



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 05:19 AM BST

PDB ID : 3PVD  
Title : Crystal structure of P domain dimer of Norovirus VA207 complexed with 3'-sialyl-Lewis x tetrasaccharide  
Authors : Chen, Y.; Tan, M.; Xia, M.; Hao, N.; Zhang, X.C.; Huang, P.; Jiang, X.; Li, X.; Rao, Z.  
Deposited on : 2010-12-06  
Resolution : 1.90 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](mailto: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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

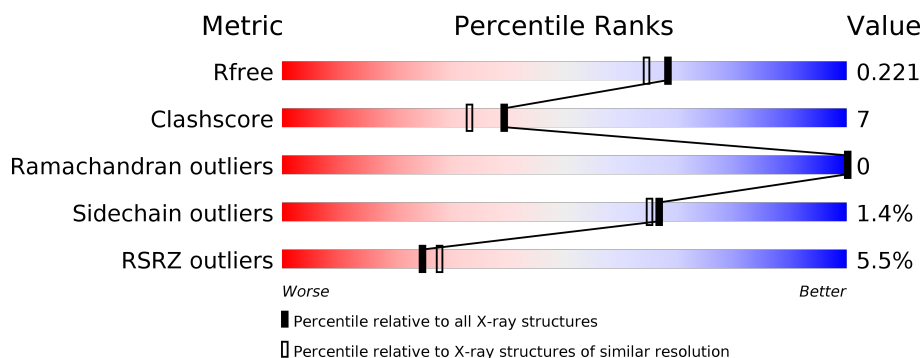
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on 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	316	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>• 5%</div> </div> </div>
1	B	316	<div> <div>7%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>•</div> </div> </div>
2	C	4	<div> <div></div> <div>100%</div> </div>
2	D	4	<div> <div>25%</div> <div>25%</div> <div>50%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5121 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.

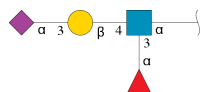
- Molecule 1 is a protein called Capsid.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2322	1476	396	442	8			
1	B	302	Total	C	N	O	S	0	0	0
			2340	1485	400	447	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ASN	THR	engineered mutation	UNP Q91H09
A	374	ASP	ASN	engineered mutation	UNP Q91H09
A	425	GLY	ARG	engineered mutation	UNP Q91H09
A	466	ARG	GLN	engineered mutation	UNP Q91H09
A	482	ALA	VAL	engineered mutation	UNP Q91H09
B	289	ASN	THR	engineered mutation	UNP Q91H09
B	374	ASP	ASN	engineered mutation	UNP Q91H09
B	425	GLY	ARG	engineered mutation	UNP Q91H09
B	466	ARG	GLN	engineered mutation	UNP Q91H09
B	482	ALA	VAL	engineered mutation	UNP Q91H09

- Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			56	31	2	23			
2	D	4	Total	C	N	O	0	0	0
			56	31	2	23			

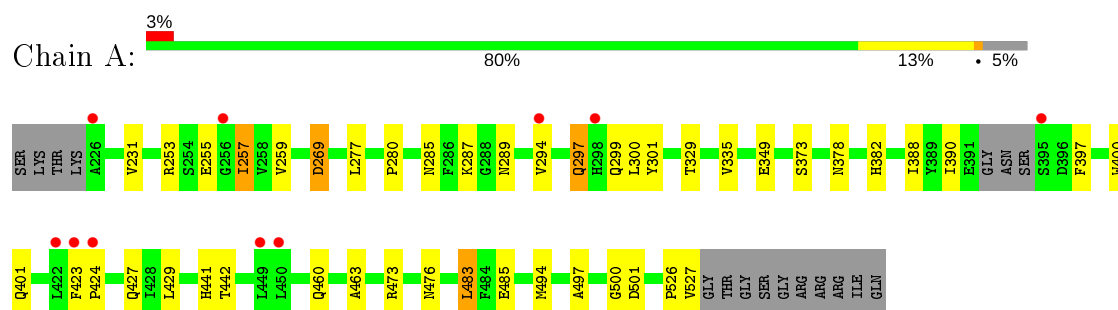
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	181	Total 181	O 181	0	0
3	B	166	Total 166	O 166	0	0

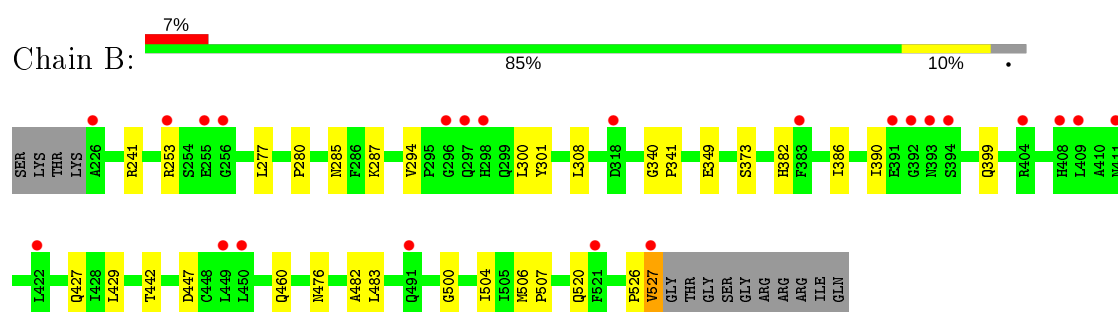
### 3 Residue-property plots [i](#)

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.

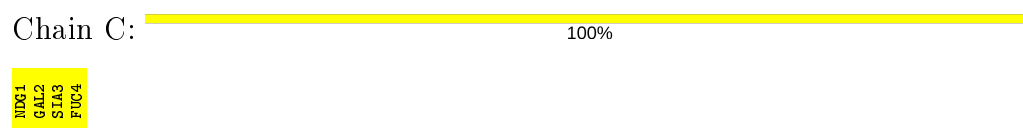
#### • Molecule 1: Capsid



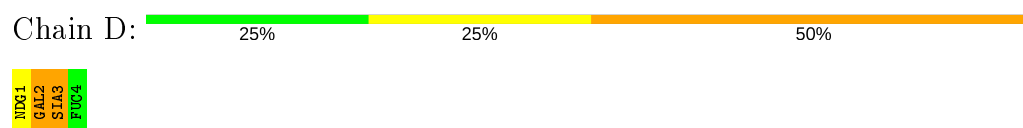
#### • Molecule 1: Capsid



#### • Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-alpha-D-glucopyranose



#### • Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-alpha-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.30 Å 96.00 Å 101.63 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.06 – 1.90 28.06 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.6 (28.06-1.90) 98.5 (28.06-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 1.91 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.186 , 0.228 0.192 , 0.221	Depositor DCC
$R_{free}$ test set	2634 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.1	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 41.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5121	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SIA, GAL, FUC, NDG

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	0.45	0/2388	0.58	0/3256
1	B	0.41	0/2407	0.55	0/3283
All	All	0.43	0/4795	0.56	0/6539

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

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	2322	0	2219	43	0
1	B	2340	0	2234	35	0
2	C	56	0	46	0	0
2	D	56	0	46	2	0
3	A	181	0	0	3	0
3	B	166	0	0	1	0
All	All	5121	0	4545	69	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 7.

All (69) 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:B:399:GLN:HE22	1:B:447:ASP:H	1.22	0.85
1:A:294:VAL:HG21	1:A:300:LEU:HD23	1.61	0.82
1:A:231:VAL:H	1:B:460:GLN:NE2	1.78	0.80
1:A:441:HIS:CE1	2:D:3:SIA:H32	2.20	0.77
1:A:257:ILE:HD13	1:A:400:TRP:CD1	2.22	0.74
1:A:231:VAL:H	1:B:460:GLN:HE22	1.37	0.69
1:A:287:LYS:NZ	1:A:382:HIS:HD2	1.94	0.66
1:A:257:ILE:HD11	1:A:259:VAL:HG22	1.79	0.64
1:A:429:LEU:HD23	1:A:494:MET:HE2	1.79	0.63
1:B:427:GLN:HE22	1:B:500:GLY:H	1.48	0.61
1:B:285:ASN:OD1	1:B:382:HIS:HE1	1.84	0.59
1:A:427:GLN:HE22	1:A:500:GLY:H	1.50	0.59
1:B:287:LYS:NZ	1:B:382:HIS:HD2	2.00	0.59
1:A:526:PRO:O	1:A:527:VAL:HG22	2.04	0.58
1:A:390:ILE:HG13	1:A:442:THR:HB	1.87	0.57
1:A:388:ILE:HG12	1:A:397:PHE:HB2	1.88	0.56
1:A:257:ILE:HG13	1:A:257:ILE:O	2.02	0.56
1:A:231:VAL:N	1:B:460:GLN:HE22	2.03	0.55
1:B:294:VAL:HG21	1:B:300:LEU:HD23	1.89	0.55
1:A:473:ARG:HG2	1:A:485:GLU:HG2	1.89	0.54
1:B:294:VAL:HG22	1:B:300:LEU:HB3	1.90	0.54
1:A:253:ARG:HG3	1:A:501:ASP:OD1	2.08	0.53
1:A:335:VAL:HG21	1:B:386:ILE:HD13	1.90	0.53
1:A:476:ASN:HB2	1:A:483:LEU:HD11	1.91	0.52
1:B:301:TYR:OH	1:B:373:SER:HA	2.10	0.51
1:B:241:ARG:HH12	1:B:399:GLN:HE21	1.59	0.51
1:A:285:ASN:OD1	1:A:382:HIS:HE1	1.95	0.50
1:A:231:VAL:N	1:B:460:GLN:NE2	2.56	0.50
1:A:280:PRO:HG3	3:B:23:HOH:O	2.10	0.50
1:A:287:LYS:HZ3	1:A:382:HIS:HD2	1.60	0.49
1:A:297:GLN:HG2	1:A:300:LEU:HD22	1.95	0.48
1:B:287:LYS:HZ3	1:B:382:HIS:HD2	1.62	0.48
1:B:483:LEU:CD2	1:B:507:PRO:HD2	2.44	0.48
1:B:390:ILE:HG13	1:B:442:THR:HB	1.97	0.47
1:B:476:ASN:HB2	1:B:483:LEU:HD11	1.97	0.47
1:A:301:TYR:OH	1:A:373:SER:HA	2.15	0.47
1:A:287:LYS:NZ	1:A:382:HIS:CD2	2.79	0.47
1:A:349:GLU:HG3	1:B:349:GLU:HG3	1.97	0.46
1:B:527:VAL:O	1:B:527:VAL:HG13	2.14	0.46
1:B:253:ARG:CZ	1:B:500:GLY:HA2	2.46	0.46
1:A:329:THR:HG23	1:A:401:GLN:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:483:LEU:HD12	1:B:483:LEU:N	2.31	0.45
1:B:520:GLN:CD	1:B:520:GLN:H	2.20	0.45
1:A:287:LYS:HG3	1:A:382:HIS:CD2	2.52	0.45
1:A:335:VAL:CG2	1:B:386:ILE:HD13	2.47	0.45
1:B:340:GLY:HA2	1:B:341:PRO:C	2.36	0.45
1:A:460:GLN:HG2	3:A:102:HOH:O	2.18	0.44
1:B:483:LEU:HD23	1:B:506:MET:SD	2.58	0.43
1:B:287:LYS:NZ	1:B:382:HIS:CD2	2.84	0.43
1:B:399:GLN:NE2	1:B:447:ASP:H	2.02	0.43
1:A:253:ARG:HB2	1:A:255:GLU:HG3	2.01	0.42
1:B:429:LEU:CD1	1:B:504:ILE:HD12	2.49	0.42
1:A:349:GLU:CG	1:B:349:GLU:HG3	2.49	0.42
1:A:349:GLU:HG3	1:B:349:GLU:OE2	2.18	0.42
1:B:482:ALA:C	1:B:483:LEU:HD12	2.40	0.42
1:A:441:HIS:HE1	2:D:2:GAL:O3	2.03	0.42
1:A:257:ILE:HD11	1:A:259:VAL:CG2	2.47	0.41
1:A:257:ILE:HD13	1:A:400:TRP:CG	2.55	0.41
1:A:497:ALA:HB3	1:A:526:PRO:HA	2.02	0.41
1:B:526:PRO:O	1:B:527:VAL:HB	2.19	0.41
3:A:564:HOH:O	1:B:280:PRO:HG3	2.20	0.41
1:A:527:VAL:HG22	3:A:609:HOH:O	2.20	0.41
1:A:289:ASN:OD1	1:A:378:ASN:HA	2.21	0.41
1:B:301:TYR:HH	1:B:373:SER:HA	1.85	0.41
1:B:308:LEU:HD23	1:B:308:LEU:HA	1.95	0.41
1:A:294:VAL:HG23	1:A:297:GLN:HB2	2.03	0.41
1:A:269:ASP:HB3	1:A:463:ALA:O	2.20	0.40
1:A:423:PHE:HA	1:A:424:PRO:HD3	1.97	0.40
1:A:299:GLN:NE2	1:A:373:SER:HB3	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	295/316 (93%)	287 (97%)	8 (3%)	0	100	100
1	B	300/316 (95%)	294 (98%)	6 (2%)	0	100	100
All	All	595/632 (94%)	581 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	253/266 (95%)	248 (98%)	5 (2%)	55	51
1	B	255/266 (96%)	253 (99%)	2 (1%)	81	82
All	All	508/532 (96%)	501 (99%)	7 (1%)	67	65

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	ILE
1	A	269	ASP
1	A	277	LEU
1	A	297	GLN
1	A	483	LEU
1	B	277	LEU
1	B	527	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	248	GLN
1	A	382	HIS
1	A	408	HIS
1	A	427	GLN
1	A	441	HIS
1	A	509	ASN

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Mol	Chain	Res	Type
1	B	248	GLN
1	B	382	HIS
1	B	399	GLN
1	B	408	HIS
1	B	427	GLN
1	B	460	GLN
1	B	509	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 ⓘ

8 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	$\# Z  > 2$
2	NDG	C	1	2	15,15,15	2.75	2 (13%)	21,21,21	1.11	1 (4%)
2	GAL	C	2	2	11,11,12	0.42	0	15,15,17	0.96	1 (6%)
2	SIA	C	3	2	17,20,21	2.10	1 (5%)	21,28,31	1.29	2 (9%)
2	FUC	C	4	2	10,10,11	0.47	0	14,14,16	0.88	1 (7%)
2	NDG	D	1	2	15,15,15	2.18	1 (6%)	21,21,21	1.62	3 (14%)
2	GAL	D	2	2	11,11,12	0.41	0	15,15,17	1.35	2 (13%)
2	SIA	D	3	2	17,20,21	2.09	1 (5%)	21,28,31	1.26	2 (9%)
2	FUC	D	4	2	10,10,11	0.46	0	14,14,16	0.51	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDG	C	1	2	-	0/6/26/26	0/1/1/1
2	GAL	C	2	2	-	2/2/19/22	0/1/1/1
2	SIA	C	3	2	-	0/14/34/38	0/1/1/1
2	FUC	C	4	2	-	-	0/1/1/1
2	NDG	D	1	2	-	0/6/26/26	0/1/1/1
2	GAL	D	2	2	-	0/2/19/22	0/1/1/1
2	SIA	D	3	2	-	3/14/34/38	0/1/1/1
2	FUC	D	4	2	-	-	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	SIA	C11-C10	-8.52	1.32	1.50
2	D	3	SIA	C11-C10	-8.47	1.32	1.50
2	C	1	NDG	C8-C7	-8.33	1.33	1.50
2	D	1	NDG	C8-C7	-8.21	1.33	1.50
2	C	1	NDG	O1-C1	-6.57	1.18	1.39

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NDG	O1-C1-O5	-5.18	94.83	110.38
2	D	2	GAL	C1-C2-C3	3.49	113.96	109.67
2	C	3	SIA	C8-C7-C6	-3.23	106.92	113.03
2	D	3	SIA	C6-O6-C2	3.18	118.13	111.34
2	D	1	NDG	C1-C2-N2	-2.96	107.29	110.73
2	D	1	NDG	O5-C1-C2	2.73	112.26	109.52
2	C	2	GAL	C1-C2-C3	2.70	112.98	109.67
2	C	3	SIA	C4-C3-C2	2.48	114.26	109.81
2	D	2	GAL	O5-C5-C6	2.39	110.95	107.20
2	D	3	SIA	C3-C2-C1	-2.35	106.79	111.93
2	C	1	NDG	C8-C7-N2	2.20	119.83	116.10
2	C	4	FUC	C1-O5-C5	2.04	117.40	112.78

There are no chirality outliers.

All (5) torsion outliers are listed below:

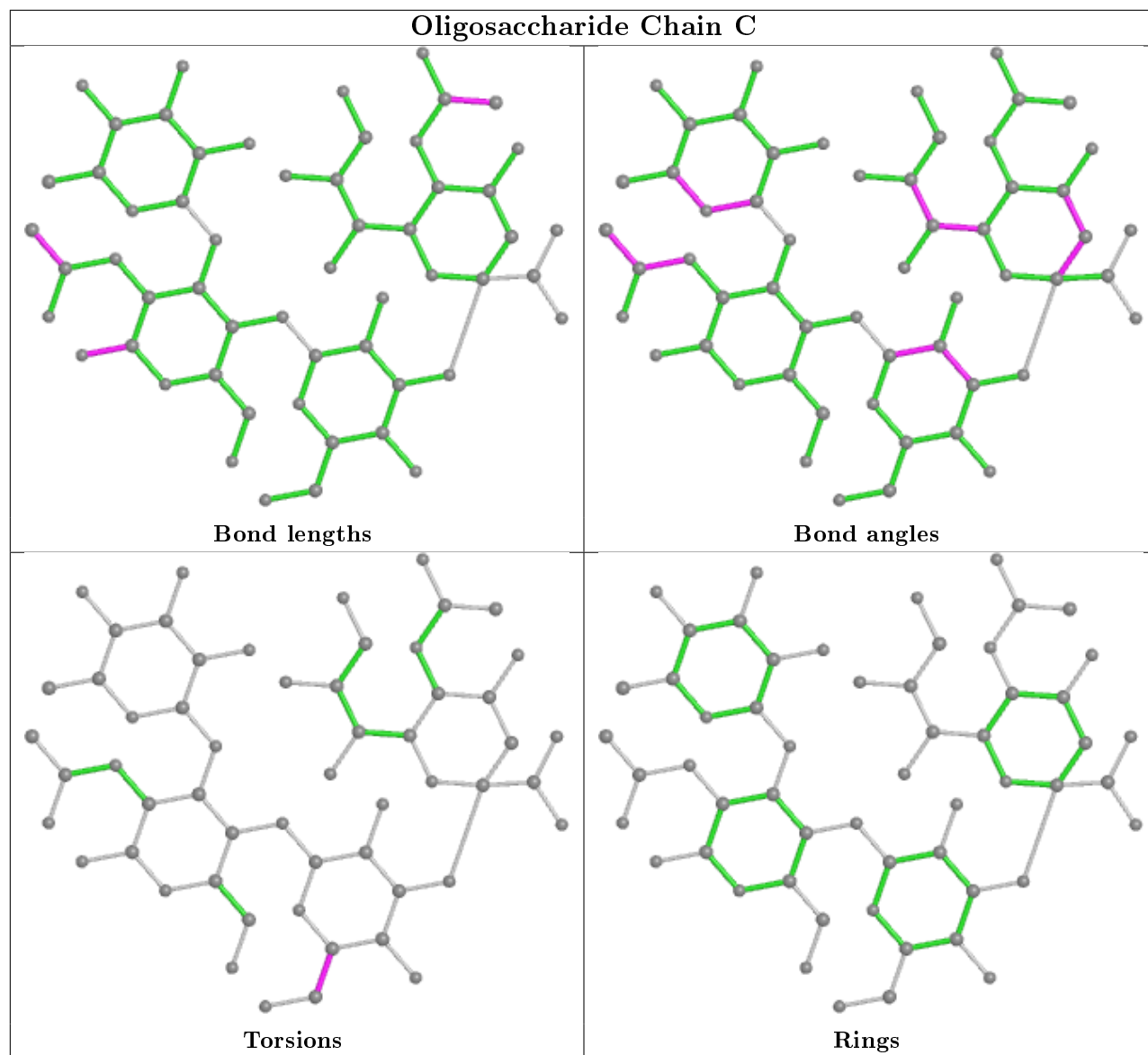
Mol	Chain	Res	Type	Atoms
2	C	2	GAL	C4-C5-C6-O6
2	C	2	GAL	O5-C5-C6-O6
2	D	3	SIA	C11-C10-N5-C5
2	D	3	SIA	O10-C10-N5-C5
2	D	3	SIA	C4-C5-N5-C10

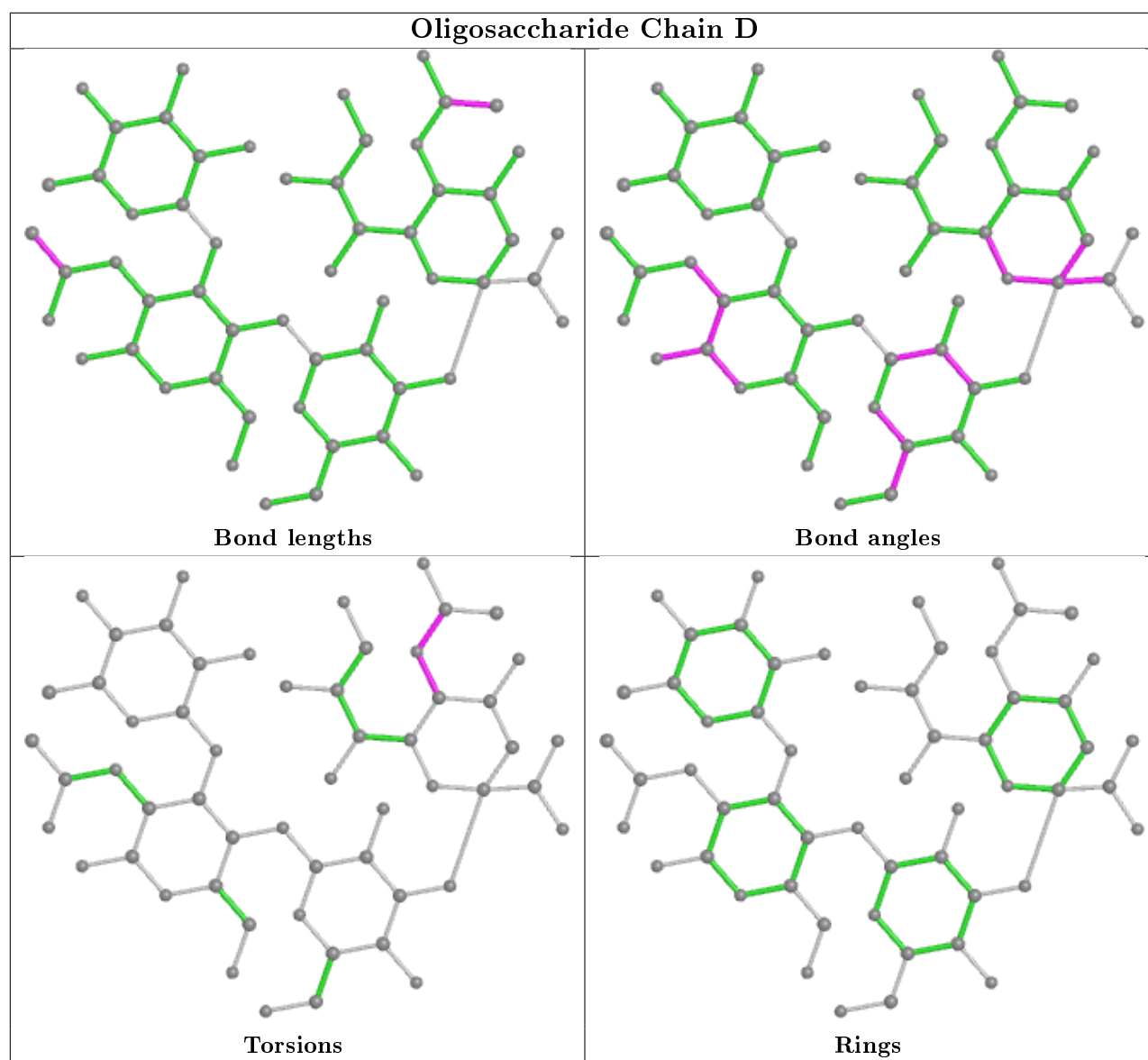
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	SIA	1	0
2	D	2	GAL	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](#)

There are no ligands in this entry.

## 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 ⓘ

### 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, 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	299/316 (94%)	0.21	10 (3%) 46 49	20, 34, 49, 60	0
1	B	302/316 (95%)	0.43	23 (7%) 13 15	25, 36, 54, 72	0
All	All	601/632 (95%)	0.32	33 (5%) 25 28	20, 36, 52, 72	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	409	LEU	11.4
1	A	226	ALA	7.4
1	B	296	GLY	6.0
1	B	298	HIS	5.9
1	B	408	HIS	4.8
1	B	392	GLY	4.7
1	B	297	GLN	3.7
1	B	527	VAL	3.6
1	B	394	SER	3.5
1	B	255	GLU	3.5
1	A	422	LEU	3.4
1	A	298	HIS	3.2
1	B	256	GLY	3.0
1	B	411	ASN	2.9
1	B	393	ASN	2.8
1	A	450	LEU	2.7
1	B	521	PHE	2.6
1	B	450	LEU	2.6
1	B	422	LEU	2.5
1	A	294	VAL	2.4
1	B	253	ARG	2.4
1	B	404	ARG	2.4
1	A	395	SER	2.4
1	B	491	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	449	LEU	2.3
1	A	449	LEU	2.2
1	A	256	GLY	2.2
1	B	226	ALA	2.1
1	B	383	PHE	2.1
1	B	391	GLU	2.1
1	A	423	PHE	2.0
1	B	318	ASP	2.0
1	A	424	PRO	2.0

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

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

## 6.3 Carbohydrates [i](#)

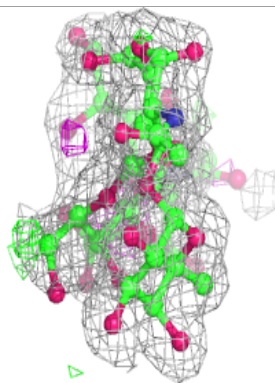
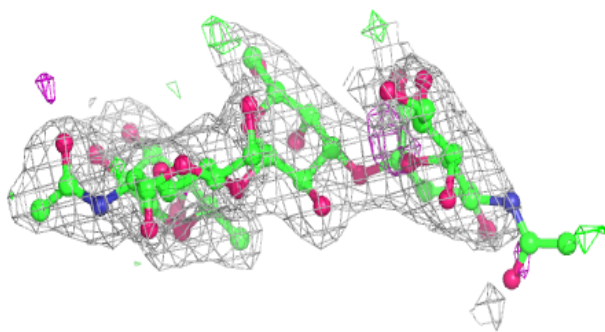
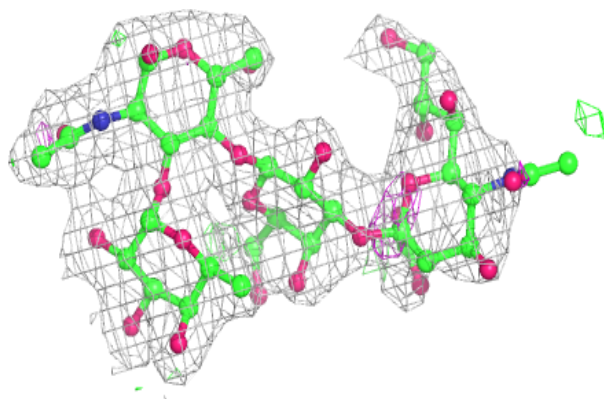
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	SIA	C	3	20/21	0.77	0.29	67,72,83,83	0
2	SIA	D	3	20/21	0.78	0.31	59,64,77,78	0
2	NDG	C	1	15/15	0.89	0.12	44,48,56,57	0
2	NDG	D	1	15/15	0.89	0.12	40,44,47,54	0
2	GAL	C	2	11/12	0.90	0.13	52,57,62,63	0
2	GAL	D	2	11/12	0.92	0.11	45,49,58,60	0
2	FUC	D	4	10/11	0.96	0.08	34,37,39,40	0
2	FUC	C	4	10/11	0.96	0.07	36,40,43,45	0

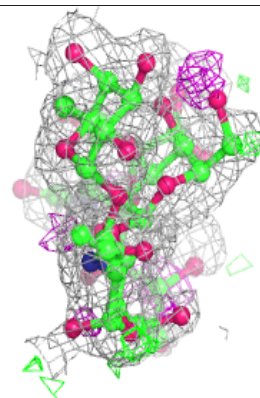
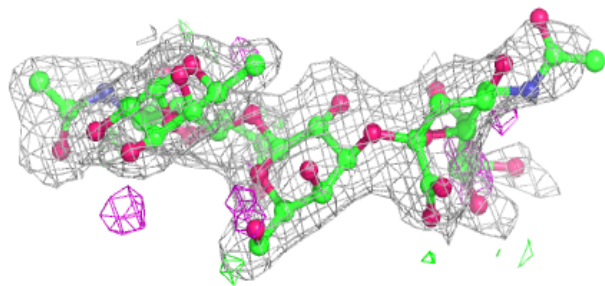
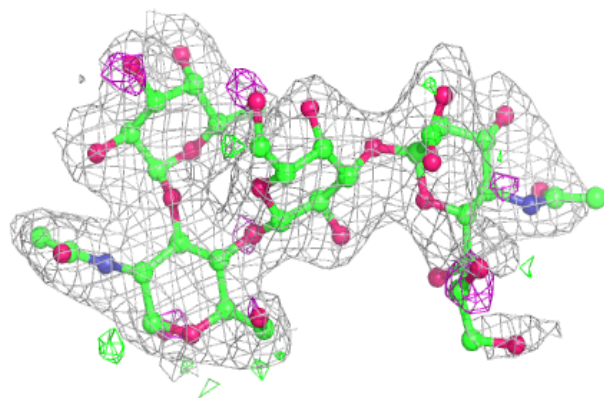
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain C:**

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

**Electron density around Chain D:**

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



## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.