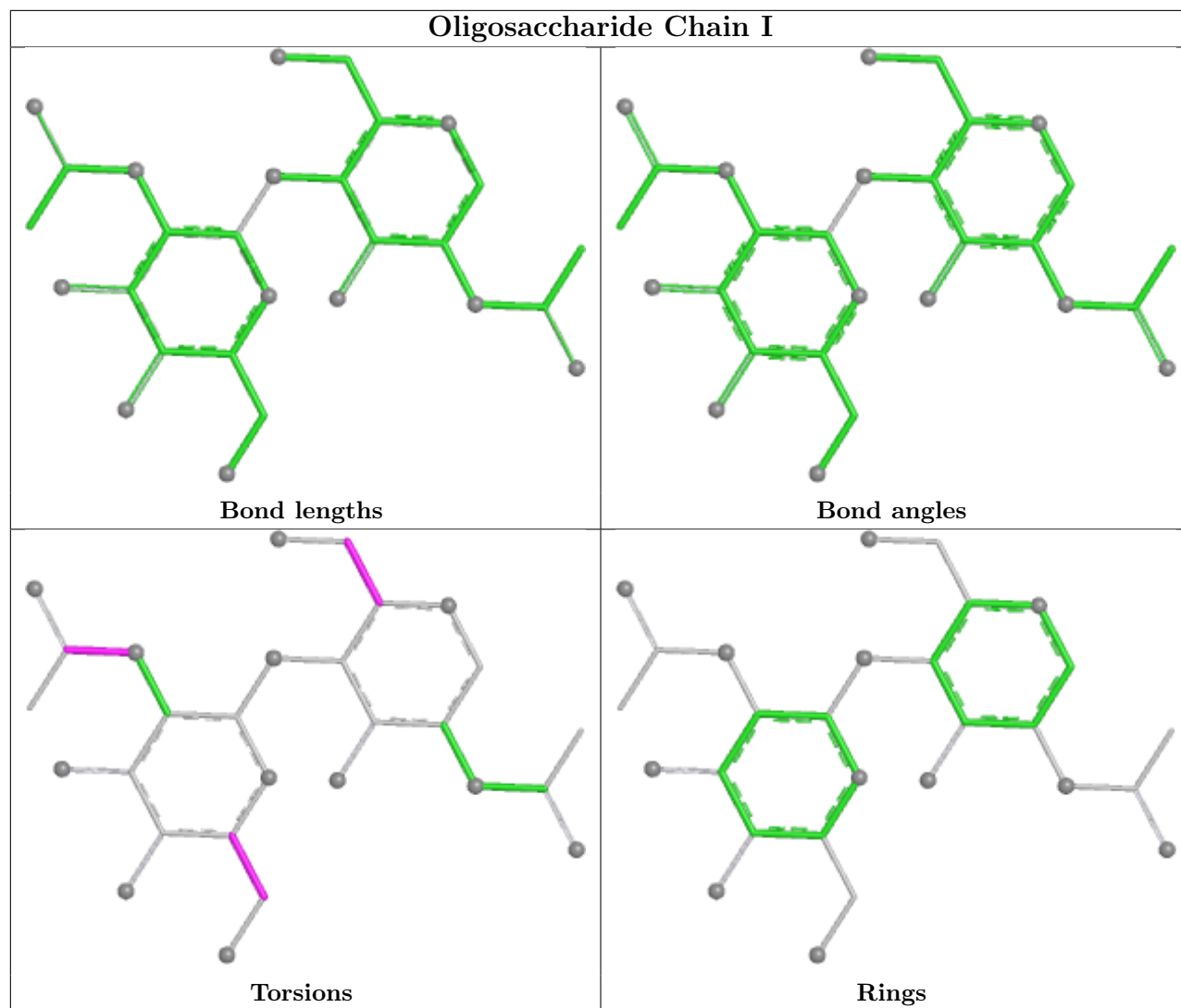
There are no ring outliers.

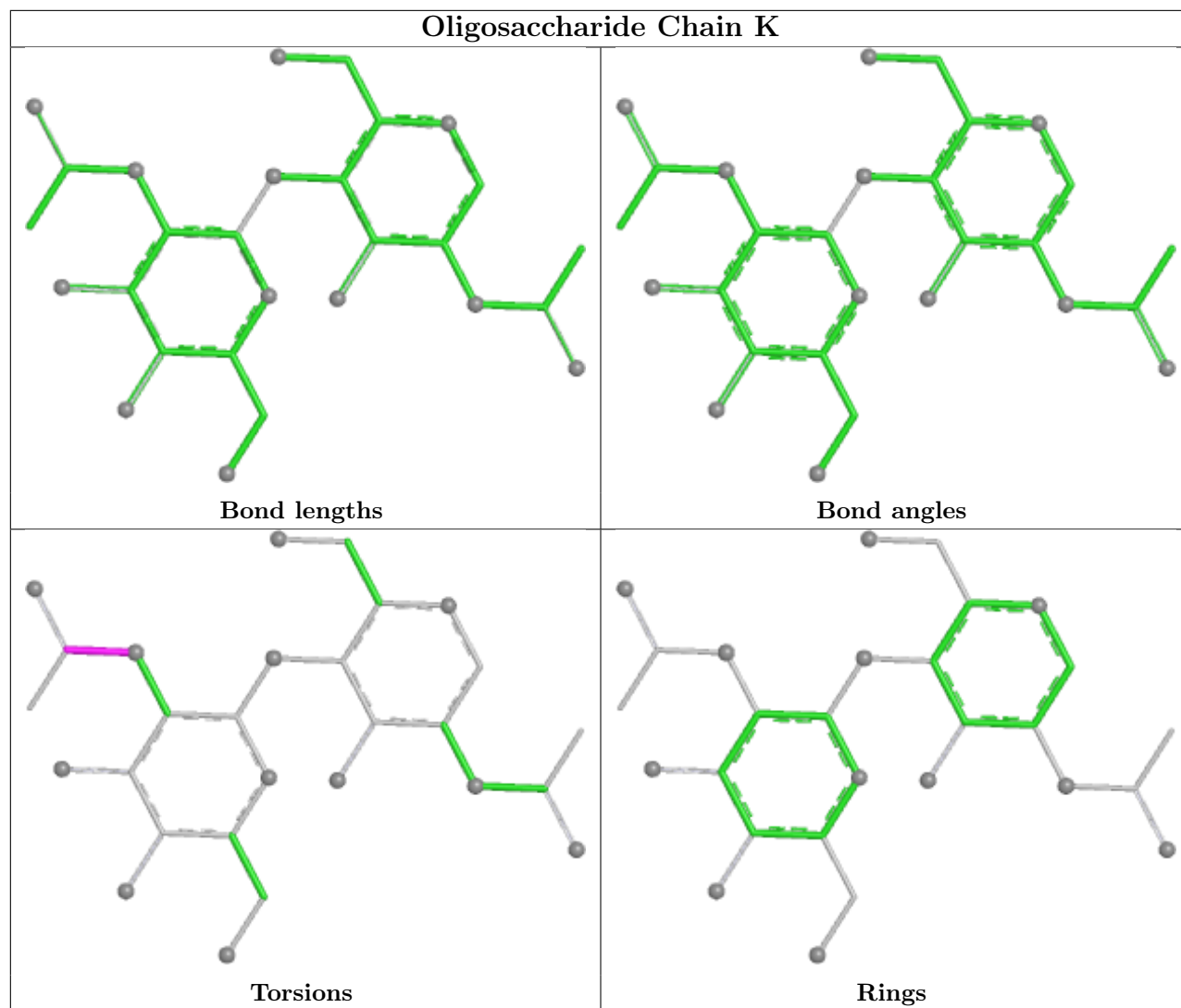
1 monomer is involved in 1 short contact:

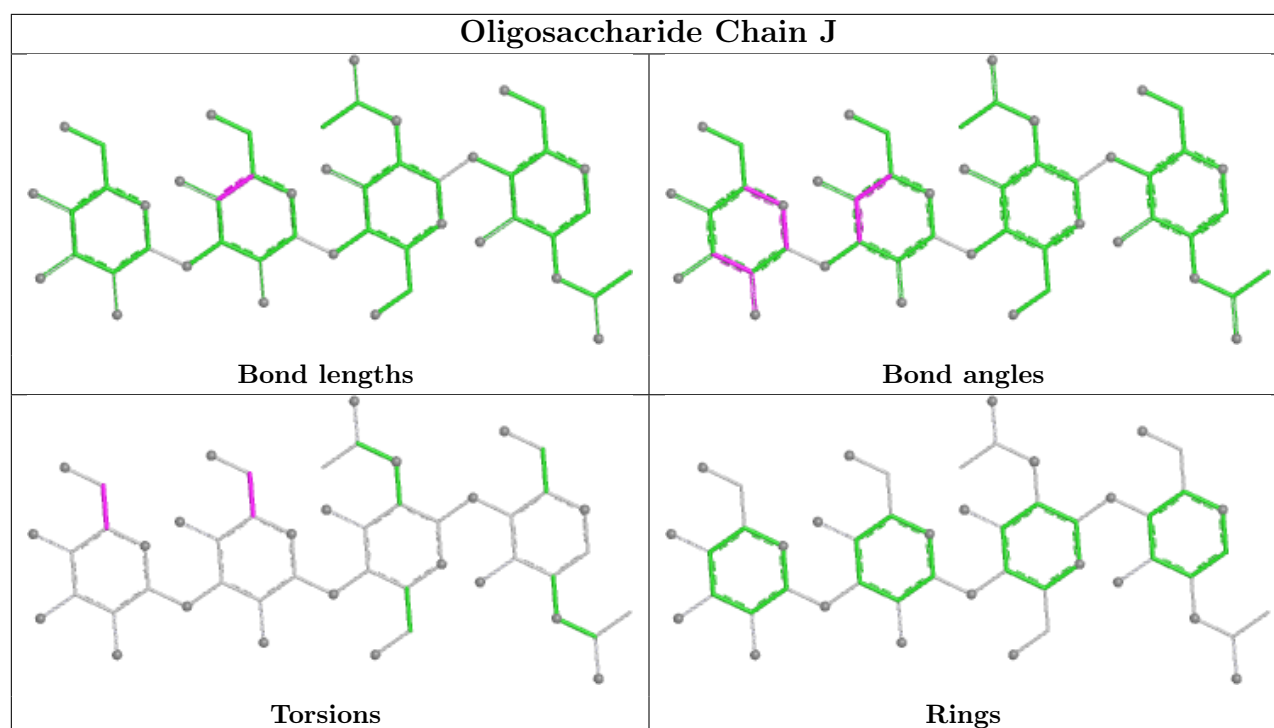
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	1	NAG	1	0

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 30 ligands modelled in this entry, 17 are monoatomic - leaving 13 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$
8	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	502	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.08	0
8	SO4	A	508	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	501	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	A	501	-	4,4,4	0.25	0	6,6,6	0.08	0
8	SO4	A	507	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	503	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	510	-	4,4,4	0.24	0	6,6,6	0.07	0
11	NAG	B	2004	2	14,14,15	0.40	0	17,19,21	0.43	0
11	NAG	D	2004	2	14,14,15	0.47	0	17,19,21	0.77	1 (5%)
12	M6K	B	2005	10	27,27,27	2.96	12 (44%)	31,37,37	1.57	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	M6K	D	2006	10	27,27,27	2.94	12 (44%)	31,37,37	1.59	5 (16%)

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	M6K	D	2006	10	-	5/16/35/35	0/3/3/3
12	M6K	B	2005	10	-	5/16/35/35	0/3/3/3
11	NAG	D	2004	2	-	2/6/23/26	0/1/1/1
11	NAG	B	2004	2	-	0/6/23/26	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	2005	M6K	C15-N16	-8.23	1.30	1.47
12	D	2006	M6K	C15-N16	-8.09	1.30	1.47
12	B	2005	M6K	C10-N11	4.95	1.40	1.28
12	D	2006	M6K	C10-N11	4.94	1.40	1.28
12	D	2006	M6K	C02-N01	4.79	1.47	1.27
12	B	2005	M6K	C02-N01	4.78	1.47	1.27
12	D	2006	M6K	C09-C04	4.27	1.45	1.39
12	B	2005	M6K	C09-C04	4.18	1.45	1.39
12	B	2005	M6K	C14-C13	-4.08	1.46	1.52
12	D	2006	M6K	C06-C05	3.96	1.45	1.38
12	D	2006	M6K	C14-C13	-3.91	1.46	1.52
12	B	2005	M6K	C06-C05	3.83	1.45	1.38
12	B	2005	M6K	C20-N19	-3.68	1.37	1.46
12	D	2006	M6K	C20-N19	-3.68	1.37	1.46
12	B	2005	M6K	C17-N16	-3.14	1.38	1.46
12	D	2006	M6K	C17-N16	-3.14	1.38	1.46
12	B	2005	M6K	C21-N16	-3.12	1.38	1.46
12	D	2006	M6K	C21-N16	-3.06	1.38	1.46
12	B	2005	M6K	C05-C04	-2.88	1.35	1.39
12	D	2006	M6K	C05-C04	-2.77	1.35	1.39
12	D	2006	M6K	C18-N19	-2.55	1.40	1.46
12	B	2005	M6K	C18-N19	-2.49	1.40	1.46
12	B	2005	M6K	C14-C10	-2.46	1.46	1.50
12	D	2006	M6K	C14-C10	-2.31	1.47	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	D	2006	M6K	C13-C14-C10	5.09	105.37	100.82
12	B	2005	M6K	C13-C14-C10	4.83	105.14	100.82
11	D	2004	NAG	C1-O5-C5	2.73	115.85	112.19
12	D	2006	M6K	C14-C10-N11	-2.68	108.08	114.31
12	B	2005	M6K	C14-C10-N11	-2.56	108.36	114.31
12	D	2006	M6K	C14-C10-C07	2.53	128.27	124.83
12	B	2005	M6K	C22-N19-C20	-2.52	107.22	111.14
12	B	2005	M6K	O12-C13-C14	2.21	106.37	104.37
12	B	2005	M6K	C06-C07-C10	-2.07	118.38	120.84
12	D	2006	M6K	C22-N19-C20	-2.06	107.94	111.14
12	D	2006	M6K	C06-C07-C10	-2.05	118.41	120.84

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	B	2005	M6K	C14-C13-C15-N16
12	B	2005	M6K	O12-C13-C15-N16
12	B	2005	M6K	N03-C02-C04-C05
12	B	2005	M6K	N03-C02-C04-C09
12	D	2006	M6K	C14-C13-C15-N16
12	D	2006	M6K	O12-C13-C15-N16
12	D	2006	M6K	N03-C02-C04-C05
12	D	2006	M6K	N03-C02-C04-C09
11	D	2004	NAG	O5-C5-C6-O6
11	D	2004	NAG	C4-C5-C6-O6
12	B	2005	M6K	N01-C02-C04-C09
12	D	2006	M6K	C08-C07-C10-C14

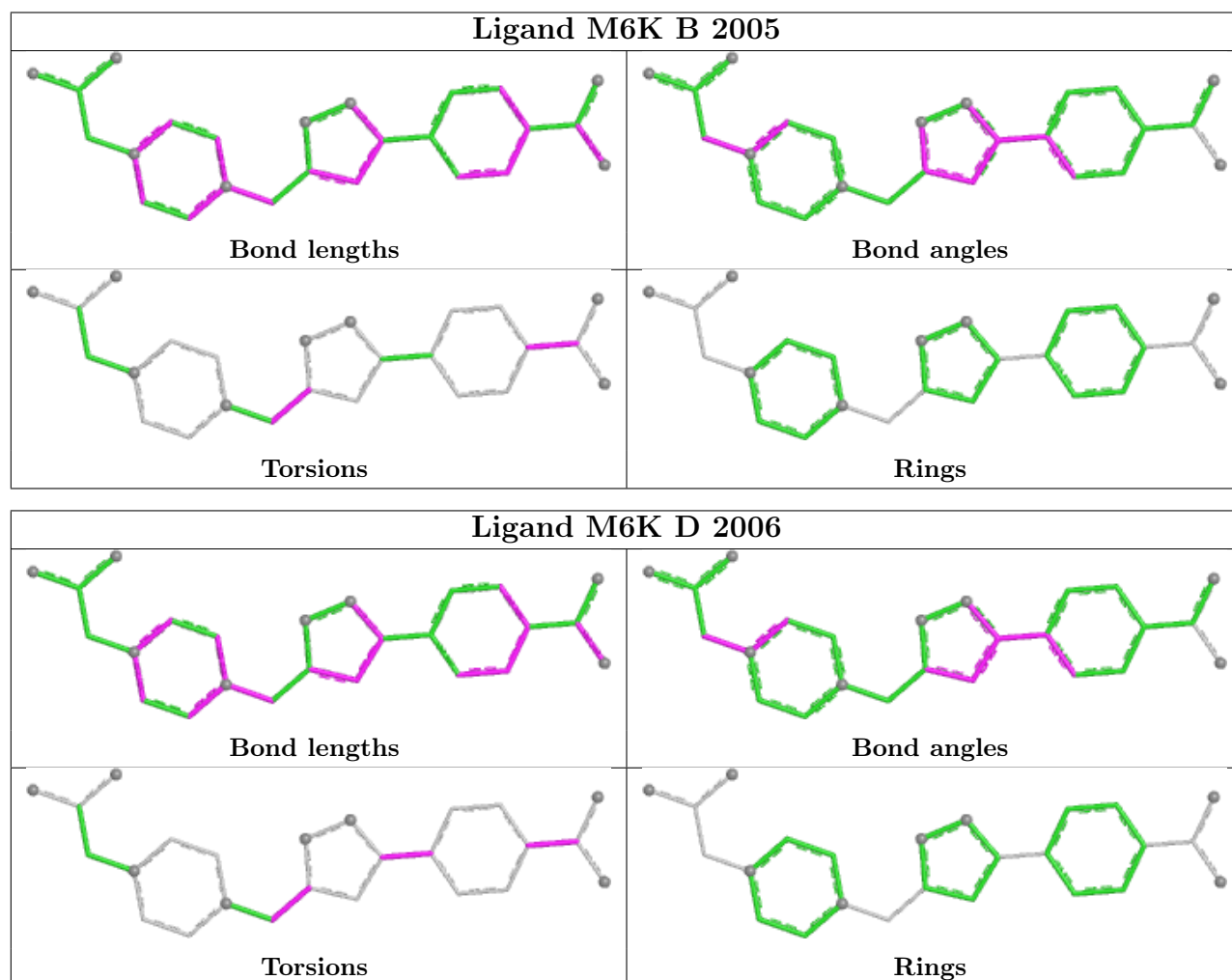
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	D	2006	M6K	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	134:CYS	C	138:THR	N	6.98

6 Fit of model and data

6.1 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	454/454 (100%)	-0.18	3 (0%) 84 85	23, 42, 67, 108	4 (0%)
1	C	453/454 (99%)	0.17	5 (1%) 78 79	27, 58, 88, 121	4 (0%)
2	B	466/471 (98%)	0.46	29 (6%) 26 24	19, 66, 148, 179	8 (1%)
2	D	471/471 (100%)	0.63	25 (5%) 32 30	38, 76, 126, 152	2 (0%)
3	E	214/216 (99%)	1.56	55 (25%) 1 1	69, 121, 172, 195	0
3	H	216/216 (100%)	0.93	20 (9%) 14 13	49, 97, 148, 160	0
4	F	214/214 (100%)	1.25	42 (19%) 3 2	71, 121, 171, 191	0
4	L	214/214 (100%)	0.55	3 (1%) 73 74	53, 85, 112, 151	0
All	All	2702/2710 (99%)	0.53	182 (6%) 24 22	19, 72, 152, 195	18 (0%)

All (182) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	129[A]	TRP	8.4
1	A	454	VAL	5.5
3	E	160	TRP	5.4
3	E	212	VAL	5.3
2	D	375	LEU	4.9
3	E	147	LEU	4.7
2	B	33	LEU	4.6
4	F	135	PHE	4.5
2	D	178	TYR	4.5
4	F	180	THR	4.5
3	E	165	LEU	4.5
3	E	144	LEU	4.4
4	F	178	THR	4.3
3	E	216	ILE	4.2
1	C	453	VAL	4.1
3	E	201	CYS	4.0

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Mol	Chain	Res	Type	RSRZ
3	E	199	ILE	3.9
3	E	189	VAL	3.9
3	E	132	PRO	3.9
3	E	131	ALA	3.9
4	F	134	CYS	3.8
3	E	145	GLY	3.8
2	B	375	LEU	3.8
4	F	159	VAL	3.8
3	E	127	VAL	3.8
4	F	125	LEU	3.8
4	F	160	LEU	3.8
3	H	133	VAL	3.7
3	E	130	LEU	3.7
3	E	194	TRP	3.7
3	E	203	VAL	3.6
3	E	176	LEU	3.6
4	F	117	ILE	3.5
2	B	178	TYR	3.5
2	D	2	PRO	3.4
3	E	204	ALA	3.4
4	F	126	THR	3.4
2	B	129	TRP	3.3
4	F	181	LEU	3.3
2	B	36	PRO	3.3
3	E	142	VAL	3.2
3	E	129	PRO	3.2
3	E	128	TYR	3.2
3	E	133	VAL	3.2
3	H	189	VAL	3.2
4	F	131	SER	3.2
2	D	181	LYS	3.2
3	E	168	GLY	3.2
3	E	169	VAL	3.2
2	D	51	PRO	3.1
4	F	196	ALA	3.1
2	B	466	TRP	3.1
2	B	181	LYS	3.1
4	F	115	VAL	3.1
4	F	132	VAL	3.1
3	E	214	LYS	3.1
2	D	471	CYS	3.0
4	F	204	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
3	H	217	GLU	3.0
3	E	143	THR	2.9
2	B	11	SER	2.9
3	H	130	LEU	2.9
3	E	187	VAL	2.9
4	F	130	ALA	2.9
2	B	4	ILE	2.9
2	B	2	PRO	2.9
3	E	85	SER	2.8
2	D	466	TRP	2.8
2	B	76	ASP	2.8
3	E	11	LEU	2.8
4	F	136	LEU	2.8
3	H	138	THR	2.8
2	B	446	HIS	2.8
3	H	11	LEU	2.8
2	D	10	VAL	2.8
4	F	150	ILE	2.8
3	E	217	GLU	2.8
2	B	432	ASP	2.7
4	F	209	PHE	2.7
3	E	190	THR	2.7
4	F	202	THR	2.7
3	E	183	LEU	2.7
4	L	135	PHE	2.7
3	E	156	VAL	2.7
2	D	180	MET	2.7
4	F	192	TYR	2.6
2	D	4	ILE	2.6
4	F	122	SER	2.6
4	F	177	SER	2.6
2	D	33	LEU	2.6
3	E	86	LEU	2.6
3	E	192	SER	2.6
3	H	177	GLN	2.5
3	H	165	LEU	2.5
3	H	195	PRO	2.5
3	E	196	SER	2.5
3	H	17	SER	2.5
3	H	168	GLY	2.5
2	D	446	HIS	2.5
2	D	468	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
3	E	146	CYS	2.5
1	A	217	SER	2.5
4	F	133	VAL	2.5
4	F	205	ILE	2.5
4	F	179	LEU	2.5
2	B	132[A]	GLN	2.5
2	B	378	GLU	2.4
2	D	312	GLU	2.4
2	B	78	SER	2.4
2	D	467	LEU	2.4
3	E	149	LYS	2.4
2	D	177	CYS	2.4
2	D	32	PRO	2.4
3	E	124	ALA	2.4
3	E	167	SER	2.4
3	H	142	VAL	2.4
4	F	118	PHE	2.4
4	F	116	SER	2.4
4	F	163	TRP	2.4
1	C	300	GLY	2.3
3	E	211	LYS	2.3
4	F	142	LYS	2.3
3	E	54	ALA	2.3
2	D	469	SER	2.3
3	H	192	SER	2.3
2	B	10	VAL	2.3
1	C	340	LEU	2.3
4	F	15	LEU	2.3
3	E	188	THR	2.3
4	F	201	SER	2.3
2	B	58	VAL	2.3
4	F	146	VAL	2.3
2	D	46	LYS	2.3
4	F	210	ASN	2.3
3	H	206	PRO	2.3
2	D	61	ALA	2.3
4	F	182	THR	2.3
2	B	44	LEU	2.2
3	H	144	LEU	2.2
4	F	169	LYS	2.2
3	E	180	LEU	2.2
1	A	319	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
3	E	195	PRO	2.2
3	E	198	SER	2.2
2	D	22	MET	2.2
1	C	130	CYS	2.2
2	B	26	CYS	2.2
3	H	194	TRP	2.2
2	B	449	ASN	2.2
3	E	153	PRO	2.2
2	B	30	ALA	2.2
3	E	200	THR	2.2
4	F	193	THR	2.2
3	E	158	LEU	2.1
3	H	216	ILE	2.1
2	B	34	GLY	2.1
2	D	53	SER	2.1
2	B	434	ASP	2.1
4	L	184	ASP	2.1
3	E	175	VAL	2.1
2	B	458	GLY	2.1
1	C	46	SER	2.1
3	H	157	THR	2.1
4	F	197	THR	2.1
3	E	207	ALA	2.1
3	H	176	LEU	2.1
2	B	49	CYS	2.1
2	D	27	SER	2.1
4	L	157	ASN	2.1
2	B	32	PRO	2.1
3	E	181	TYR	2.1
3	H	140	SER	2.0
2	B	374	CYS	2.0
3	E	161	ASN	2.0
4	F	119	PRO	2.0
4	F	141	PRO	2.0
3	E	134	CYS	2.0
2	B	366	LEU	2.0
2	D	45	LEU	2.0
4	F	36	LEU	2.0
3	E	219	ARG	2.0
4	F	199	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

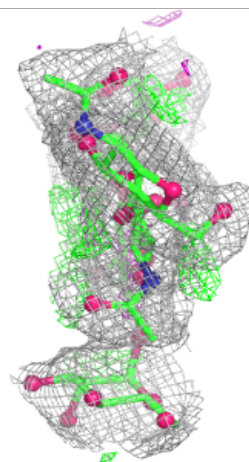
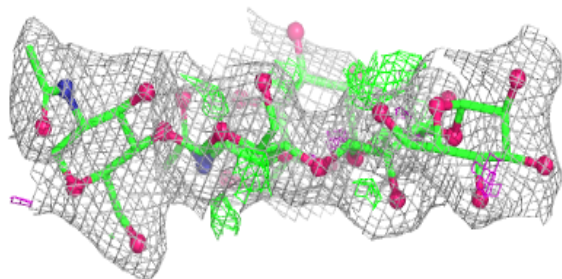
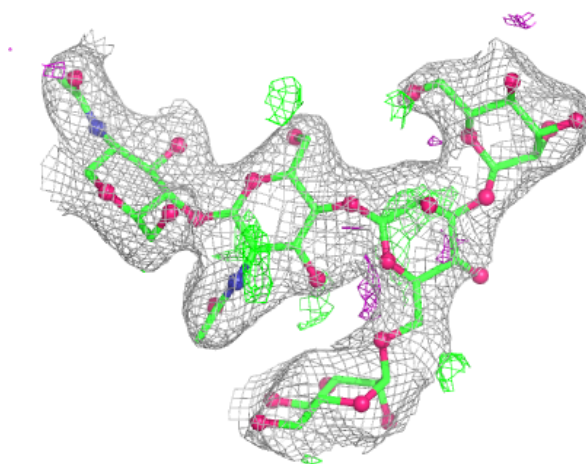
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	G	1	14/15	-	-	51,51,51,51	0
5	NAG	G	2	14/15	-	-	72,72,72,72	0
5	BMA	G	3	11/12	-	-	93,93,93,93	0
5	MAN	G	4	11/12	-	-	90,90,90,90	0
5	MAN	G	5	11/12	-	-	102,102,102,102	0
7	NAG	J	2	14/15	0.54	0.14	87,87,87,87	0
6	NAG	K	2	14/15	0.83	0.12	117,117,117,117	0
6	NAG	I	2	14/15	0.83	0.12	114,114,114,114	0
7	NAG	J	1	14/15	0.84	0.12	69,69,69,69	0
6	NAG	K	1	14/15	0.90	0.11	107,107,107,107	0
6	NAG	I	1	14/15	0.95	0.07	106,106,106,106	0
7	BMA	J	3	11/12	-	-	100,100,100,100	0
7	MAN	J	4	11/12	-	-	100,100,100,100	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.

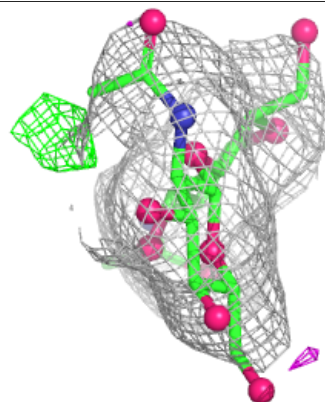
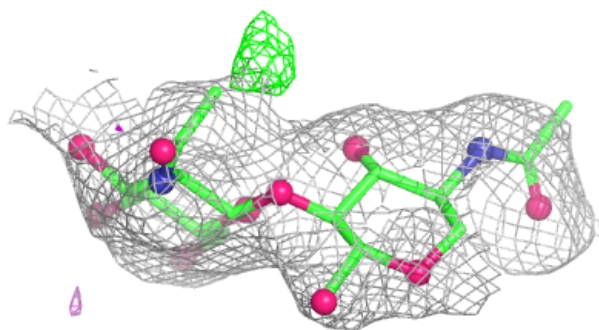
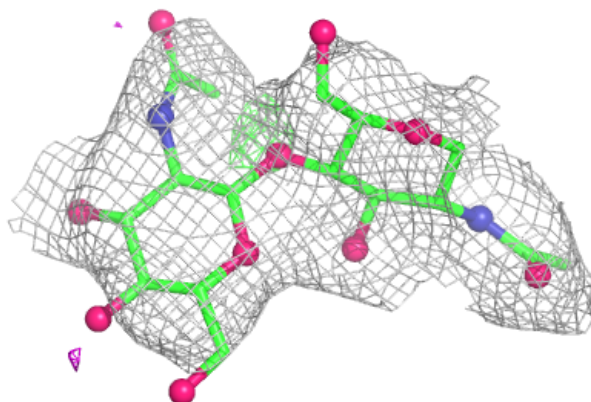
Electron density around Chain G:

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

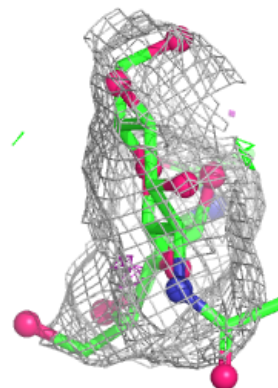
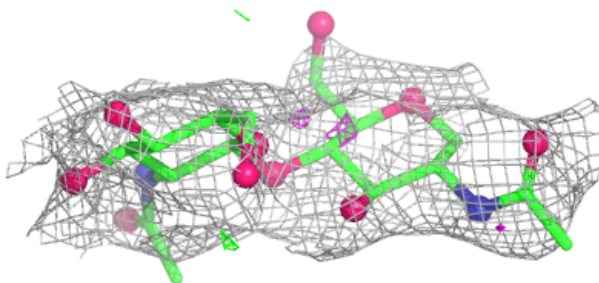
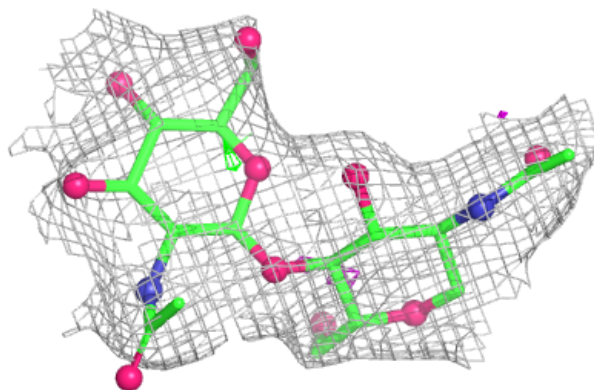


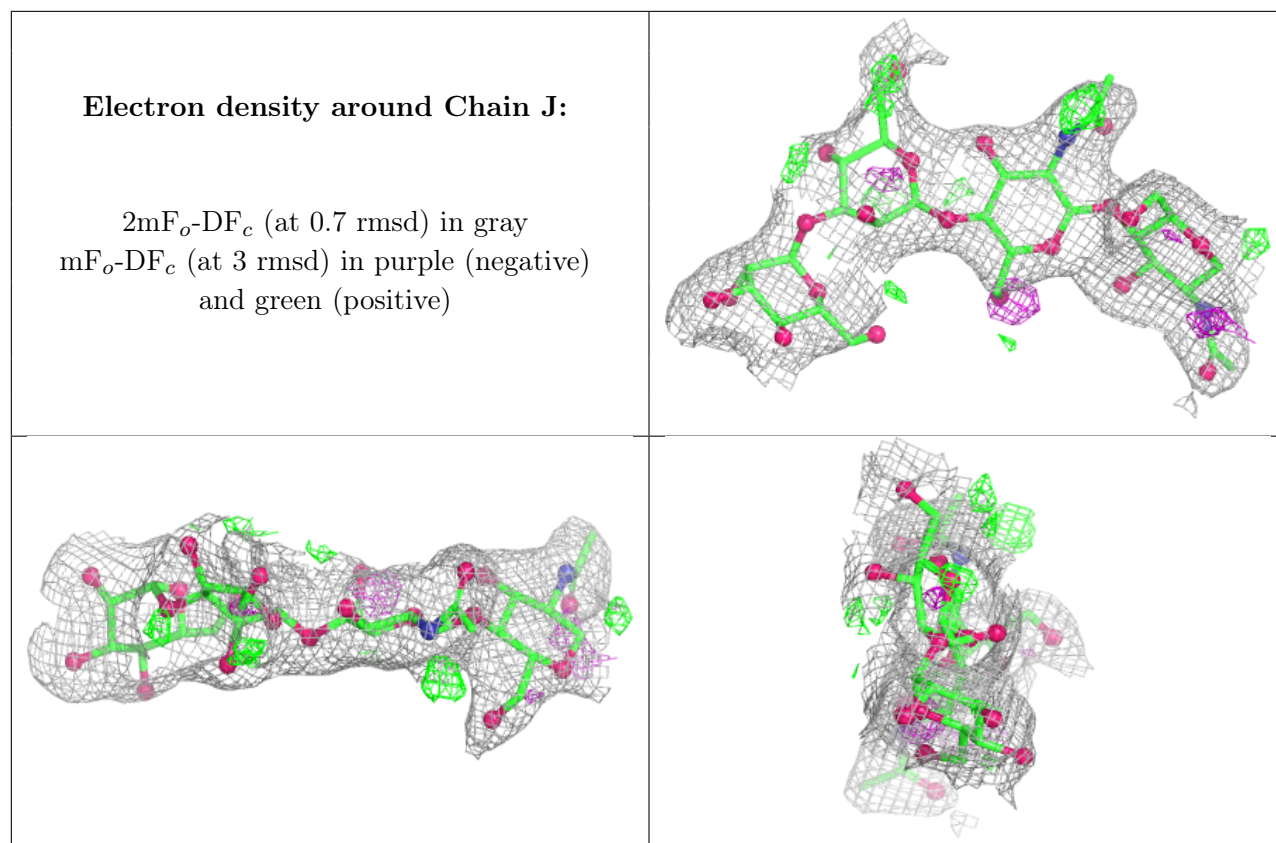
Electron density around Chain I:

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

**Electron density around Chain K:**

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





6.4 Ligands [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.

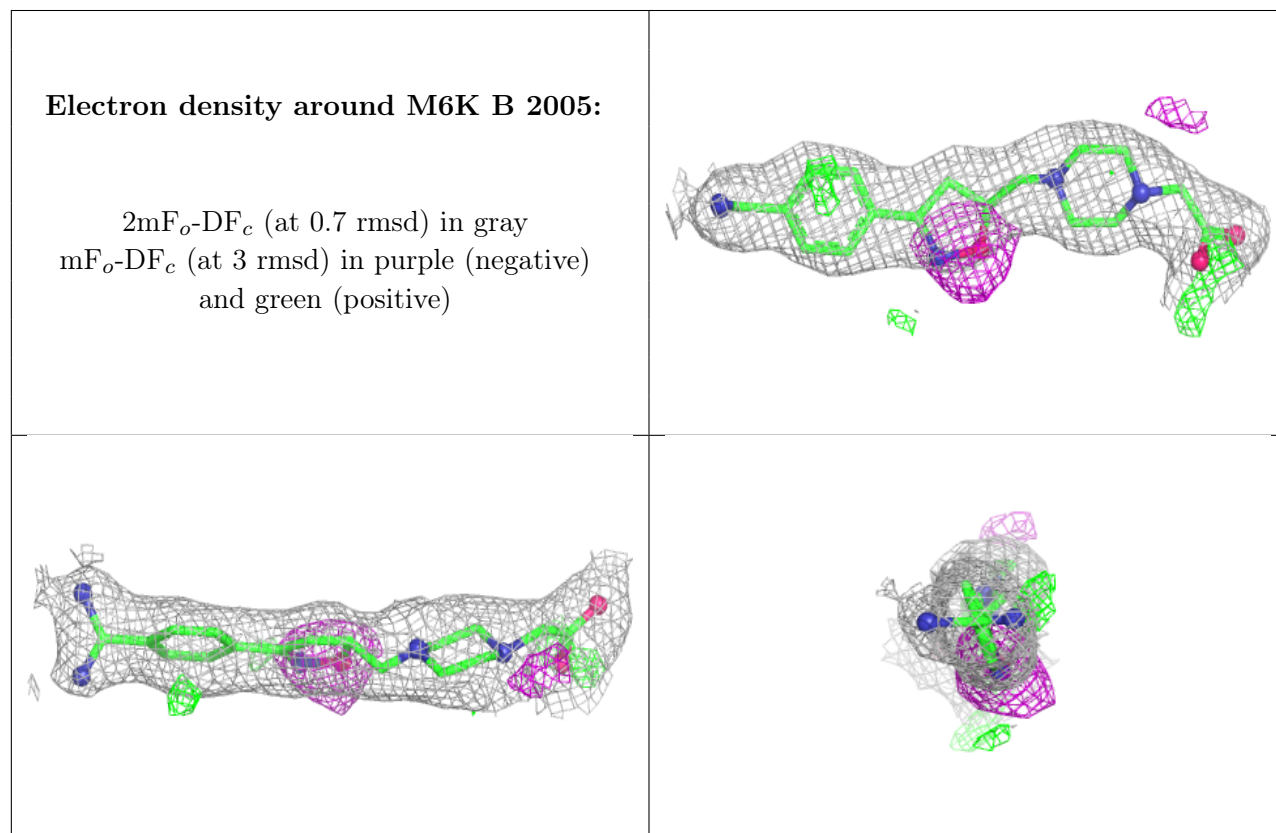
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	NAG	B	2004	14/15	0.57	0.14	111,111,111,111	0
8	SO4	C	502	5/5	0.60	0.16	99,99,99,99	0
8	SO4	A	508	5/5	0.68	0.14	95,95,95,95	0
8	SO4	C	503	5/5	0.72	0.12	104,104,104,104	0
11	NAG	D	2004	14/15	0.72	0.16	108,108,108,108	0
8	SO4	C	501	5/5	0.73	0.18	88,88,88,88	0
8	SO4	A	507	5/5	0.76	0.14	83,83,83,83	0
8	SO4	C	510	5/5	0.83	0.10	98,98,98,98	0
8	SO4	L	301	5/5	0.84	0.11	88,88,88,88	0
8	SO4	A	501	5/5	0.85	0.13	72,72,72,72	0
13	CL	D	2005	1/1	0.86	0.18	91,91,91,91	0
13	CL	C	505	1/1	0.90	0.22	93,93,93,93	0
12	M6K	B	2005	25/25	0.90	0.11	47,47,47,47	0
13	CL	C	504	1/1	0.91	0.21	85,85,85,85	0

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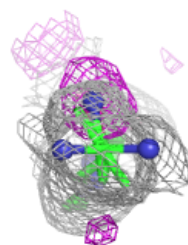
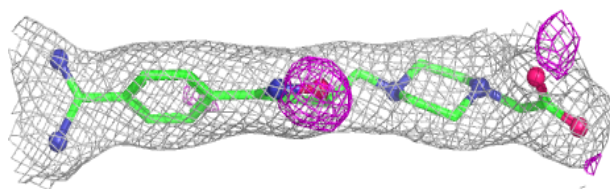
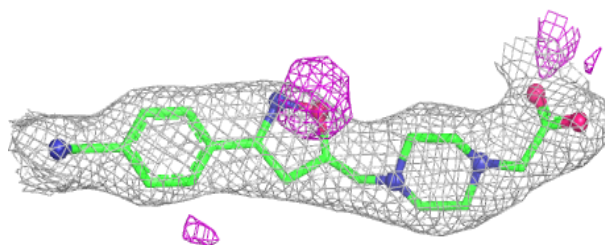
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
12	M6K	D	2006	25/25	0.92	0.11	57,57,57,57	0
10	MN	B	2002	1/1	0.93	0.22	78,78,78,78	0
10	MN	D	2002	1/1	0.93	0.10	66,66,66,66	0
8	SO4	A	502	5/5	0.93	0.09	66,66,66,66	0
9	CA	C	506	1/1	0.95	0.06	81,81,81,81	0
9	CA	A	505	1/1	0.97	0.04	36,36,36,36	0
9	CA	C	507	1/1	0.98	0.04	66,66,66,66	0
9	CA	C	509	1/1	0.98	0.04	56,56,56,56	0
9	CA	A	503	1/1	0.98	0.03	47,47,47,47	0
9	CA	A	506	1/1	0.98	0.03	36,36,36,36	0
10	MN	D	2003	1/1	0.98	0.05	48,48,48,48	0
9	CA	A	504	1/1	0.98	0.03	37,37,37,37	0
9	CA	C	508	1/1	0.99	0.03	59,59,59,59	0
10	MN	B	2003	1/1	0.99	0.02	35,35,35,35	0
10	MN	D	2001	1/1	0.99	0.07	47,47,47,47	0
10	MN	B	2001	1/1	0.99	0.02	34,34,34,34	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around M6K D 2006:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.