



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 23, 2024 – 12:10 AM EDT

PDB ID : 7UKO  
Title : Integrin alpha IIB beta3 complex with sibrifiban (Mn)  
Authors : Lin, F.-Y.; Zhu, J.; Zhu, J.; Springer, T.A.  
Deposited on : 2022-04-01  
Resolution : 2.60 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](mailto:validation@mail.wwpdb.org)

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<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>.

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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
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.3

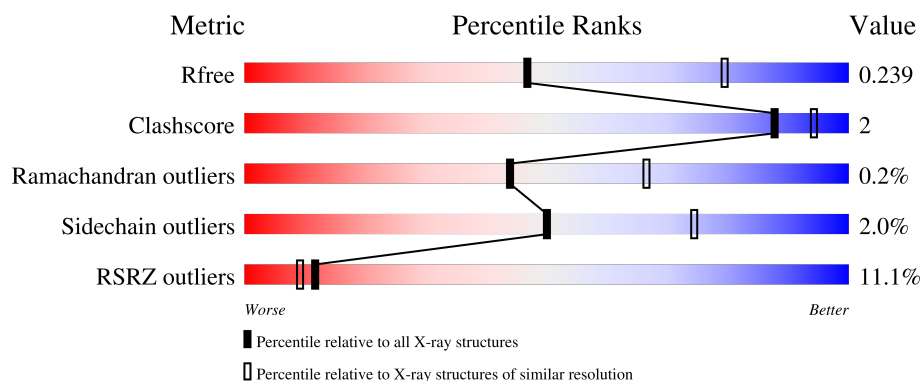
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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  $\geq 3$ , 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	457	<div> <div>2%</div> <div>94%</div> <div>5%</div> </div>
1	C	457	<div> <div>2%</div> <div>93%</div> <div>7%</div> </div>
2	B	472	<div> <div>8%</div> <div>90%</div> <div>8%</div> </div>
2	D	472	<div> <div>9%</div> <div>91%</div> <div>8%</div> </div>
3	E	221	<div> <div>38%</div> <div>88%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	221	
4	F	214	
4	L	214	
5	G	5	
6	I	2	
6	K	2	
7	J	4	

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 21809 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 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	5	0
			3508	2230	605	665	8			
1	C	453	Total	C	N	O	S	0	3	0
			3495	2219	602	666	8			

- Molecule 2 is a protein called Isoform Beta-3C of Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	466	Total	C	N	O	S	4	3	0
			3610	2248	616	713	33			
2	D	471	Total	C	N	O	S	3	1	0
			3631	2260	620	716	35			

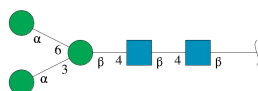
- Molecule 3 is a protein called 10E5 Fab heavy chain.

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 Fab 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 (three-letter code: SO4) (formula: O<sub>4</sub>S).



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	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 (three-letter code: 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 GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

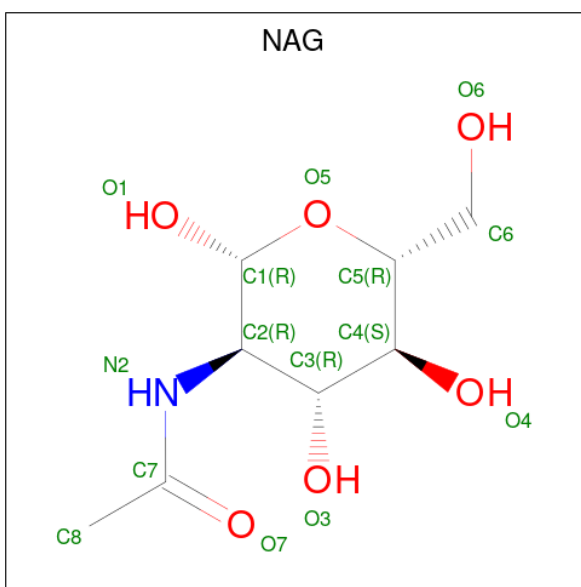


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	3	3		
10	A	1	Total	C	O	0	0
			6	3	3		

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

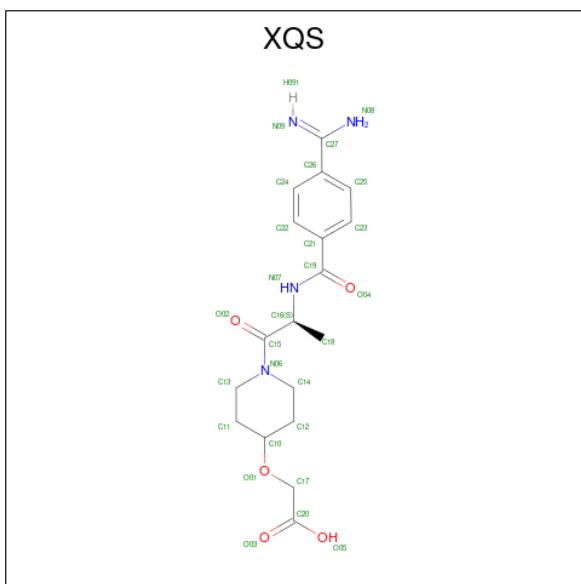
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	3	Total	Mn	0	0
			3	3		
11	D	3	Total	Mn	0	0
			3	3		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 13 is sibrifiban (active form) (three-letter code: XQS) (formula:  $C_{18}H_{24}N_4O_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	B	1	Total	C	N	O	0	0
			27	18	4	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	D	1	Total	C	N	O	0	0
			27	18	4	5		

- Molecule 14 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

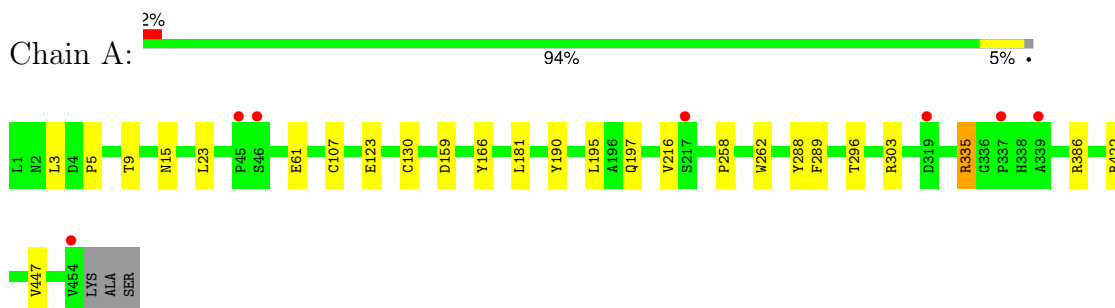
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	299	Total	O	0	0
			299	299		
15	B	150	Total	O	0	0
			150	150		
15	C	92	Total	O	0	0
			92	92		
15	D	85	Total	O	0	0
			85	85		
15	E	11	Total	O	0	0
			11	11		
15	F	18	Total	O	0	0
			18	18		
15	H	24	Total	O	0	0
			24	24		
15	L	38	Total	O	0	0
			38	38		

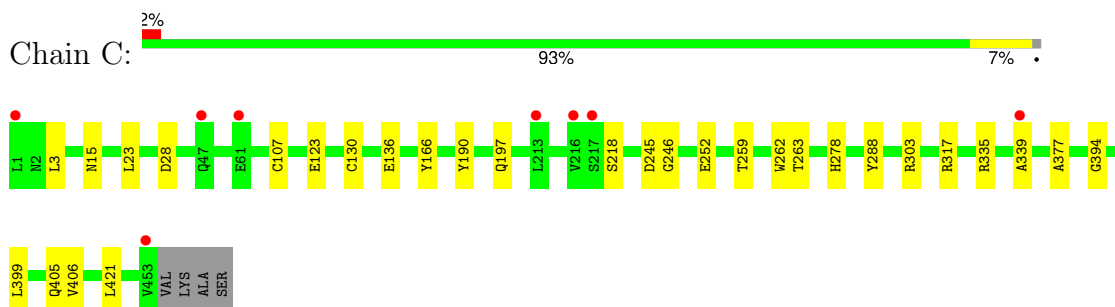
### 3 Residue-property plots [i](#)

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.

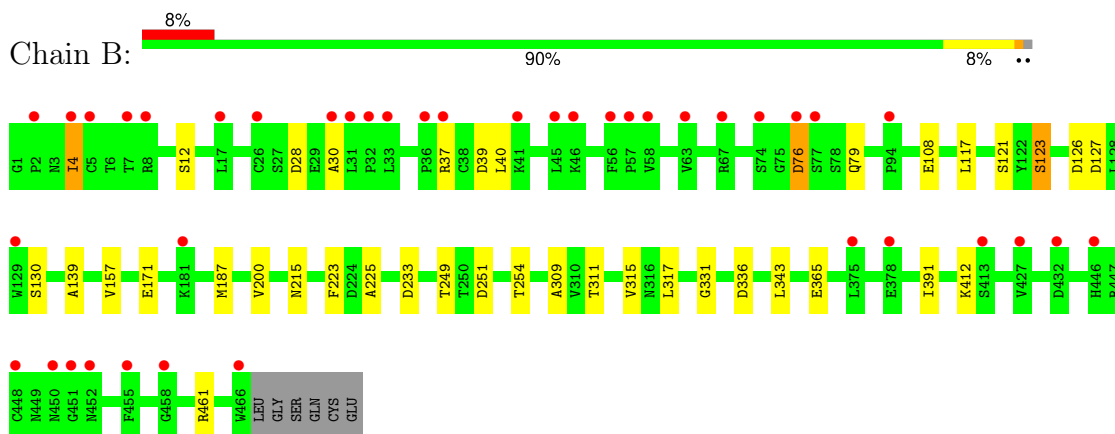
- Molecule 1: Integrin alpha-IIb heavy chain



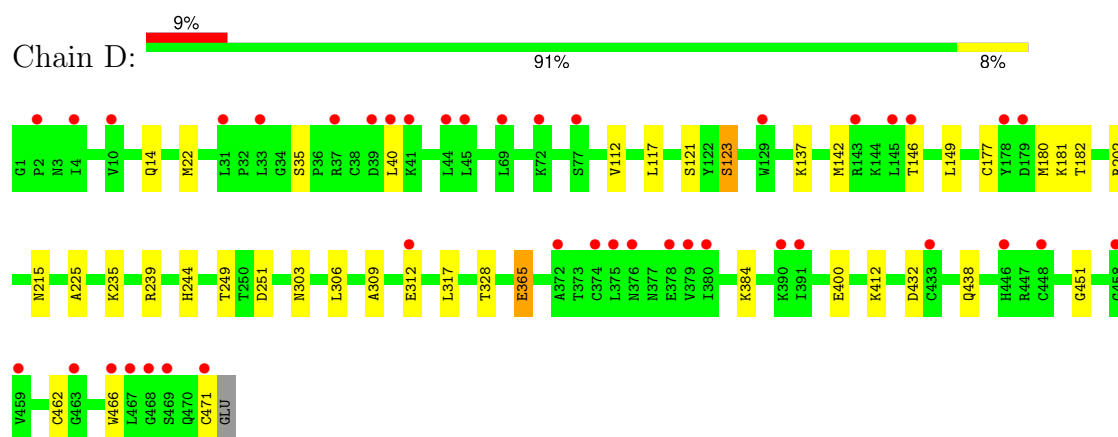
- Molecule 1: Integrin alpha-IIb heavy chain



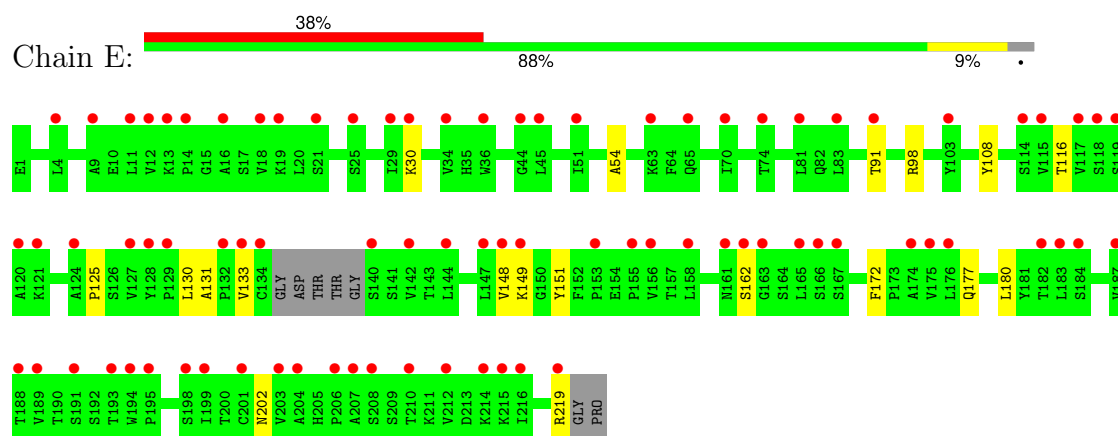
- Molecule 2: Isoform Beta-3C of Integrin beta-3



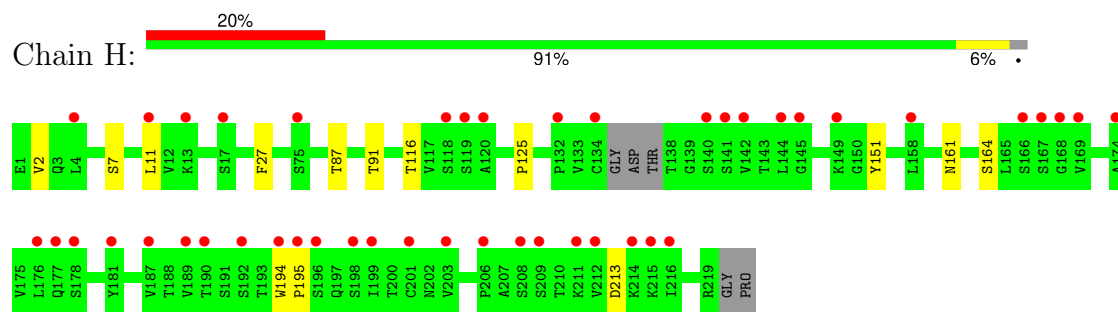
- Molecule 2: Isoform Beta-3C of Integrin beta-3



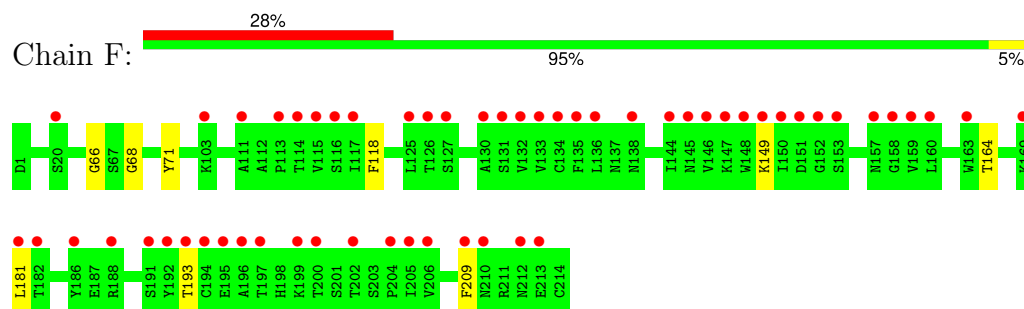
- Molecule 3: 10E5 Fab heavy chain



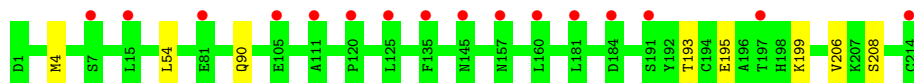
- Molecule 3: 10E5 Fab heavy chain



- Molecule 4: 10E5 Fab light chain



- Molecule 4: 10E5 Fab 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



- 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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	258.39Å 144.60Å 104.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.29 – 2.60 49.29 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.29-2.60) 88.8 (49.29-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.84 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, $R_{free}$	0.214 , 0.239 0.214 , 0.239	Depositor DCC
$R_{free}$ test set	118716 reflections (1.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.9	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	21809	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: BMA, GOL, NAG, SO4, MN, MAN, CL, XQS, CA

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	0.27	0/3620	0.49	0/4933
1	C	0.26	0/3594	0.47	0/4897
2	B	0.26	0/3680	0.46	0/4991
2	D	0.25	0/3698	0.45	0/5013
3	E	0.25	0/1673	0.45	0/2290
3	H	0.25	0/1684	0.46	0/2305
4	F	0.25	0/1673	0.46	0/2269
4	L	0.25	0/1673	0.45	0/2269
All	All	0.26	0/21295	0.46	0/28967

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	3508	0	3355	11	0
1	C	3495	0	3327	11	0
2	B	3610	0	3526	20	0
2	D	3631	0	3548	16	0
3	E	1631	0	1590	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	0	1600	5	0
4	F	1637	0	1553	7	0
4	L	1637	0	1553	4	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	10	0	0	0	0
8	C	10	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	A	12	0	16	2	0
11	B	3	0	0	0	0
11	D	3	0	0	0	0
12	B	14	0	13	0	0
12	D	14	0	13	0	0
13	B	27	0	0	1	0
13	D	27	0	0	1	0
14	C	1	0	0	0	0
15	A	299	0	0	1	0
15	B	150	0	0	0	0
15	C	92	0	0	0	0
15	D	85	0	0	0	0
15	E	11	0	0	0	0
15	F	18	0	0	0	0
15	H	24	0	0	0	0
15	L	38	0	0	1	0
All	All	21809	0	20239	79	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 2.

The worst 5 of 79 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)
3:E:149:LYS:NZ	4:F:180:THR:HG21	2.02	0.74
1:C:245:ASP:OD1	1:C:246:GLY:N	2.26	0.68
1:A:386:ARG:HH11	10:A:507:GOL:H31	1.58	0.67
2:B:121:SER:HB2	13:B:2005:XQS:O03	1.94	0.67
2:B:39:ASP:OD1	2:B:40:LEU:N	2.29	0.64

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	457/457 (100%)	443 (97%)	13 (3%)	1 (0%)	44	66
1	C	454/457 (99%)	443 (98%)	10 (2%)	1 (0%)	44	66
2	B	467/472 (99%)	445 (95%)	20 (4%)	2 (0%)	30	52
2	D	470/472 (100%)	448 (95%)	21 (4%)	1 (0%)	44	66
3	E	210/221 (95%)	191 (91%)	19 (9%)	0	100	100
3	H	212/221 (96%)	201 (95%)	11 (5%)	0	100	100
4	F	212/214 (99%)	198 (93%)	13 (6%)	1 (0%)	25	47
4	L	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
All	All	2694/2728 (99%)	2574 (96%)	114 (4%)	6 (0%)	44	66

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
2	B	76	ASP
1	C	123	GLU
2	D	451	GLY
2	B	157	VAL

### 5.3.2 Protein sidechains [i](#)

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	367/364 (101%)	358 (98%)	9 (2%)	42	68
1	C	364/364 (100%)	354 (97%)	10 (3%)	40	66
2	B	415/417 (100%)	407 (98%)	8 (2%)	52	75
2	D	417/417 (100%)	404 (97%)	13 (3%)	35	62
3	E	186/190 (98%)	186 (100%)	0	100	100
3	H	187/190 (98%)	183 (98%)	4 (2%)	48	73
4	F	188/188 (100%)	187 (100%)	1 (0%)	86	95
4	L	188/188 (100%)	187 (100%)	1 (0%)	86	95
All	All	2312/2318 (100%)	2266 (98%)	46 (2%)	50	74

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	123	SER
2	D	312	GLU
2	D	180	MET
2	D	215	ASN
2	D	384	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2	ASN
1	C	333	GLN
2	D	438	GLN
4	F	138	ASN
4	F	156	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 ⓘ

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	0.49	0	17,19,21	0.41	0
5	NAG	G	2	5	14,14,15	0.41	0	17,19,21	0.51	0
5	BMA	G	3	5	11,11,12	1.24	2 (18%)	15,15,17	0.92	1 (6%)
5	MAN	G	4	5	11,11,12	0.76	0	15,15,17	0.89	1 (6%)
5	MAN	G	5	5	11,11,12	1.15	1 (9%)	15,15,17	1.07	1 (6%)
6	NAG	I	1	6,2	14,14,15	0.36	0	17,19,21	0.45	0
6	NAG	I	2	6	14,14,15	0.50	0	17,19,21	0.41	0
7	NAG	J	1	7,2	14,14,15	0.51	0	17,19,21	0.52	0
7	NAG	J	2	7	14,14,15	0.42	0	17,19,21	0.38	0
7	BMA	J	3	7	11,11,12	0.88	0	15,15,17	0.84	1 (6%)
7	MAN	J	4	7	11,11,12	0.75	0	15,15,17	0.87	1 (6%)
6	NAG	K	1	6,2	14,14,15	0.47	0	17,19,21	0.38	0
6	NAG	K	2	6	14,14,15	0.37	0	17,19,21	0.42	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
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	-	0/2/19/22	0/1/1/1
5	MAN	G	5	5	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	4/6/23/26	0/1/1/1
7	NAG	J	1	7,2	-	2/6/23/26	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	J	4	7	-	0/2/19/22	0/1/1/1
6	NAG	K	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	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	G	5	MAN	C1-C2	2.25	1.57	1.52
5	G	3	BMA	C2-C3	2.16	1.55	1.52
5	G	3	BMA	C4-C5	2.13	1.57	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	5	MAN	C1-C2-C3	2.92	113.90	109.64
7	J	4	MAN	O2-C2-C3	-2.28	105.44	110.15
5	G	4	MAN	O2-C2-C3	-2.25	105.48	110.15
5	G	3	BMA	C2-C3-C4	2.20	114.73	110.86
7	J	3	BMA	C1-O5-C5	2.04	114.92	112.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

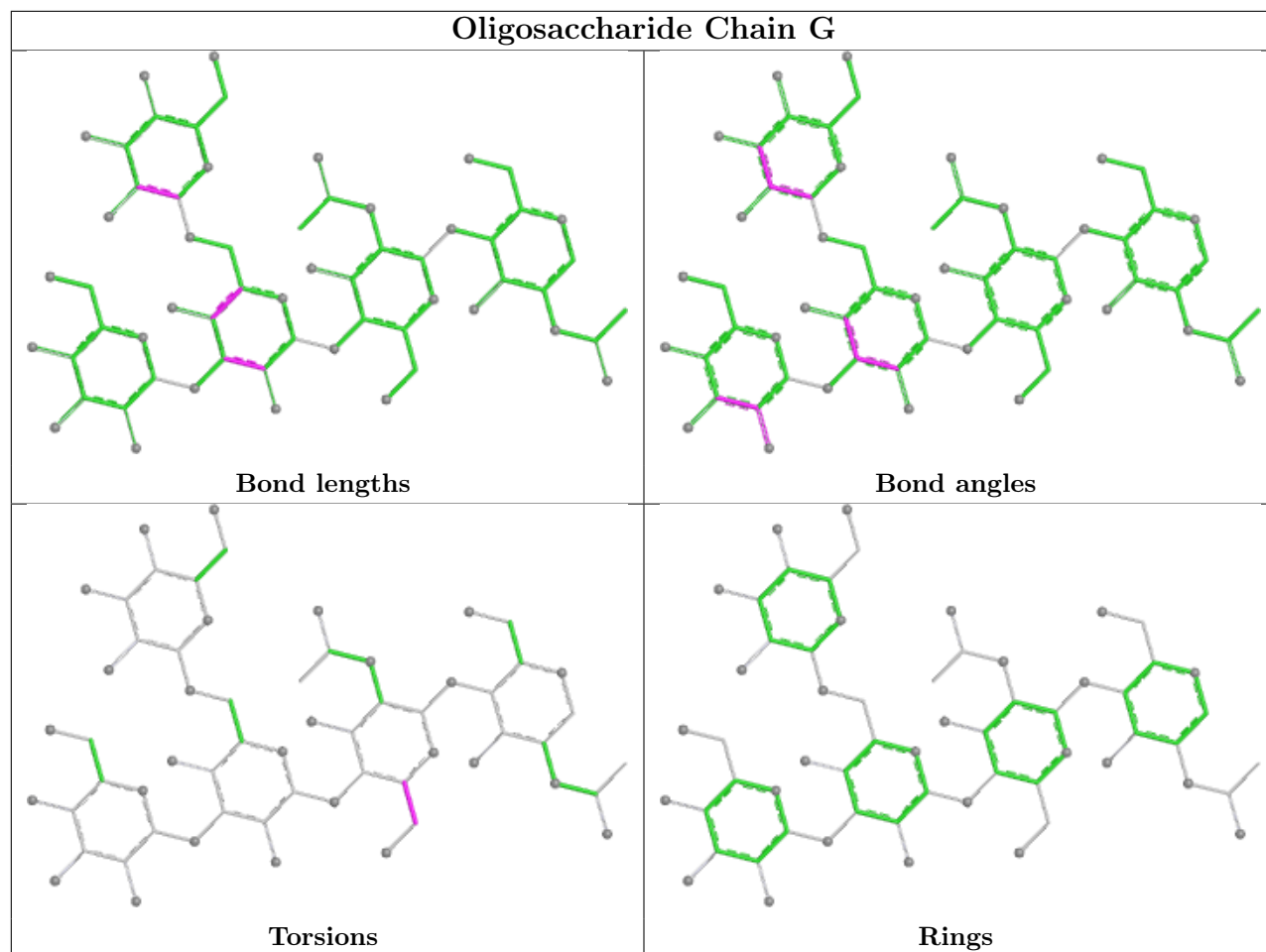
Mol	Chain	Res	Type	Atoms
6	I	2	NAG	C4-C5-C6-O6
6	K	2	NAG	C4-C5-C6-O6
7	J	3	BMA	O5-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2

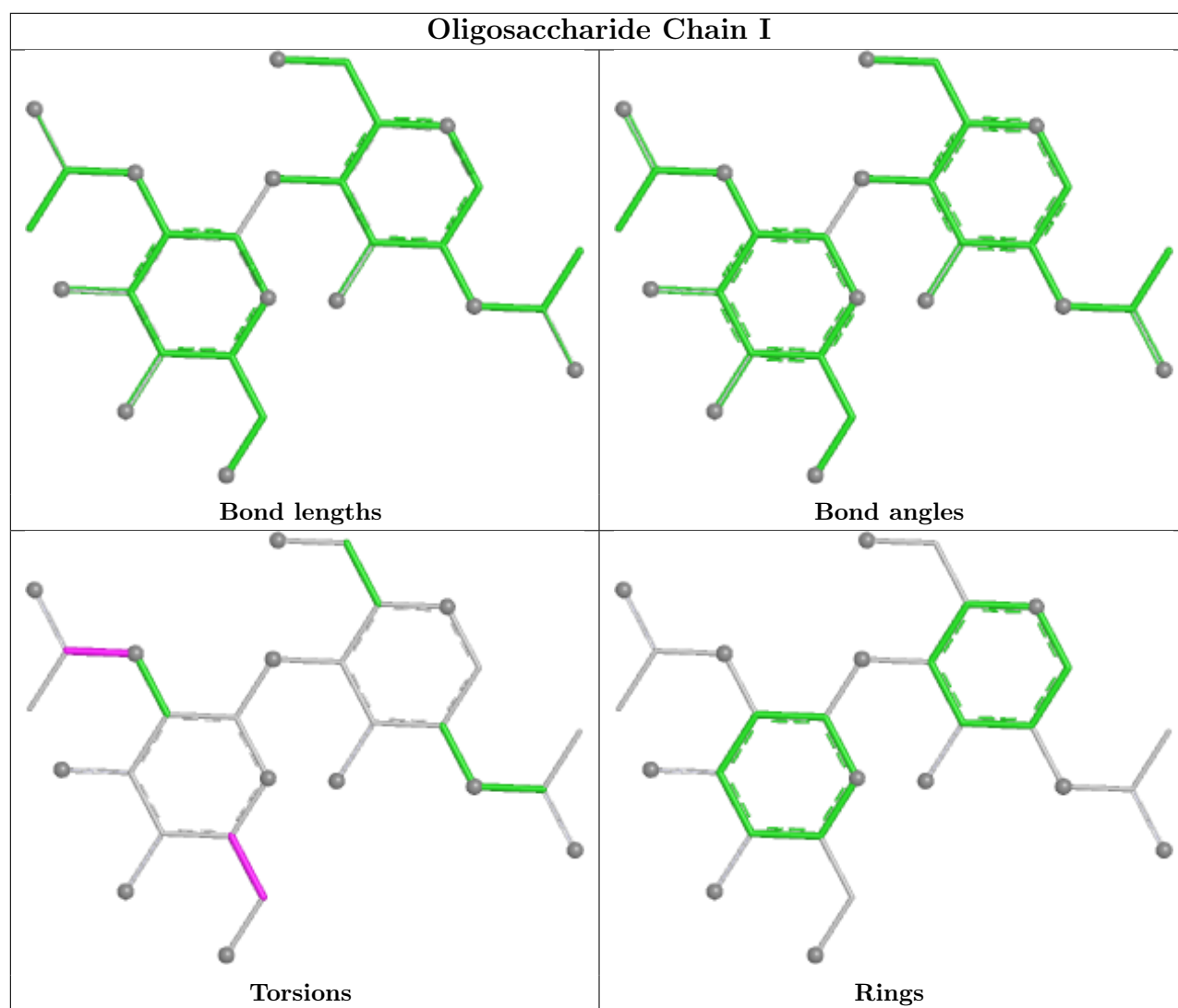
There are no ring outliers.

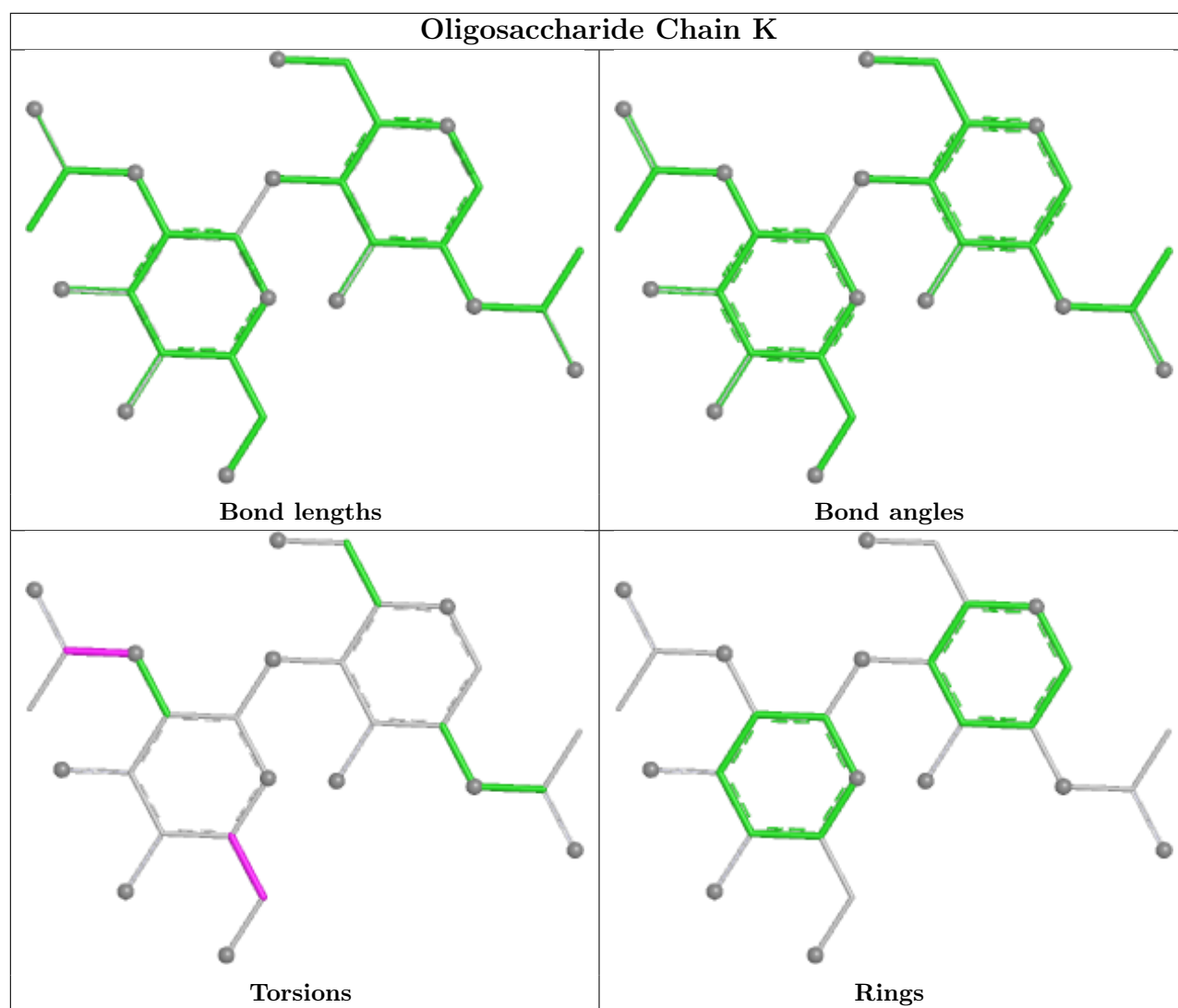
1 monomer is involved in 1 short contact:

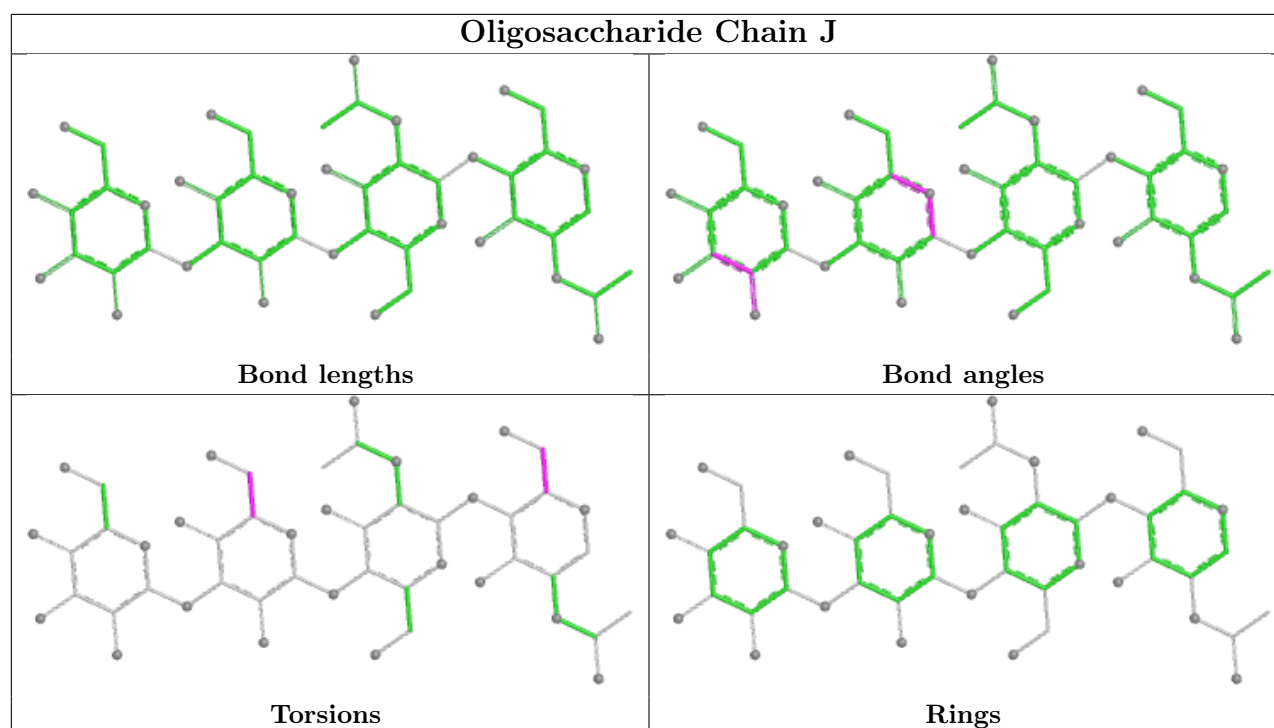
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	1	NAG	1	0

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 26 ligands modelled in this entry, 15 are monoatomic - leaving 11 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	0.33	0	17,19,21	0.54	0
8	SO4	L	301	-	4,4,4	0.25	0	6,6,6	0.19	0
13	XQS	B	2005	11	28,28,28	3.10	10 (35%)	33,38,38	1.72	5 (15%)
10	GOL	A	508	-	5,5,5	0.37	0	5,5,5	0.66	0
8	SO4	C	507	-	4,4,4	0.25	0	6,6,6	0.07	0
8	SO4	A	501	-	4,4,4	0.22	0	6,6,6	0.24	0
8	SO4	A	506	-	4,4,4	0.26	0	6,6,6	0.48	0
13	XQS	D	2005	11	28,28,28	3.15	11 (39%)	33,38,38	1.61	4 (12%)
8	SO4	C	501	-	4,4,4	0.24	0	6,6,6	0.16	0
10	GOL	A	507	-	5,5,5	0.38	0	5,5,5	0.51	0
12	NAG	D	2004	2	14,14,15	0.46	0	17,19,21	0.50	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	B	2004	2	-	2/6/23/26	0/1/1/1
13	XQS	B	2005	11	-	2/25/35/35	0/2/2/2
10	GOL	A	508	-	-	4/4/4/4	-
13	XQS	D	2005	11	-	3/25/35/35	0/2/2/2
10	GOL	A	507	-	-	0/4/4/4	-
12	NAG	D	2004	2	-	0/6/23/26	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	D	2005	XQS	C22-C21	8.03	1.51	1.39
13	D	2005	XQS	C25-C23	7.97	1.51	1.38
13	D	2005	XQS	C24-C26	7.94	1.51	1.39
13	B	2005	XQS	C25-C23	7.81	1.51	1.38
13	B	2005	XQS	C22-C21	7.73	1.51	1.39

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	2005	XQS	C14-N06-C13	5.44	123.78	112.68
13	D	2005	XQS	C14-N06-C13	4.97	122.82	112.68
13	B	2005	XQS	C14-C12-C10	-4.11	105.88	110.32
13	D	2005	XQS	C11-C13-N06	4.09	118.68	110.66
13	B	2005	XQS	C11-C13-N06	3.64	117.79	110.66

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

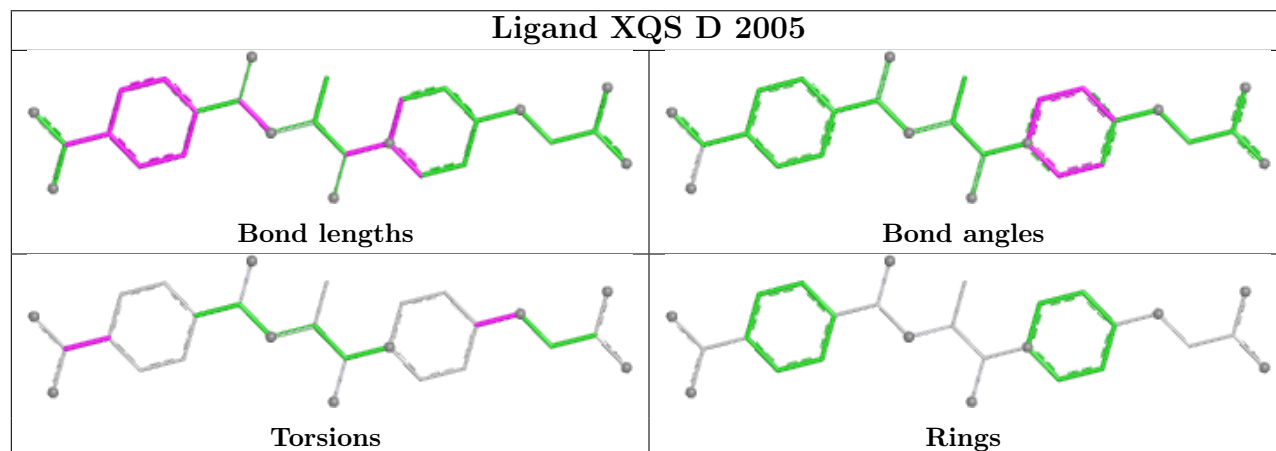
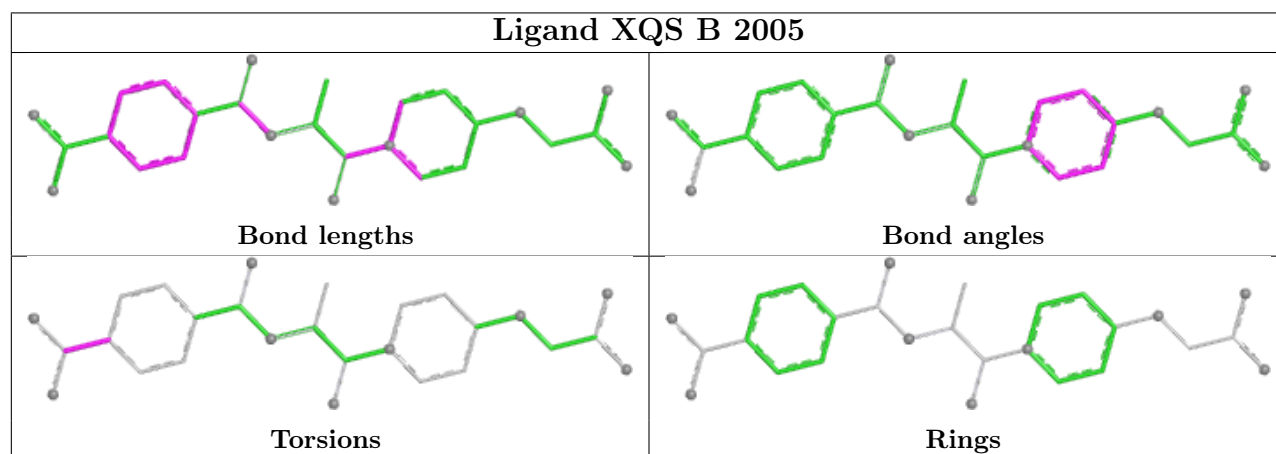
Mol	Chain	Res	Type	Atoms
10	A	508	GOL	C1-C2-C3-O3
10	A	508	GOL	O2-C2-C3-O3
13	B	2005	XQS	C24-C26-C27-N08
13	D	2005	XQS	C24-C26-C27-N08
10	A	508	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	B	2005	XQS	1	0
10	A	508	GOL	1	0
13	D	2005	XQS	1	0
10	A	507	GOL	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	454/457 (99%)	-0.22	7 (1%) 71 67	21, 35, 52, 72	5 (1%)
1	C	453/457 (99%)	0.23	8 (1%) 67 62	21, 49, 69, 91	3 (0%)
2	B	466/472 (98%)	0.51	40 (8%) 18 15	20, 57, 120, 136	4 (0%)
2	D	471/472 (99%)	0.81	41 (8%) 17 14	24, 67, 111, 128	2 (0%)
3	E	214/221 (96%)	1.81	83 (38%) 1 1	67, 112, 153, 163	0
3	H	216/221 (97%)	1.23	45 (20%) 3 2	47, 84, 118, 126	0
4	F	214/214 (100%)	1.65	60 (28%) 2 1	69, 111, 156, 175	0
4	L	214/214 (100%)	0.91	16 (7%) 22 17	51, 74, 89, 115	0
All	All	2702/2728 (99%)	0.67	300 (11%) 12 9	20, 63, 133, 175	14 (0%)

The worst 5 of 300 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	147	LEU	5.8
3	E	165	LEU	5.6
2	D	471	CYS	4.9
3	E	212	VAL	4.8
2	D	375	LEU	4.7

### 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 ⓘ

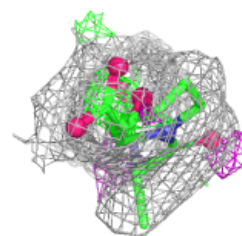
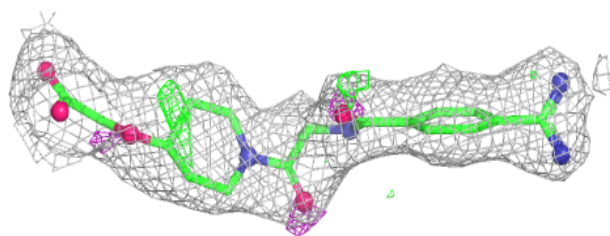
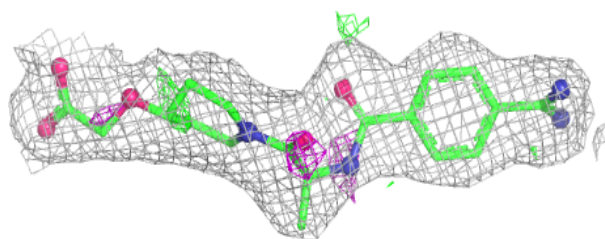
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
12	NAG	B	2004	14/15	0.66	0.17	86,86,86,86	0
12	NAG	D	2004	14/15	0.67	0.16	81,81,81,81	0
11	MN	B	2002	1/1	0.82	0.35	66,66,66,66	0
10	GOL	A	508	6/6	0.83	0.14	39,39,39,39	0
8	SO4	C	507	5/5	0.85	0.20	73,73,73,73	0
8	SO4	A	506	5/5	0.87	0.22	58,58,58,58	0
10	GOL	A	507	6/6	0.88	0.14	35,35,35,35	0
8	SO4	L	301	5/5	0.89	0.23	70,70,70,70	0
8	SO4	A	501	5/5	0.89	0.15	49,49,49,49	0
13	XQS	B	2005	27/27	0.90	0.11	33,33,33,33	0
13	XQS	D	2005	27/27	0.90	0.12	48,48,48,48	0
8	SO4	C	501	5/5	0.91	0.17	69,69,69,69	0
11	MN	D	2002	1/1	0.95	0.18	65,65,65,65	0
14	CL	C	502	1/1	0.95	0.07	53,53,53,53	0
9	CA	A	504	1/1	0.96	0.04	31,31,31,31	0
9	CA	A	503	1/1	0.97	0.05	33,33,33,33	0
9	CA	C	503	1/1	0.97	0.05	67,67,67,67	0
9	CA	C	506	1/1	0.97	0.04	49,49,49,49	0
9	CA	C	504	1/1	0.98	0.06	55,55,55,55	0
11	MN	B	2003	1/1	0.98	0.07	32,32,32,32	0
9	CA	A	502	1/1	0.99	0.03	44,44,44,44	0
9	CA	A	505	1/1	0.99	0.02	31,31,31,31	0
11	MN	D	2001	1/1	0.99	0.04	44,44,44,44	0
9	CA	C	505	1/1	0.99	0.03	50,50,50,50	0
11	MN	D	2003	1/1	0.99	0.08	45,45,45,45	0
11	MN	B	2001	1/1	1.00	0.03	29,29,29,29	0

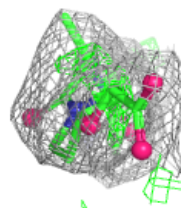
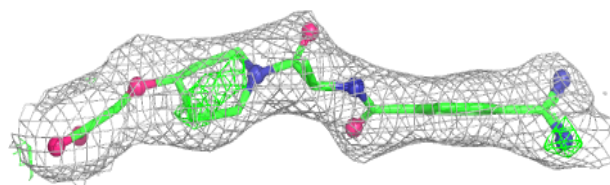
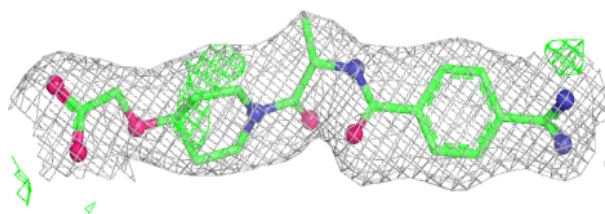
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around XQS B 2005:**

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

**Electron density around XQS D 2005:**

$2mF_o-DF_c$  (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.