



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 22, 2018 – 07:46 AM EST

PDB ID : 5Y92
Title : Crystal structure of ANXUR2 extracellular domain from Arabidopsis thaliana
Authors : Du, S.; Xiao, J.Y.
Deposited on : 2017-08-22
Resolution : 2.00 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030736

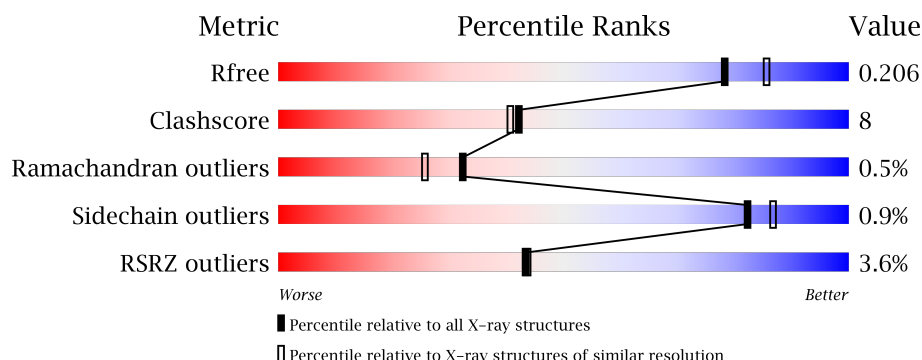
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 ≥ 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	387	<div> <div>4%</div> <div>87%</div> <div>12%</div> </div>

2 Entry composition [i](#)

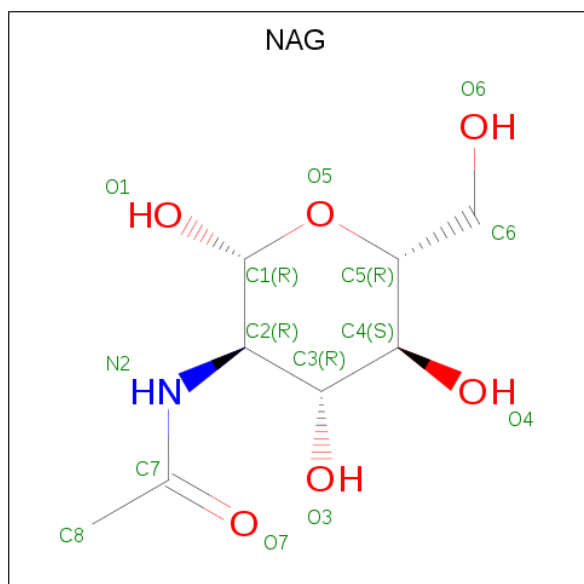
There are 4 unique types of molecules in this entry. The entry contains 3240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Receptor-like protein kinase ANXUR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	0
			3015	1921	494	587	13			

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



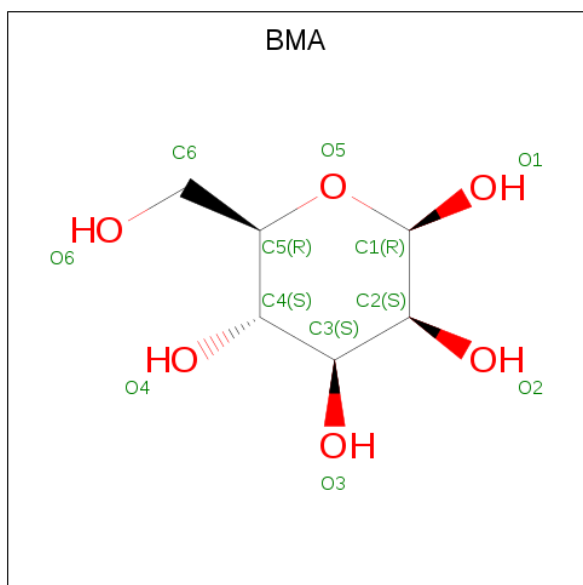
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	A	1	Total	C	O	0	0
			11	6	5		

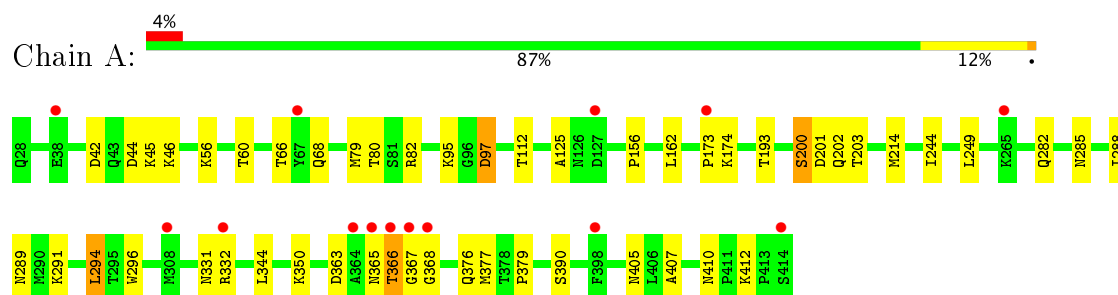
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		

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 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: Receptor-like protein kinase ANXUR2



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	103.19Å 103.19Å 121.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.15 – 2.00 46.74 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.15-2.00) 93.6 (46.74-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.184 , 0.208 0.180 , 0.206	Depositor DCC
R_{free} test set	1861 reflections (4.67%)	DCC
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.636	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.036 for -h,k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3240	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: BMA, NAG

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	0.43	0/3092	0.62	2/4211 (0.0%)

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
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	214	MET	CG-SD-CE	-6.21	90.26	100.20
1	A	97	ASP	CB-CG-OD2	5.42	123.18	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	366	THR	Peptide

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	3015	0	2928	48	0
2	A	98	0	86	6	0
3	A	22	0	20	3	0
4	A	105	0	0	4	0
All	All	3240	0	3034	49	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 8.

All (49) 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:363:ASP:OD1	1:A:365:ASN:ND2	1.94	1.00
1:A:200:SER:O	1:A:202:GLN:N	1.98	0.96
1:A:285:ASN:ND2	1:A:288:ILE:HB	1.99	0.76
1:A:376:GLN:NE2	2:A:504:NAG:H61	2.03	0.74
1:A:376:GLN:HE22	2:A:504:NAG:H61	1.55	0.72
1:A:412:LYS:NZ	3:A:503:BMA:H2	2.07	0.69
1:A:80:THR:O	4:A:601:HOH:O	2.13	0.65
1:A:410:ASN:HD22	2:A:501:NAG:H61	1.64	0.63
1:A:66:THR:HG21	1:A:112:THR:HG23	1.79	0.63
1:A:366:THR:OG1	1:A:367:GLY:N	2.31	0.63
1:A:289:ASN:OD1	4:A:602:HOH:O	2.16	0.59
1:A:288:ILE:HD13	1:A:291:LYS:HD2	1.86	0.57
1:A:412:LYS:HZ3	3:A:503:BMA:H2	1.72	0.55
1:A:60:THR:OG1	1:A:82:ARG:HD3	2.07	0.54
1:A:285:ASN:HD22	1:A:288:ILE:HB	1.72	0.53
1:A:173:PRO:O	1:A:174:LYS:HB2	2.08	0.53
1:A:412:LYS:HZ2	3:A:503:BMA:H2	1.74	0.51
1:A:377:MET:HE3	1:A:390:SER:HB2	1.92	0.51
1:A:97:ASP:N	1:A:97:ASP:OD1	2.21	0.51
1:A:350:LYS:NZ	4:A:605:HOH:O	2.29	0.51
2:A:509:NAG:H3	2:A:509:NAG:H83	1.92	0.50
1:A:68:GLN:HA	1:A:79:MET:CE	2.42	0.50
1:A:193:THR:HB	1:A:203:THR:HG23	1.96	0.47
1:A:95:LYS:HD3	1:A:97:ASP:OD1	2.14	0.47
1:A:285:ASN:HD21	1:A:288:ILE:HB	1.76	0.47
1:A:285:ASN:HD21	1:A:288:ILE:CG1	2.28	0.46
1:A:125:ALA:HB1	1:A:162:LEU:HD11	1.98	0.45
1:A:405:ASN:ND2	1:A:407:ALA:H	2.14	0.45
1:A:377:MET:HE3	1:A:390:SER:CB	2.46	0.45
1:A:44:ASP:C	1:A:45:LYS:HG2	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:ILE:HA	1:A:291:LYS:HD2	1.99	0.44
1:A:376:GLN:NE2	4:A:606:HOH:O	2.32	0.44
1:A:285:ASN:HD21	1:A:288:ILE:CB	2.30	0.44
1:A:66:THR:HG21	1:A:112:THR:CG2	2.45	0.44
1:A:285:ASN:O	1:A:285:ASN:ND2	2.52	0.43
1:A:376:GLN:HE22	2:A:504:NAG:C6	2.28	0.43
1:A:282:GLN:OE1	1:A:379:PRO:HD3	2.19	0.43
1:A:331:ASN:HA	2:A:504:NAG:O6	2.19	0.43
1:A:367:GLY:HA3	1:A:368:GLY:C	2.39	0.42
1:A:365:ASN:ND2	1:A:366:THR:HG23	2.35	0.42
1:A:68:GLN:HA	1:A:79:MET:HE3	2.01	0.41
1:A:365:ASN:CG	1:A:366:THR:N	2.74	0.41
1:A:405:ASN:HD21	1:A:407:ALA:HB3	1.85	0.41
1:A:42:ASP:OD2	1:A:46:LYS:HB3	2.21	0.41
1:A:294:LEU:HD13	1:A:296:TRP:CH2	2.56	0.40
1:A:97:ASP:HA	1:A:156:PRO:HB3	2.03	0.40
1:A:244:ILE:HG21	1:A:249:LEU:HD23	2.03	0.40
1:A:344:LEU:HA	1:A:344:LEU:HD23	1.91	0.40
1:A:68:GLN:HA	1:A:79:MET:HE1	2.02	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	385/387 (100%)	371 (96%)	12 (3%)	2 (0%)	32 26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	SER
1	A	201	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	332/332 (100%)	329 (99%)	3 (1%)	82	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LYS
1	A	294	LEU
1	A	332	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	285	ASN
1	A	376	GLN
1	A	405	ASN

5.3.3 RNA [i](#)

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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

9 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	$\# Z > 2$
2	NAG	A	501	1,2	14,14,15	0.44	0	15,19,21	1.09	1 (6%)
2	NAG	A	502	3,2	14,14,15	0.34	0	15,19,21	0.68	0
3	BMA	A	503	2	11,11,12	1.00	1 (9%)	13,15,17	0.87	0
2	NAG	A	504	1,2	14,14,15	0.67	0	15,19,21	2.26	2 (13%)
2	NAG	A	505	2	14,14,15	0.39	0	15,19,21	0.60	0
2	NAG	A	506	1,2	14,14,15	0.57	0	15,19,21	0.76	1 (6%)
2	NAG	A	507	3,2	14,14,15	0.53	0	15,19,21	0.66	0
3	BMA	A	508	2	11,11,12	1.92	3 (27%)	13,15,17	1.73	3 (23%)
2	NAG	A	509	1	14,14,15	0.53	0	15,19,21	1.43	2 (13%)

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	501	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	502	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	503	2	-	0/2/19/22	0/1/1/1
2	NAG	A	504	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	505	2	-	0/6/23/26	0/1/1/1
2	NAG	A	506	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	507	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	508	2	-	0/2/19/22	0/1/1/1
2	NAG	A	509	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	508	BMA	C4-C5	2.19	1.57	1.53
3	A	503	BMA	O5-C5	2.57	1.48	1.43
3	A	508	BMA	C1-C2	2.58	1.58	1.52
3	A	508	BMA	C2-C3	4.65	1.58	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	508	BMA	C3-C4-C5	2.02	113.78	110.22
2	A	509	NAG	C1-C2-N2	2.17	114.20	110.49
2	A	506	NAG	C1-O5-C5	2.28	115.30	112.17
2	A	504	NAG	C3-C4-C5	3.22	115.89	110.22
3	A	508	BMA	C2-C3-C4	3.24	116.52	110.88
3	A	508	BMA	C1-C2-C3	3.77	114.43	109.65
2	A	501	NAG	C1-O5-C5	3.78	117.37	112.17
2	A	509	NAG	C2-N2-C7	4.25	129.14	122.94
2	A	504	NAG	C1-O5-C5	7.65	122.71	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	NAG	1	0
3	A	503	BMA	3	0
2	A	504	NAG	4	0
2	A	509	NAG	1	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 [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, 95th 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 ²)	Q<0.9
1	A	387/387 (100%)	0.37	14 (3%)	43 44	35, 53, 83, 110	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	365	ASN	7.1
1	A	414	SER	4.6
1	A	366	THR	4.5
1	A	364	ALA	4.0
1	A	368	GLY	3.5
1	A	265	LYS	3.4
1	A	38	GLU	3.3
1	A	67	TYR	2.9
1	A	367	GLY	2.8
1	A	332	ARG	2.5
1	A	173	PRO	2.5
1	A	398	PHE	2.2
1	A	127	ASP	2.2
1	A	308	MET	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](#)

There are no carbohydrates in this entry.

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. 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, 95th 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 ²)	Q<0.9
2	NAG	A	509	14/15	0.74	0.34	1.26	99,109,117,120	0
2	NAG	A	501	14/15	0.87	0.17	0.47	63,72,84,85	0
2	NAG	A	504	14/15	0.94	0.13	-0.28	56,66,70,87	0
3	BMA	A	508	11/12	0.49	0.42	-	116,126,132,132	0
2	NAG	A	505	14/15	0.79	0.25	-	80,115,130,130	0
2	NAG	A	502	14/15	0.88	0.41	-	75,95,110,113	0
3	BMA	A	503	11/12	0.72	0.44	-	100,104,110,112	0
2	NAG	A	506	14/15	0.75	0.21	-	80,86,95,98	0
2	NAG	A	507	14/15	0.55	0.34	-	98,104,112,122	0

6.5 Other polymers [i](#)

There are no such residues in this entry.