



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:17 PM GMT

PDB ID : 1SYT  
Title : Crystal structure of signalling protein from goat SPG-40 in the presense of N, N',N''-triacetyl-chitotriose at 2.6A resolution  
Authors : Kumar, J.; Prem Kumar, R.; Srivastava, D.B.; Sharma, S.; Singh, T.P.  
Deposited on : 2004-04-02  
Resolution : 2.60 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

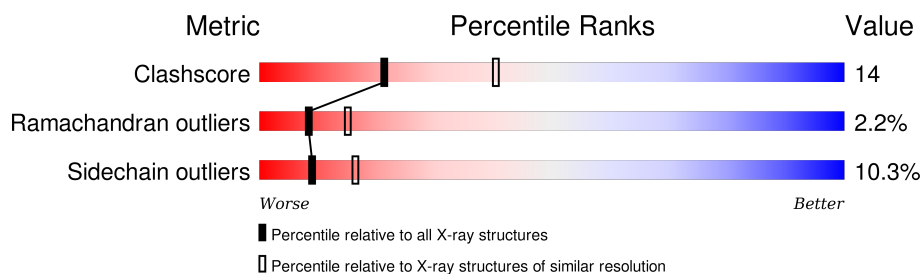
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (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 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.

Note EDS was not executed.

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	-	-	-
3	NAG	A	364	X	-	-	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3117 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.

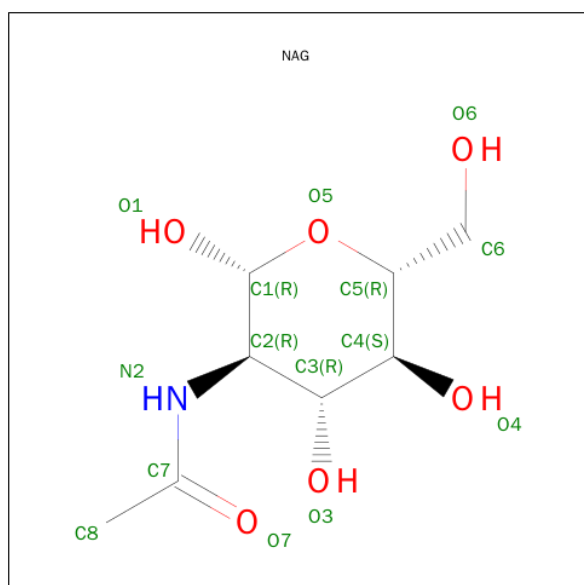
- Molecule 1 is a protein called BP40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	361	2874	1833	508	524	9	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	VAL	ILE	SEE REMARK 999	GB 19526603
A	131	ALA	GLY	SEE REMARK 999	GB 19526603
A	205	ASN	GLN	SEE REMARK 999	GB 19526603
A	206	SER	GLU	SEE REMARK 999	GB 19526603
A	?	-	ASP	SEE REMARK 999	GB 19526603
A	253	GLY	VAL	SEE REMARK 999	GB 19526603
A	361	ARG	GLU	SEE REMARK 999	GB 19526603

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			25	14	1	10		

- Molecule 4 is water.

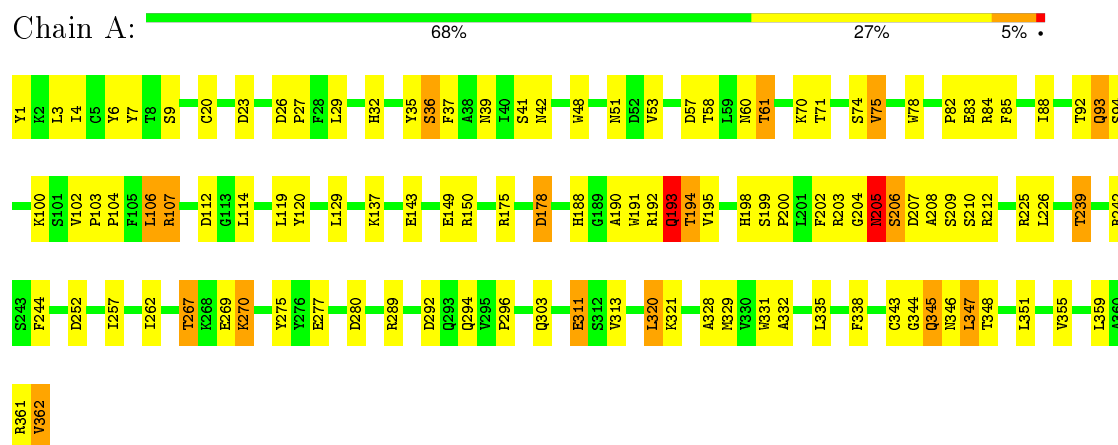
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	204	Total	O	0	0
			204	204		

### 3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: BP40



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.11Å 66.04Å 107.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 – 2.60	Depositor
% Data completeness (in resolution range)	100.0 (19.80-2.60)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.180 , 0.217	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3117	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

## 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: NAG, 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	0.94	2/2950 (0.1%)	0.90	7/3996 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	6	TYR	CD1-CE1	-5.94	1.30	1.39
1	A	6	TYR	CD2-CE2	-5.43	1.31	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	361	ARG	NE-CZ-NH1	10.29	125.45	120.30
1	A	361	ARG	NE-CZ-NH2	-7.71	116.45	120.30
1	A	280	ASP	CB-CG-OD2	7.41	124.97	118.30
1	A	178	ASP	CB-CG-OD2	6.65	124.28	118.30
1	A	320	LEU	CA-CB-CG	6.40	130.01	115.30
1	A	112	ASP	CB-CG-OD2	6.05	123.74	118.30
1	A	252	ASP	CB-CG-OD2	5.12	122.91	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	364	NAG	C1

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	2874	0	2811	80	0
2	A	14	0	12	0	0
3	A	25	0	22	1	0
4	A	204	0	0	5	0
All	All	3117	0	2845	81	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 (81) 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:A:57:ASP:O	1:A:61:THR:HG22	1.69	0.93
1:A:204:GLY:HA2	1:A:292:ASP:HB3	1.48	0.92
1:A:205:ASN:HD22	1:A:205:ASN:H	1.20	0.89
1:A:321:LYS:HE3	1:A:362:VAL:HG12	1.54	0.89
1:A:269:GLU:HG3	4:A:541:HOH:O	1.84	0.76
1:A:58:THR:O	1:A:61:THR:HG23	1.87	0.74
1:A:212:ARG:HD2	1:A:212:ARG:O	1.86	0.74
1:A:204:GLY:CA	1:A:292:ASP:HB3	2.19	0.73
1:A:191:TRP:HE3	1:A:192:ARG:HG3	1.57	0.69
1:A:203:ARG:HB3	1:A:212:ARG:HH11	1.57	0.69
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.76	0.68
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.25	0.67
1:A:191:TRP:CE3	1:A:192:ARG:HG3	2.30	0.67
1:A:205:ASN:HD22	1:A:205:ASN:N	1.93	0.67
1:A:93:GLN:HG2	1:A:94:SER:N	2.10	0.66
1:A:332:ALA:HB3	1:A:335:LEU:HD12	1.79	0.65
1:A:267:THR:HG22	4:A:370:HOH:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:PRO:HD2	1:A:83:GLU:OE2	2.02	0.60
1:A:262:ILE:H	1:A:303:GLN:HE22	1.49	0.60
1:A:4:ILE:N	1:A:4:ILE:HD12	2.17	0.60
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.83	0.59
1:A:39:ASN:HB2	1:A:48:TRP:CE3	2.40	0.56
1:A:262:ILE:H	1:A:303:GLN:NE2	2.04	0.56
1:A:193:GLN:N	1:A:193:GLN:OE1	2.32	0.55
1:A:239:THR:HG21	1:A:332:ALA:O	2.07	0.55
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.37	0.54
1:A:103:PRO:HB2	1:A:104:PRO:HD3	1.89	0.54
1:A:83:GLU:CD	1:A:83:GLU:H	2.11	0.53
1:A:203:ARG:HD3	1:A:212:ARG:CZ	2.38	0.53
1:A:84:ARG:O	1:A:88:ILE:HG12	2.08	0.52
1:A:199:SER:N	1:A:200:PRO:HD3	2.24	0.52
1:A:205:ASN:H	1:A:205:ASN:ND2	1.97	0.52
1:A:313:VAL:HG13	1:A:355:VAL:HG22	1.89	0.52
1:A:267:THR:HB	1:A:277:GLU:OE1	2.11	0.51
1:A:289:ARG:NH1	1:A:311:GLU:HG2	2.26	0.51
1:A:244:PHE:HB3	1:A:257:ILE:HD12	1.92	0.51
1:A:347:LEU:HD23	1:A:348:THR:N	2.26	0.50
1:A:244:PHE:HB3	1:A:257:ILE:CD1	2.42	0.49
1:A:7:TYR:O	1:A:36:SER:HB2	2.12	0.49
1:A:239:THR:HG23	1:A:239:THR:O	2.12	0.49
1:A:347:LEU:HD23	1:A:348:THR:H	1.78	0.49
1:A:9:SER:OG	1:A:35:TYR:CE2	2.66	0.48
1:A:58:THR:O	1:A:61:THR:CG2	2.59	0.48
1:A:239:THR:O	1:A:275:TYR:HB2	2.14	0.48
1:A:320:LEU:HD11	1:A:328:ALA:HB2	1.96	0.47
1:A:37:PHE:HA	1:A:74:SER:O	2.14	0.47
1:A:78:TRP:HZ3	1:A:331:TRP:CZ2	2.33	0.47
1:A:257:ILE:HD13	1:A:257:ILE:HA	1.77	0.47
1:A:188:HIS:HE1	1:A:194:THR:O	1.98	0.46
1:A:344:GLY:O	1:A:345:GLN:C	2.53	0.46
1:A:205:ASN:N	1:A:205:ASN:ND2	2.59	0.46
1:A:270:LYS:H	1:A:270:LYS:HG2	1.39	0.46
1:A:137:LYS:HE3	1:A:150:ARG:NH1	2.31	0.46
1:A:212:ARG:CD	1:A:212:ARG:O	2.59	0.45
1:A:188:HIS:H	1:A:198:HIS:HA	1.81	0.45
1:A:1:TYR:CZ	1:A:321:LYS:HG2	2.51	0.45
3:A:364:NAG:O3	3:A:365:MAN:H5	2.16	0.45
1:A:107:ARG:HD3	1:A:143:GLU:OE2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:ILE:O	1:A:329:MET:HA	2.17	0.45
1:A:39:ASN:HB2	1:A:48:TRP:HE3	1.82	0.45
1:A:321:LYS:CE	1:A:362:VAL:HG12	2.38	0.44
1:A:345:GLN:C	1:A:347:LEU:H	2.20	0.44
1:A:313:VAL:HG13	1:A:355:VAL:CG2	2.47	0.43
1:A:26:ASP:HB3	1:A:29:LEU:HB2	2.00	0.43
1:A:119:LEU:HD23	1:A:119:LEU:HA	1.60	0.43
1:A:209:SER:O	1:A:210:SER:OG	2.27	0.43
1:A:60:ASN:ND2	1:A:71:THR:OG1	2.51	0.43
1:A:343:CYS:O	1:A:345:GLN:HG2	2.19	0.42
1:A:32:HIS:HA	1:A:70:LYS:O	2.19	0.42
1:A:311:GLU:HB2	4:A:398:HOH:O	2.18	0.42
1:A:208:ALA:HA	4:A:530:HOH:O	2.19	0.42
1:A:51:ASN:HA	4:A:393:HOH:O	2.20	0.42
1:A:102:VAL:HG12	1:A:106:LEU:HD22	2.01	0.41
1:A:41:SER:O	1:A:42:ASN:C	2.58	0.41
1:A:202:PHE:HE2	1:A:294:GLN:NE2	2.19	0.41
1:A:107:ARG:NH1	1:A:143:GLU:OE1	2.54	0.41
1:A:100:LYS:HB3	1:A:100:LYS:HE2	1.74	0.41
1:A:203:ARG:HB3	1:A:212:ARG:NH1	2.29	0.40
1:A:20:CYS:HB2	1:A:338:PHE:CZ	2.56	0.40
1:A:150:ARG:NH2	1:A:178:ASP:OD1	2.54	0.40
1:A:26:ASP:HA	1:A:27:PRO:HD3	1.91	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%)	332 (92%)	19 (5%)	8 (2%)	<b>8</b> <b>15</b>

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	205	ASN
1	A	206	SER
1	A	345	GLN
1	A	346	ASN
1	A	120	TYR
1	A	190	ALA
1	A	207	ASP

### 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	301/301 (100%)	270 (90%)	31 (10%)	9	16

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	23	ASP
1	A	36	SER
1	A	53	VAL
1	A	61	THR
1	A	75	VAL
1	A	85	PHE
1	A	92	THR
1	A	93	GLN
1	A	106	LEU
1	A	107	ARG
1	A	129	LEU
1	A	149	GLU
1	A	175	ARG
1	A	193	GLN
1	A	194	THR
1	A	195	VAL
1	A	205	ASN
1	A	206	SER

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Mol	Chain	Res	Type
1	A	225	ARG
1	A	226	LEU
1	A	239	THR
1	A	242	ARG
1	A	267	THR
1	A	270	LYS
1	A	296	PRO
1	A	311	GLU
1	A	347	LEU
1	A	351	LEU
1	A	359	LEU
1	A	362	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	188	HIS
1	A	205	ASN
1	A	303	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 ⓘ

2 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
3	NAG	A	364	3,2	14,14,15	0.74	0	15,19,21	1.42	3 (20%)
3	MAN	A	365	3	11,11,12	0.73	0	14,15,17	1.47	3 (21%)

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	364	3,2	1/1/5/7	0/6/23/26	0/1/1/1
3	MAN	A	365	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	365	MAN	O5-C1-C2	-2.59	106.66	110.86
3	A	364	NAG	O7-C7-C8	-2.19	118.05	122.06
3	A	365	MAN	C3-C4-C5	-2.14	106.47	110.20
3	A	365	MAN	O3-C3-C2	2.14	113.86	110.00
3	A	364	NAG	O4-C4-C5	2.84	116.77	109.24
3	A	364	NAG	O4-C4-C3	3.17	117.47	110.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	364	NAG	C1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	364	NAG	1	0
3	A	365	MAN	1	0

## 5.6 Ligand geometry

1 ligand is 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	1,3	14,14,15	1.07	0	15,19,21	3.58	8 (53%)

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	1,3	1/1/5/7	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	363	NAG	O4-C4-C3	-5.68	97.56	110.34
2	A	363	NAG	C8-C7-N2	-4.63	107.25	116.11
2	A	363	NAG	C6-C5-C4	2.17	118.37	113.02
2	A	363	NAG	C3-C4-C5	2.73	114.96	110.20
2	A	363	NAG	O7-C7-N2	3.11	128.21	121.86
2	A	363	NAG	O5-C5-C6	3.68	115.32	107.35
2	A	363	NAG	C3-C2-N2	3.77	119.59	110.56
2	A	363	NAG	C1-O5-C5	8.74	123.34	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	363	NAG	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.