



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2024 – 08:41 AM EDT

PDB ID : 3BES  
Title : Structure of a Poxvirus ifngbp/ifng Complex  
Authors : Nuara, A.A.; Walter, M.R.  
Deposited on : 2007-11-20  
Resolution : 2.20 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)

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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
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

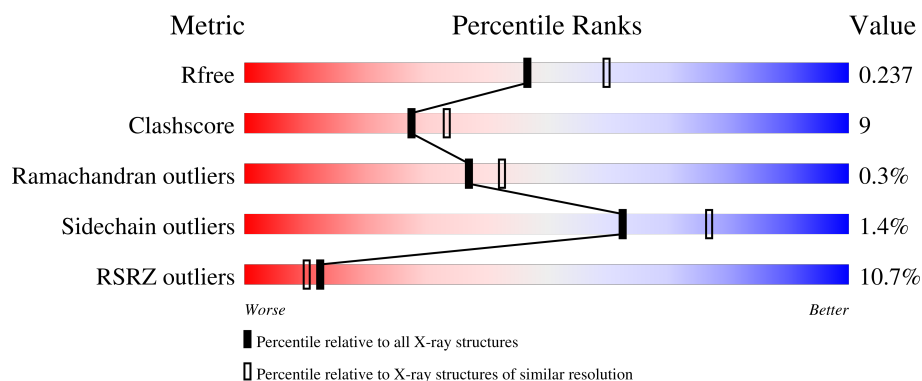
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	L	139	<div> <div>14%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>.</div> </div> </div>
2	R	250	<div> <div>8%</div> <div> <div></div> <div>83%</div> <div>17%</div> </div> </div>
3	A	3	<div> <div>33%</div> <div>33%</div> <div>33%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3420 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 Interferon gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	133	Total	C	N	O	S	0	0	0
			1096	695	190	207	4			

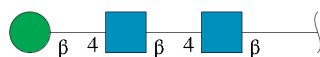
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	0	MET	-	initiating methionine	UNP P01579

- Molecule 2 is a protein called Interferon-gamma binding protein C4R.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	250	Total	C	N	O	S	0	1	0
			2019	1291	317	398	13			

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



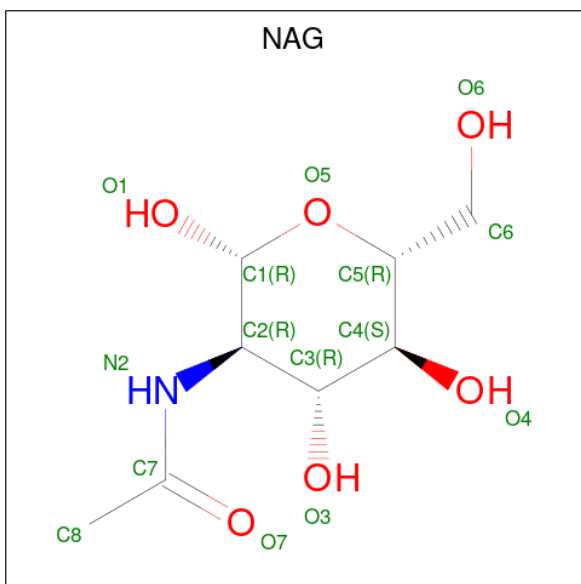
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	O	P	0	0
			5	4	1		
4	R	1	Total	O	P	0	0
			5	4	1		
4	R	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

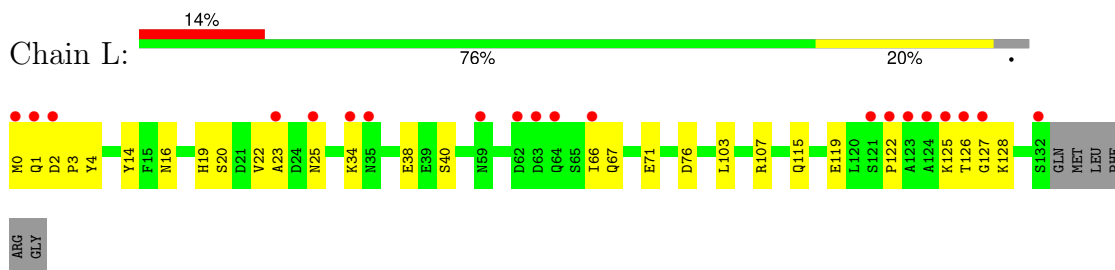
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	L	62	Total	O	0	0
			62	62		
6	R	175	Total	O	0	0
			175	175		

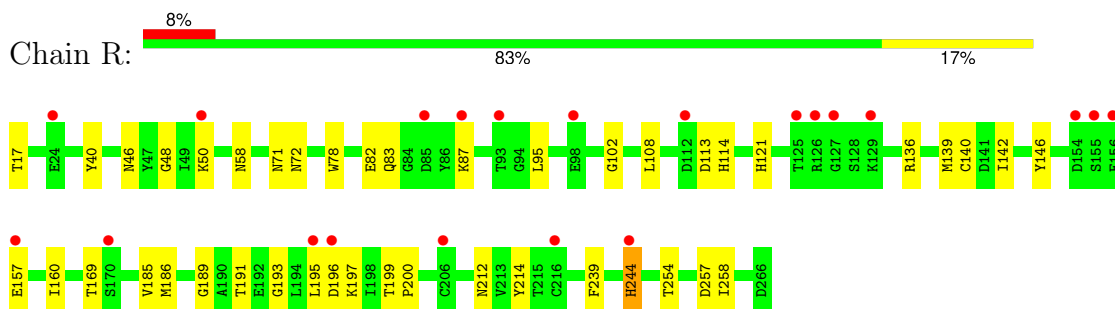
### 3 Residue-property plots

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.

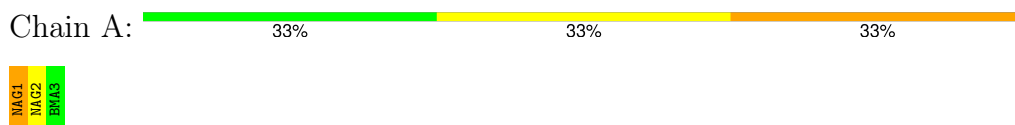
- Molecule 1: Interferon gamma



- Molecule 2: Interferon-gamma binding protein C4R



- Molecule 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	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.63Å 119.13Å 184.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.20) 99.3 (20.00-2.20)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.24 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.219 , 0.245 0.209 , 0.237	Depositor DCC
$R_{free}$ test set	2595 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.6	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.4	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	0.95	EDS
Total number of atoms	3420	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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: PO4, NAG, BMA

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	L	0.35	0/1114	0.53	0/1487
2	R	0.35	0/2074	0.61	0/2813
All	All	0.35	0/3188	0.58	0/4300

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	L	1096	0	1108	26	0
2	R	2019	0	1945	32	0
3	A	39	0	34	3	0
4	L	5	0	0	0	0
4	R	10	0	0	1	0
5	R	14	0	13	2	0
6	L	62	0	0	2	0
6	R	175	0	0	2	0
All	All	3420	0	3100	56	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.



All (56) 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:R:58:ASN:HD21	3:A:1:NAG:HN2	1.23	0.87
2:R:189:GLY:H	2:R:199:THR:HG22	1.45	0.82
1:L:1:GLN:HB3	1:L:3:PRO:HD2	1.63	0.81
2:R:239:PHE:O	2:R:244:HIS:HE1	1.65	0.79
1:L:0:MET:O	1:L:1:GLN:HG3	1.90	0.72
1:L:122:PRO:HB2	1:L:125:LYS:HB2	1.72	0.71
2:R:46:ASN:HD21	2:R:71:ASN:H	1.39	0.68
2:R:189:GLY:H	2:R:199:THR:CG2	2.05	0.68
2:R:46:ASN:ND2	2:R:71:ASN:H	1.93	0.67
2:R:199:THR:HG23	2:R:200:PRO:O	1.95	0.66
1:L:1:GLN:CB	1:L:3:PRO:HD2	2.27	0.64
2:R:17:THR:N	2:R:40:TYR:HH	1.97	0.63
2:R:58:ASN:ND2	3:A:1:NAG:HN2	1.96	0.62
2:R:140:CYS:HB2	2:R:142:ILE:HG13	1.81	0.62
1:L:34:LYS:NZ	1:L:34:LYS:HB2	2.15	0.61
2:R:121:HIS:HE1	2:R:169:THR:O	1.84	0.60
2:R:83:GLN:HA	3:A:1:NAG:H81	1.82	0.60
2:R:239:PHE:O	2:R:244:HIS:CE1	2.53	0.58
1:L:0:MET:O	1:L:1:GLN:CG	2.54	0.56
1:L:122:PRO:O	1:L:126:THR:HG23	2.05	0.56
2:R:257:ASP:OD2	4:R:1:PO4:O4	2.26	0.54
1:L:2:ASP:N	1:L:3:PRO:CD	2.71	0.53
2:R:136:ARG:HD3	2:R:139:MET:CE	2.38	0.53
2:R:121:HIS:HD2	2:R:146:TYR:OH	1.92	0.52
2:R:136:ARG:HD3	2:R:139:MET:HE3	1.92	0.52
1:L:1:GLN:HB3	1:L:3:PRO:CD	2.39	0.51
1:L:4:TYR:CD2	1:L:76:ASP:HB2	2.45	0.51
1:L:126:THR:O	1:L:128:LYS:N	2.40	0.51
1:L:107:ARG:HD2	6:L:162:HOH:O	2.11	0.51
2:R:102:GLY:O	2:R:199:THR:OG1	2.27	0.51
2:R:72:ASN:OD1	2:R:95:LEU:HD23	2.12	0.50
2:R:82:GLU:OE2	2:R:87:LYS:HE2	2.13	0.49
1:L:4:TYR:CE2	1:L:76:ASP:HB2	2.48	0.48
2:R:195:LEU:HD12	6:R:358:HOH:O	2.14	0.48
2:R:212:ASN:HB2	2:R:214:TYR:CZ	2.49	0.47
1:L:0:MET:SD	2:R:193:GLY:HA2	2.55	0.46
1:L:103:LEU:O	1:L:103:LEU:HD23	2.14	0.46
1:L:14:TYR:CD2	1:L:66:ILE:HG21	2.50	0.46
2:R:113:ASP:O	2:R:114:HIS:HB3	2.16	0.46
2:R:254:THR:O	2:R:258:ILE:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:19:HIS:O	1:L:22:VAL:HG12	2.16	0.46
1:L:67:GLN:HG3	1:L:71:GLU:OE2	2.18	0.44
1:L:23:ALA:HB1	2:R:48:GLY:H	1.83	0.44
2:R:160:ILE:HD11	5:R:270:NAG:O5	2.18	0.44
1:L:38:GLU:OE1	1:L:40:SER:HB2	2.19	0.43
1:L:115:GLN:O	1:L:119:GLU:HG2	2.19	0.43
1:L:34:LYS:HB2	1:L:34:LYS:HZ2	1.81	0.43
2:R:50:LYS:H	2:R:50:LYS:HG2	1.66	0.42
1:L:0:MET:C	1:L:1:GLN:HG3	2.38	0.42
1:L:14:TYR:CG	1:L:66:ILE:HG21	2.55	0.42
2:R:185:VAL:HG12	2:R:186:MET:N	2.34	0.42
1:L:25:ASN:N	6:L:168:HOH:O	2.53	0.42
1:L:20:SER:HA	2:R:78:TRP:CE2	2.55	0.42
5:R:270:NAG:H62	6:R:326:HOH:O	2.19	0.41
2:R:191:THR:OG1	2:R:195:LEU:O	2.37	0.41
2:R:191:THR:HG23	2:R:197:LYS:HB2	2.02	0.41

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	L	131/139 (94%)	127 (97%)	3 (2%)	1 (1%)	16	16
2	R	249/250 (100%)	240 (96%)	9 (4%)	0	100	100
All	All	380/389 (98%)	367 (97%)	12 (3%)	1 (0%)	37	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	127	GLY

### 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	L	122/127 (96%)	121 (99%)	1 (1%)	79	88
2	R	231/230 (100%)	227 (98%)	4 (2%)	56	71
All	All	353/357 (99%)	348 (99%)	5 (1%)	62	77

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	16	ASN
2	R	108	LEU
2	R	157	GLU
2	R	196	ASP
2	R	244	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	10	ASN
1	L	83	ASN
2	R	37	ASN
2	R	46	ASN
2	R	58	ASN
2	R	114	HIS
2	R	116	ASN
2	R	121	HIS
2	R	137	ASN
2	R	244	HIS
2	R	256	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

3 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	$\# Z  > 2$
3	NAG	A	1	3,2	14,14,15	0.51	0	17,19,21	0.67	1 (5%)
3	NAG	A	2	3	14,14,15	0.48	0	17,19,21	0.70	1 (5%)
3	BMA	A	3	3	11,11,12	0.45	0	15,15,17	0.24	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
3	NAG	A	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	A	2	3	-	4/6/23/26	0/1/1/1
3	BMA	A	3	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	NAG	C2-N2-C7	-2.09	120.10	122.90
3	A	1	NAG	C2-N2-C7	-2.01	120.21	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

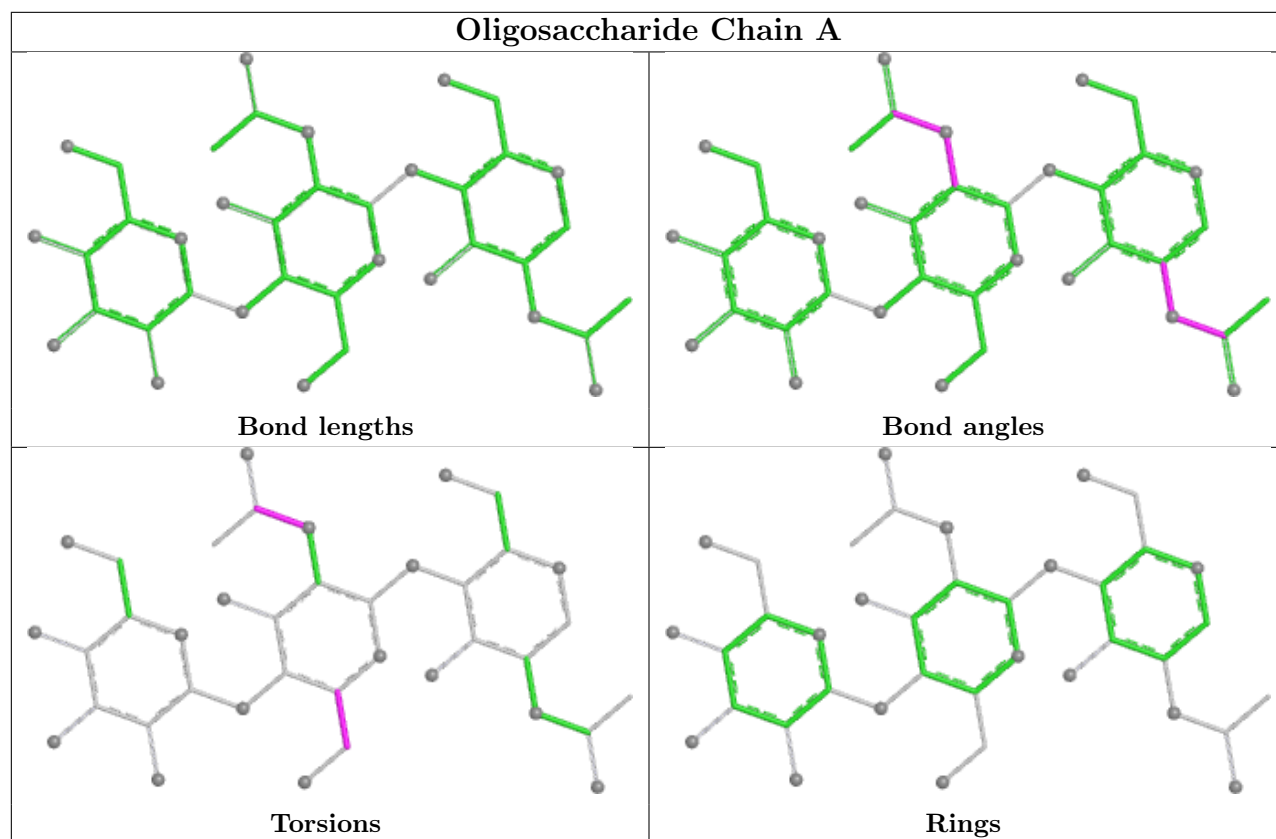
Mol	Chain	Res	Type	Atoms
3	A	2	NAG	C8-C7-N2-C2
3	A	2	NAG	O7-C7-N2-C2
3	A	2	NAG	C4-C5-C6-O6
3	A	2	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	NAG	3	0

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



## 5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PO4	R	1	-	4,4,4	1.26	1 (25%)	6,6,6	0.97	0
5	NAG	R	270	2	14,14,15	0.58	0	17,19,21	0.66	0
4	PO4	L	139	-	4,4,4	1.70	0	6,6,6	0.45	0
4	PO4	R	3	-	4,4,4	1.61	0	6,6,6	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	R	270	2	-	5/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	1	PO4	P-O1	-2.10	1.45	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	R	270	NAG	C8-C7-N2-C2
5	R	270	NAG	O7-C7-N2-C2
5	R	270	NAG	C4-C5-C6-O6
5	R	270	NAG	O5-C5-C6-O6
5	R	270	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	1	PO4	1	0
5	R	270	NAG	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	L	133/139 (95%)	0.78	20 (15%) <b>6</b> <b>5</b>	26, 44, 80, 85	0
2	R	250/250 (100%)	0.36	21 (8%) <b>18</b> <b>16</b>	28, 39, 58, 81	1 (0%)
All	All	383/389 (98%)	0.50	41 (10%) <b>12</b> <b>10</b>	26, 41, 72, 85	1 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	0	MET	6.8
1	L	124	ALA	5.8
1	L	1	GLN	5.7
1	L	126	THR	5.6
1	L	123	ALA	5.2
1	L	122	PRO	4.6
1	L	127	GLY	4.4
1	L	121	SER	3.9
2	R	129	LYS	3.9
1	L	25	ASN	3.9
2	R	126	ARG	3.8
2	R	157	GLU	3.8
2	R	195	LEU	3.4
1	L	64	GLN	3.3
2	R	206	CYS	3.3
2	R	156	GLU	3.2
1	L	62	ASP	3.2
2	R	216	CYS	3.0
2	R	127	GLY	3.0
1	L	132	SER	2.9
2	R	196	ASP	2.9
2	R	50	LYS	2.9
2	R	93	THR	2.9
2	R	85	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	L	23	ALA	2.7
2	R	244	HIS	2.7
2	R	154	ASP	2.6
1	L	125	LYS	2.5
2	R	170	SER	2.5
2	R	24	GLU	2.4
2	R	87	LYS	2.4
2	R	125	THR	2.4
1	L	34	LYS	2.4
2	R	112	ASP	2.4
1	L	2	ASP	2.4
1	L	35	ASN	2.3
2	R	155	SER	2.2
1	L	66	ILE	2.2
1	L	63	ASP	2.2
2	R	98	GLU	2.1
1	L	59	ASN	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](#)

SUGAR-RSR INFOmissingINFO

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
5	NAG	R	270	14/15	0.69	0.20	72,78,79,81	0
4	PO4	R	3	5/5	0.71	0.33	82,83,85,85	0
4	PO4	R	1	5/5	0.88	0.13	102,102,102,102	5
4	PO4	L	139	5/5	0.92	0.16	83,83,84,84	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.