Full wwPDB X-ray Structure Validation Report (i)

Jan 4, 2017 – 11:14 AM EST

PDB ID	:	5HYX
Title	:	Plant peptide hormone receptor RGFR1 in complex with RGF1
Authors	:	Song, W.; Han, Z.; Chai, J.
Deposited on	:	2016-02-02
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*
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

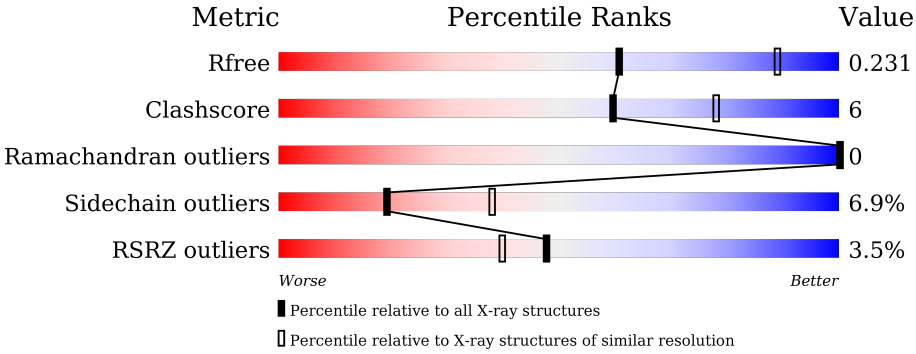
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

1 Overall quality at a glance (i)

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))
R_{free}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (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 >=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 <=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	B	633	3% 81% 17% • •
2	A	13	8% 62% 31% 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5032 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 Probable LRR receptor-like serine/threonine-protein kinase At4g26540.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	626	4783	3024	809	935	15	0	0	0

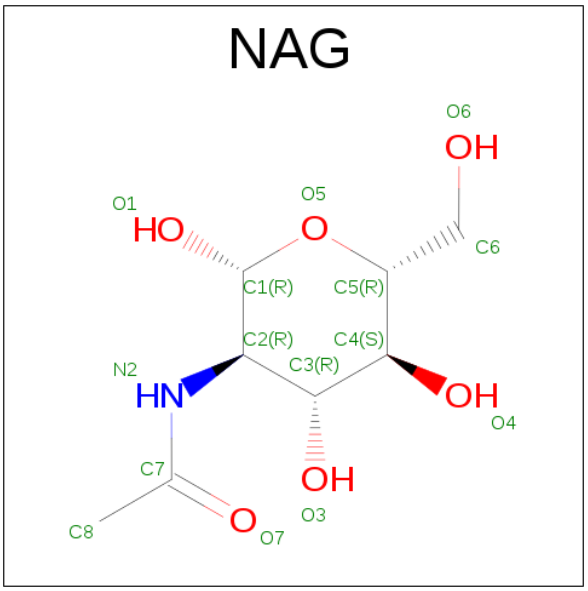
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	64	THR	VAL	engineered mutation	UNP C0LGR3
B	81	GLU	GLY	engineered mutation	UNP C0LGR3
B	82	LYS	MET	engineered mutation	UNP C0LGR3
B	83	GLN	ASP	engineered mutation	UNP C0LGR3
B	104	GLN	ASN	engineered mutation	UNP C0LGR3

- Molecule 2 is a protein called PTR-SER-ASN-PRO-GLY-HIS-HIS-PRO-HYP-ARG-HIS-ASN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	A	13	114	65	24	24	1	0	0	0

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is water.

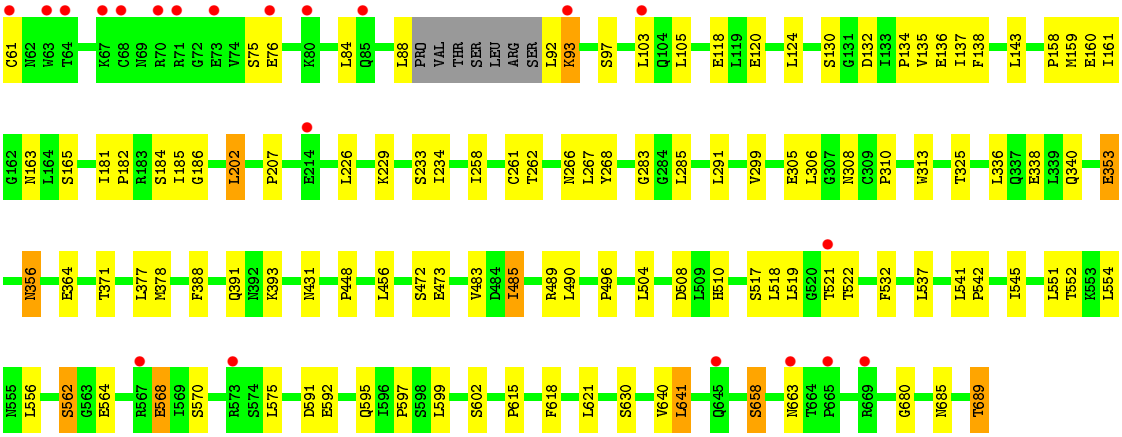
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	B	76	76	76	0	0
			Total	O		
4	A	3	3	3	0	0

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.

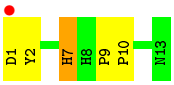
- Molecule 1: Probable LRR receptor-like serine/threonine-protein kinase At4g26540

Chain B:



- Molecule 2: PTR-SER-ASN-PRO-GLY-HIS-HIS-PRO-HYP-ARG-HIS-ASN

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	182.34Å 182.34Å 87.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.02 – 2.60 12.02 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (12.02-2.60) 99.7 (12.02-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.19 (at 2.59Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.191 , 0.233 0.181 , 0.231	Depositor DCC
R_{free} test set	1678 reflections (5.08%)	DCC
Wilson B-factor (Å^2)	53.4	Xtriage
Anisotropy	0.571	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.014 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5032	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: PTR, HZP, 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	B	0.45	0/4853	0.66	0/6585
2	A	0.48	0/92	0.61	0/120
All	All	0.45	0/4945	0.66	0/6705

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	93	LYS	Peptide

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	B	4783	0	4884	55	0
2	A	114	0	88	4	0
3	B	56	0	51	1	0
4	A	3	0	0	0	0
4	B	76	0	0	4	0
All	All	5032	0	5023	57	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 6.

All (57) 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:61:CYS:N	4:B:801:HOH:O	2.17	0.77
1:B:483:VAL:HG12	1:B:504:LEU:HD11	1.70	0.74
1:B:496:PRO:HA	1:B:522:THR:HG23	1.69	0.73
1:B:391:GLN:NE2	4:B:802:HOH:O	2.18	0.71
1:B:640:VAL:HG13	1:B:641:LEU:HD13	1.73	0.71
1:B:570:SER:HB3	1:B:592:GLU:HB3	1.75	0.69
1:B:76:GLU:HG2	1:B:97:SER:HB3	1.78	0.65
1:B:181:ILE:HG13	1:B:202:LEU:HD11	1.83	0.61
1:B:658:SER:HB2	1:B:680:GLY:HA3	1.84	0.60
1:B:518:LEU:HD13	1:B:537:LEU:HD13	1.86	0.57
1:B:136:GLU:OE2	1:B:136:GLU:N	2.38	0.54
1:B:595:GLN:O	1:B:597:PRO:HD3	2.08	0.53
1:B:283:GLY:HA3	1:B:305:GLU:HB3	1.91	0.53
1:B:138:PHE:HE2	1:B:158:PRO:HG2	1.74	0.52
1:B:541:LEU:HD12	1:B:542:PRO:HD2	1.91	0.52
1:B:364:GLU:HG3	1:B:388:PHE:HB2	1.91	0.52
1:B:340:GLN:NE2	1:B:364:GLU:OE1	2.32	0.50
1:B:308:ASN:O	1:B:310:PRO:HD3	2.12	0.49
1:B:517:SER:OG	1:B:518:LEU:N	2.45	0.49
1:B:371:THR:HG22	1:B:393:LYS:HB2	1.94	0.49
1:B:689:THR:O	4:B:803:HOH:O	2.19	0.49
1:B:448:PRO:O	1:B:473:GLU:HG3	2.13	0.48
1:B:508:ASP:OD1	1:B:510:HIS:ND1	2.47	0.48
2:A:1:ASP:O	2:A:2:PTR:CD2	2.62	0.47
1:B:532:PHE:HB2	1:B:556:LEU:HD23	1.97	0.46
1:B:615:PRO:HG2	1:B:618:PHE:CD1	2.50	0.46
1:B:160:GLU:O	1:B:163:ASN:HB2	2.18	0.44
1:B:551:LEU:HD21	1:B:554:LEU:HB2	1.98	0.44
1:B:261:CYS:O	1:B:285:LEU:HD22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:ASN:HB3	1:B:268:TYR:CE1	2.53	0.44
1:B:338:GLU:OE2	2:A:7:HIS:ND1	2.50	0.43
1:B:84:LEU:HD13	1:B:103:LEU:HB3	2.01	0.43
1:B:552:THR:O	1:B:575:LEU:HD12	2.18	0.43
1:B:377:LEU:HA	1:B:377:LEU:HD23	1.85	0.43
1:B:185:ILE:HD12	1:B:186:GLY:N	2.34	0.43
1:B:340:GLN:HE22	2:A:10:HZP:HG	1.82	0.43
1:B:266:ASN:HB3	1:B:268:TYR:CZ	2.54	0.43
1:B:663:ASN:ND2	1:B:685:ASN:OD1	2.47	0.42
1:B:182:PRO:O	1:B:185:ILE:HG13	2.19	0.42
1:B:313:TRP:HA	1:B:336:LEU:HA	2.01	0.42
1:B:306:LEU:HD23	1:B:306:LEU:HA	1.82	0.42
1:B:485:ILE:HG21	1:B:490:LEU:HD11	2.00	0.42
1:B:568:GLU:HG2	1:B:568:GLU:H	1.39	0.41
2:A:9:PRO:HA	2:A:10:HZP:HDA	1.89	0.41
1:B:353:GLU:O	1:B:356:ASN:HB2	2.20	0.41
1:B:630:SER:OG	3:B:704:NAG:H82	2.20	0.41
1:B:234:ILE:HD12	1:B:234:ILE:HA	1.88	0.41
1:B:562:SER:O	4:B:804:HOH:O	2.22	0.41
1:B:132:ASP:O	1:B:134:PRO:HD3	2.21	0.41
1:B:519:LEU:HB2	1:B:522:THR:OG1	2.21	0.41
1:B:267:LEU:HB3	1:B:291:LEU:HD12	2.02	0.41
1:B:103:LEU:HB2	1:B:105:LEU:HG	2.02	0.40
1:B:185:ILE:HD11	1:B:207:PRO:HG2	2.02	0.40
1:B:120:GLU:HA	1:B:143:LEU:HA	2.03	0.40
1:B:456:LEU:HD12	1:B:456:LEU:HA	1.96	0.40
1:B:599:LEU:HD23	1:B:599:LEU:HA	1.85	0.40
1:B:621:LEU:HD23	1:B:621:LEU:HA	1.62	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	B	622/633 (98%)	597 (96%)	25 (4%)	0	100	100
2	A	9/13 (69%)	9 (100%)	0	0	100	100
All	All	631/646 (98%)	606 (96%)	25 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	B	554/568 (98%)	516 (93%)	38 (7%)	19	38
2	A	10/10 (100%)	9 (90%)	1 (10%)	9	18
All	All	564/578 (98%)	525 (93%)	39 (7%)	19	38

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	75	SER
1	B	88	LEU
1	B	92	LEU
1	B	93	LYS
1	B	118	GLU
1	B	124	LEU
1	B	130	SER
1	B	135	VAL
1	B	137	ILE
1	B	159	MET
1	B	161	ILE
1	B	165	SER
1	B	184	SER
1	B	202	LEU
1	B	226	LEU
1	B	229	LYS
1	B	233	SER
1	B	258	ILE

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Mol	Chain	Res	Type
1	B	262	THR
1	B	299	VAL
1	B	325	THR
1	B	353	GLU
1	B	356	ASN
1	B	378	MET
1	B	431	ASN
1	B	472	SER
1	B	485	ILE
1	B	489	ARG
1	B	521	THR
1	B	545	ILE
1	B	562	SER
1	B	564	GLU
1	B	568	GLU
1	B	591	ASP
1	B	602	SER
1	B	641	LEU
1	B	658	SER
1	B	689	THR
2	A	7	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	HZP	A	10	2	6,8,9	0.74	0	5,10,12	1.37	1 (20%)
2	PTR	A	2	2	13,16,17	1.55	2 (15%)	19,22,24	0.88	1 (5%)

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	HZP	A	10	2	-	0/0/11/13	0/1/1/1
2	PTR	A	2	2	-	0/9/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	PTR	OH-CZ	-4.39	1.30	1.40
2	A	2	PTR	P-O2P	-2.06	1.47	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	10	HZP	CB-CG-CD	2.52	106.16	103.06
2	A	2	PTR	CG-CB-CA	2.74	120.45	114.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	10	HZP	2	0
2	A	2	PTR	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

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	$\#\|Z\| > 2$
3	NAG	B	701	1,3	14,14,15	0.55	0	15,19,21	1.17	2 (13%)
3	NAG	B	702	3	14,14,15	0.48	0	15,19,21	0.71	0
3	NAG	B	703	1	14,14,15	0.45	0	15,19,21	1.67	1 (6%)
3	NAG	B	704	1	14,14,15	0.60	0	15,19,21	1.15	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
3	NAG	B	701	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	702	3	-	0/6/23/26	0/1/1/1
3	NAG	B	703	1	-	0/6/23/26	0/1/1/1
3	NAG	B	704	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	701	NAG	O5-C5-C6	2.06	111.76	107.34
3	B	701	NAG	C2-N2-C7	2.78	126.72	123.11
3	B	704	NAG	C1-O5-C5	2.97	116.50	112.14
3	B	703	NAG	C1-O5-C5	5.31	119.95	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	704	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	B	626/633 (98%)	-0.07	21 (3%)	49	41	6, 22, 61, 95	0
2	A	11/13 (84%)	-0.34	1 (9%)	11	7	10, 19, 37, 63	0
All	All	637/646 (98%)	-0.07	22 (3%)	48	40	6, 22, 61, 95	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	521	THR	4.8
1	B	70	ARG	4.6
1	B	663	ASN	3.6
1	B	64	THR	3.5
1	B	67	LYS	3.2
1	B	669	ARG	3.1
1	B	71	ARG	2.9
1	B	61	CYS	2.8
1	B	85	GLN	2.7
1	B	68	CYS	2.7
1	B	214	GLU	2.6
2	A	1	ASP	2.5
1	B	76	GLU	2.5
1	B	567	ARG	2.5
1	B	103	LEU	2.4
1	B	645	GLN	2.3
1	B	63	TRP	2.3
1	B	93	LYS	2.3
1	B	665	PRO	2.2
1	B	80	LYS	2.2
1	B	573	ARG	2.1
1	B	73	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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	HZP	A	10	8/9	0.96	0.10	-	16,22,26,44	0
2	PTR	A	2	16/17	0.98	0.11	-	13,14,33,36	0

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
3	NAG	B	704	14/15	0.94	0.22	1.21	13,29,37,41	0
3	NAG	B	701	14/15	0.92	0.17	0.18	21,25,32,33	0
3	NAG	B	703	14/15	0.95	0.13	-0.79	13,16,22,23	0
3	NAG	B	702	14/15	0.92	0.22	-	31,35,40,41	0

6.5 Other polymers (i)

There are no such residues in this entry.