



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:39 AM GMT

PDB ID : 2DSU  
Title : Binding of chitin-like polysaccharide to protective signalling factor: Crystal structure of the complex formed between signalling protein from sheep (SPS-40) with a tetrasaccharide at 2.2 Å resolution  
Authors : Srivastava, D.B.; Ethayathulla, A.S.; Kumar, J.; Singh, N.; Sharma, S.; Kaur, P.; Bhushan, A.; Singh, T.P.  
Deposited on : 2006-07-07  
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)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

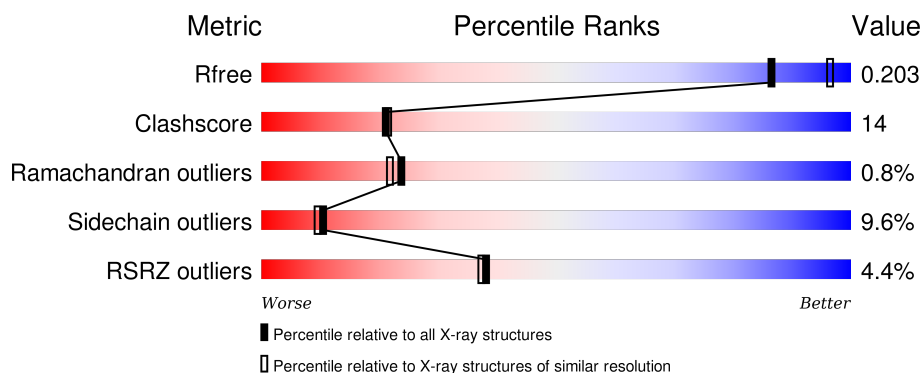
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	361	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	363	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NDG	A	367	-	-	-	X
3	NAG	A	368	-	-	X	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3144 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 Chitinase-3-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2869	1832	499	529	9			

- Molecule 2 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 3 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	4	Total	C	N	O	0	0
			57	32	4	21		

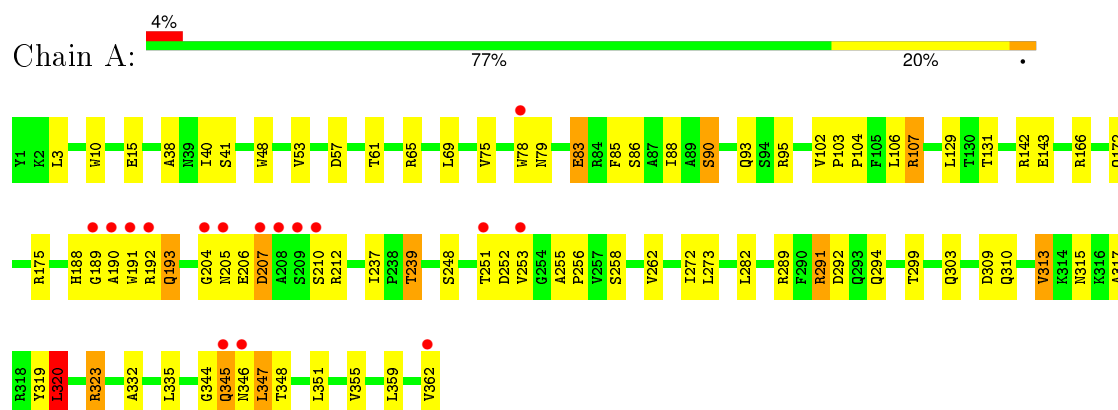
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	168	Total	O	0	0
			168	168		

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

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Chitinase-3-like protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.75Å 66.51Å 107.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.00 – 2.20 45.64 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.7 (56.00-2.20) 95.9 (45.64-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.187 , 0.209 0.187 , 0.203	Depositor DCC
$R_{free}$ test set	446 reflections (1.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.1	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 60.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 22554 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3144	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, NAG, NDG, MAN

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	0.38	0/2945	0.69	1/3995 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	320	LEU	CA-CB-CG	8.68	135.25	115.30

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	2869	0	2794	68	0
2	A	50	0	43	9	0
3	A	57	0	51	12	0
4	A	168	0	0	19	0
All	All	3144	0	2888	84	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 14.

All (84) 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:A:365:BMA:H61	2:A:366:MAN:C2	1.92	0.99
1:A:204:GLY:HA2	1:A:292:ASP:HB3	1.46	0.97
1:A:323:ARG:HH11	1:A:323:ARG:HG2	1.27	0.96
1:A:142:ARG:HD3	4:A:482:HOH:O	1.71	0.91
2:A:363:NAG:O3	2:A:364:NDG:H6C2	1.71	0.90
2:A:363:NAG:H83	2:A:363:NAG:H3	1.59	0.84
2:A:365:BMA:H61	2:A:366:MAN:O2	1.77	0.84
1:A:291:ARG:HG3	4:A:515:HOH:O	1.77	0.83
1:A:323:ARG:NH1	1:A:323:ARG:HG2	1.93	0.82
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.62	0.80
1:A:57:ASP:O	1:A:61:THR:HG23	1.83	0.78
2:A:365:BMA:C6	2:A:366:MAN:H2	2.13	0.78
2:A:365:BMA:H61	2:A:366:MAN:H2	1.66	0.77
3:A:368:NAG:H62	3:A:369:NAG:C8	2.14	0.76
3:A:368:NAG:H62	3:A:369:NAG:H81	1.66	0.76
1:A:204:GLY:CA	1:A:292:ASP:HB3	2.18	0.74
1:A:15:GLU:HB3	4:A:512:HOH:O	1.86	0.74
1:A:323:ARG:CG	1:A:323:ARG:HH11	1.99	0.71
1:A:262:VAL:H	1:A:303:GLN:HE22	1.38	0.71
1:A:191:TRP:CD1	4:A:472:HOH:O	2.43	0.71
1:A:193:GLN:HE21	1:A:193:GLN:HA	1.56	0.71
1:A:193:GLN:HE21	1:A:193:GLN:CA	2.04	0.70
1:A:53:VAL:HG22	4:A:533:HOH:O	1.90	0.70
1:A:212:ARG:HD3	4:A:428:HOH:O	1.91	0.69
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.23	0.68
1:A:107:ARG:HD3	1:A:143:GLU:OE2	1.94	0.68
1:A:38:ALA:HB3	1:A:75:VAL:HG12	1.76	0.66
3:A:367:NDG:H6C2	3:A:368:NAG:N2	2.13	0.64
2:A:363:NAG:C3	2:A:363:NAG:H83	2.26	0.63
1:A:319:TYR:CZ	1:A:323:ARG:HD2	2.33	0.63
3:A:370:NAG:O3	3:A:370:NAG:C8	2.48	0.61
1:A:262:VAL:H	1:A:303:GLN:NE2	1.98	0.61
1:A:348:THR:HG21	4:A:440:HOH:O	2.01	0.61
1:A:323:ARG:NH1	4:A:460:HOH:O	2.34	0.60
1:A:95:ARG:NH2	1:A:131:THR:HG21	2.17	0.60
1:A:291:ARG:HD2	4:A:475:HOH:O	2.03	0.59
1:A:239:THR:HG21	1:A:332:ALA:O	2.03	0.58
1:A:292:ASP:HB2	4:A:500:HOH:O	2.02	0.58
2:A:363:NAG:H3	2:A:363:NAG:C8	2.33	0.58
1:A:239:THR:HG23	1:A:239:THR:O	2.04	0.57
1:A:48:TRP:HB3	4:A:507:HOH:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:VAL:HG23	4:A:522:HOH:O	2.05	0.57
3:A:370:NAG:O3	3:A:370:NAG:H83	2.05	0.56
1:A:10:TRP:CZ2	3:A:367:NDG:H4	2.41	0.56
1:A:317:ALA:HA	1:A:320:LEU:HD13	1.86	0.56
1:A:345:GLN:O	1:A:347:LEU:N	2.39	0.56
1:A:95:ARG:CZ	1:A:131:THR:HG21	2.36	0.56
1:A:313:VAL:HG13	1:A:355:VAL:CG2	2.36	0.55
1:A:166:ARG:HD3	4:A:535:HOH:O	2.06	0.54
1:A:103:PRO:HB2	1:A:104:PRO:HD3	1.89	0.54
1:A:345:GLN:HG2	1:A:345:GLN:O	2.06	0.54
1:A:294:GLN:NE2	1:A:315:ASN:OD1	2.41	0.54
1:A:323:ARG:NH2	4:A:404:HOH:O	2.43	0.50
2:A:365:BMA:C6	2:A:366:MAN:C2	2.70	0.50
1:A:310:GLN:HE22	1:A:345:GLN:NE2	2.09	0.50
1:A:61:THR:HG22	4:A:523:HOH:O	2.10	0.50
1:A:289:ARG:HD3	4:A:408:HOH:O	2.11	0.49
1:A:206:GLU:O	1:A:207:ASP:HB2	2.13	0.49
1:A:204:GLY:HA2	1:A:292:ASP:CB	2.32	0.48
1:A:40:ILE:HG21	1:A:88:ILE:HD13	1.94	0.48
1:A:10:TRP:CG	3:A:368:NAG:H3	2.48	0.48
1:A:79:ASN:HB2	3:A:368:NAG:C8	2.44	0.48
1:A:86:SER:O	1:A:90:SER:OG	2.32	0.48
1:A:291:ARG:CD	4:A:475:HOH:O	2.59	0.47
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.95	0.47
1:A:193:GLN:NE2	1:A:193:GLN:CA	2.75	0.45
1:A:344:GLY:O	1:A:345:GLN:C	2.54	0.45
1:A:313:VAL:HG13	1:A:355:VAL:HG22	1.96	0.45
1:A:251:THR:HG22	4:A:518:HOH:O	2.15	0.45
1:A:239:THR:CG2	1:A:239:THR:O	2.65	0.44
3:A:368:NAG:C6	3:A:369:NAG:C8	2.90	0.44
1:A:189:GLY:O	1:A:191:TRP:N	2.51	0.43
1:A:40:ILE:HG21	1:A:88:ILE:CD1	2.49	0.43
1:A:78:TRP:CE3	3:A:367:NDG:O	2.72	0.43
1:A:83:GLU:CD	1:A:83:GLU:H	2.22	0.43
1:A:172:GLN:OE1	1:A:175:ARG:NH1	2.52	0.42
1:A:272:ILE:HG22	1:A:273:LEU:N	2.33	0.42
1:A:188:HIS:ND1	1:A:189:GLY:N	2.66	0.42
1:A:65:ARG:NH2	4:A:421:HOH:O	2.51	0.41
1:A:237:ILE:CG2	1:A:313:VAL:HG22	2.51	0.41
3:A:367:NDG:H6C2	3:A:368:NAG:HN2	1.84	0.41
1:A:79:ASN:HB2	3:A:368:NAG:H81	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ALA:HA	1:A:256:PRO:HD3	1.87	0.40
1:A:289:ARG:NH2	1:A:309:ASP:OD2	2.51	0.40

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	359/361 (99%)	343 (96%)	13 (4%)	3 (1%)	24 22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	ALA
1	A	346	ASN
1	A	207	ASP

### 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	302/302 (100%)	273 (90%)	29 (10%)	10 9

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	41	SER
1	A	69	LEU
1	A	83	GLU
1	A	85	PHE
1	A	90	SER
1	A	93	GLN
1	A	106	LEU
1	A	107	ARG
1	A	129	LEU
1	A	192	ARG
1	A	193	GLN
1	A	205	ASN
1	A	210	SER
1	A	239	THR
1	A	248	SER
1	A	252	ASP
1	A	253	VAL
1	A	258	SER
1	A	282	LEU
1	A	291	ARG
1	A	299	THR
1	A	313	VAL
1	A	320	LEU
1	A	323	ARG
1	A	345	GLN
1	A	347	LEU
1	A	351	LEU
1	A	359	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	150	GLN
1	A	193	GLN
1	A	205	ASN
1	A	294	GLN
1	A	303	GLN
1	A	315	ASN
1	A	345	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 ⓘ

8 carbohydrates 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	NAG	A	363	1,2	14,14,15	0.95	1 (7%)	15,19,21	1.54	5 (33%)
2	NDG	A	364	2	14,14,15	1.14	2 (14%)	15,19,21	1.06	2 (13%)
2	BMA	A	365	2	11,11,12	0.99	1 (9%)	14,15,17	3.00	5 (35%)
2	MAN	A	366	2	11,11,12	0.69	0	14,15,17	0.78	0
3	NDG	A	367	3	15,15,15	0.56	0	17,21,21	1.10	1 (5%)
3	NAG	A	368	3	14,14,15	0.89	0	15,19,21	1.26	2 (13%)
3	NAG	A	369	3	14,14,15	0.99	0	15,19,21	1.04	1 (6%)
3	NAG	A	370	3	14,14,15	0.98	1 (7%)	15,19,21	1.18	1 (6%)

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	NAG	A	363	1,2	-	0/6/23/26	0/1/1/1
2	NDG	A	364	2	-	0/6/23/26	0/1/1/1
2	BMA	A	365	2	-	0/2/19/22	0/1/1/1
2	MAN	A	366	2	-	0/2/19/22	1/1/1/1
3	NDG	A	367	3	-	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	368	3	-	0/6/23/26	0/1/1/1
3	NAG	A	369	3	-	0/6/23/26	0/1/1/1
3	NAG	A	370	3	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	364	NDG	C4-C3	2.04	1.57	1.52
2	A	365	BMA	C1-C2	2.08	1.57	1.52
2	A	363	NAG	C4-C3	2.09	1.57	1.52
2	A	364	NDG	C1-C2	2.67	1.56	1.52
3	A	370	NAG	C1-C2	3.16	1.56	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	365	BMA	C3-C4-C5	-6.93	98.12	110.20
2	A	365	BMA	C2-C3-C4	-5.67	101.42	111.04
3	A	367	NDG	C4-C3-C2	-3.43	105.67	110.43
3	A	368	NAG	C2-N2-C7	-3.21	118.91	123.04
3	A	370	NAG	C2-N2-C7	-3.02	119.17	123.04
3	A	369	NAG	C6-C5-C4	-2.34	107.23	113.02
2	A	364	NDG	C1-O-C5	-2.27	109.37	112.25
2	A	363	NAG	O7-C7-C8	-2.06	118.27	122.06
2	A	364	NDG	C2-N2-C7	-2.03	120.44	123.04
2	A	363	NAG	C2-N2-C7	2.14	125.79	123.04
2	A	365	BMA	O5-C1-C2	2.33	114.63	110.86
3	A	368	NAG	C1-O5-C5	2.38	115.27	112.25
2	A	363	NAG	C8-C7-N2	2.46	120.81	116.11
2	A	363	NAG	C3-C4-C5	2.58	114.70	110.20
2	A	365	BMA	C1-O5-C5	2.94	115.98	112.25
2	A	363	NAG	C3-C2-N2	3.09	117.96	110.56
2	A	365	BMA	C1-C2-C3	4.21	114.53	109.54

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	366	MAN	C1-C2-C3-C4-C5-O5

8 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	363	NAG	4	0
2	A	364	NDG	1	0
2	A	365	BMA	5	0
2	A	366	MAN	5	0
3	A	367	NDG	4	0
3	A	368	NAG	8	0
3	A	369	NAG	3	0
3	A	370	NAG	2	0

## 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 [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	361/361 (100%)	-0.08	16 (4%) 38 37	14, 28, 59, 98	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	208	ALA	15.6
1	A	191	TRP	9.5
1	A	189	GLY	6.8
1	A	207	ASP	6.7
1	A	209	SER	5.4
1	A	78	TRP	4.4
1	A	362	VAL	3.3
1	A	204	GLY	3.3
1	A	345	GLN	3.2
1	A	253	VAL	2.9
1	A	210	SER	2.7
1	A	346	ASN	2.3
1	A	192	ARG	2.3
1	A	205	ASN	2.3
1	A	251	THR	2.3
1	A	190	ALA	2.2

### 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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	A	363	14/15	0.78	0.33	12.23	26,32,37,44	14
3	NAG	A	368	14/15	0.67	0.66	10.57	59,63,67,67	0
3	NDG	A	367	15/15	0.63	0.55	5.34	52,58,61,61	0
2	NDG	A	364	14/15	0.67	0.43	-	50,55,59,60	14
2	MAN	A	366	11/12	0.45	0.39	-	54,55,56,56	11
2	BMA	A	365	11/12	0.29	0.38	-	55,56,56,56	11
3	NAG	A	369	14/15	0.53	0.54	-	53,55,57,57	14
3	NAG	A	370	14/15	0.76	0.35	-	52,54,56,56	14

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.