



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:16 PM UTC

PDB ID : 4UYU / pdb_00004uyu
Title : STRUCTURE OF THE WNT DEACYLASE NOTUM - CRYSTAL FORM I
IODIDE COMPLEX - 2.3A
Authors : Zebisch, M.; Jones, E.Y.
Deposited on : 2014-09-03
Resolution : 2.30 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

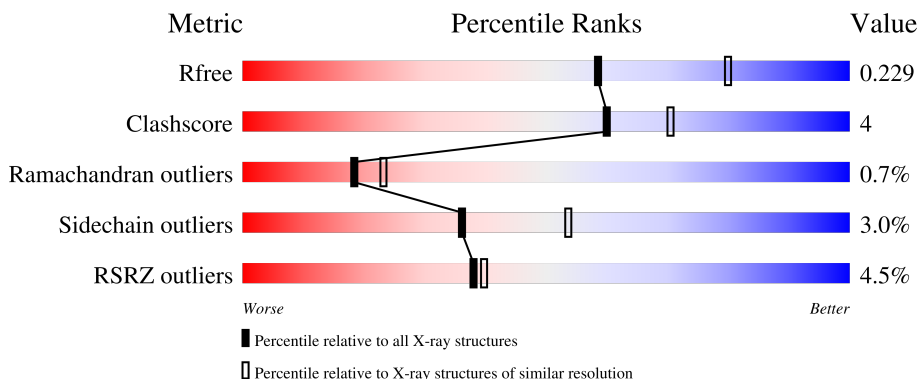
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 ≥ 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	A	383	3% 81% 9% 10%
1	B	383	5% 80% 9% 10%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5644 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 PROTEIN NOTUM HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	0	0
			2771	1753	498	502	18			
1	B	345	Total	C	N	O	S	0	0	0
			2770	1750	499	503	18			

There are 26 discrepancies between the modelled and reference sequences:

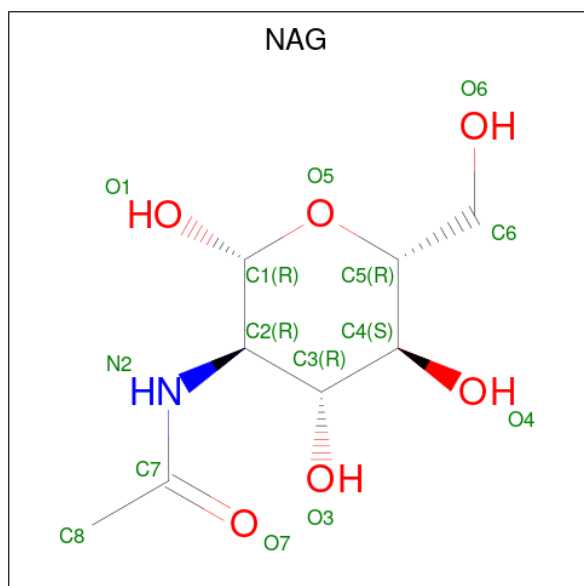
Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLU	-	expression tag	UNP Q6P988
A	79	THR	-	expression tag	UNP Q6P988
A	80	GLY	-	expression tag	UNP Q6P988
A	452	GLY	-	expression tag	UNP Q6P988
A	453	THR	-	expression tag	UNP Q6P988
A	454	LYS	-	expression tag	UNP Q6P988
A	455	HIS	-	expression tag	UNP Q6P988
A	456	HIS	-	expression tag	UNP Q6P988
A	457	HIS	-	expression tag	UNP Q6P988
A	458	HIS	-	expression tag	UNP Q6P988
A	459	HIS	-	expression tag	UNP Q6P988
A	460	HIS	-	expression tag	UNP Q6P988
A	330	SER	CYS	engineered mutation	UNP Q6P988
B	78	GLU	-	expression tag	UNP Q6P988
B	79	THR	-	expression tag	UNP Q6P988
B	80	GLY	-	expression tag	UNP Q6P988
B	452	GLY	-	expression tag	UNP Q6P988
B	453	THR	-	expression tag	UNP Q6P988
B	454	LYS	-	expression tag	UNP Q6P988
B	455	HIS	-	expression tag	UNP Q6P988
B	456	HIS	-	expression tag	UNP Q6P988
B	457	HIS	-	expression tag	UNP Q6P988
B	458	HIS	-	expression tag	UNP Q6P988
B	459	HIS	-	expression tag	UNP Q6P988
B	460	HIS	-	expression tag	UNP Q6P988

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Chain	Residue	Modelled	Actual	Comment	Reference
B	330	SER	CYS	engineered mutation	UNP Q6P988

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: 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	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	I	0	0
			5	5		
3	B	6	Total	I	0	0
			6	6		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	B	1	Total	Cl	0	0
			1	1		

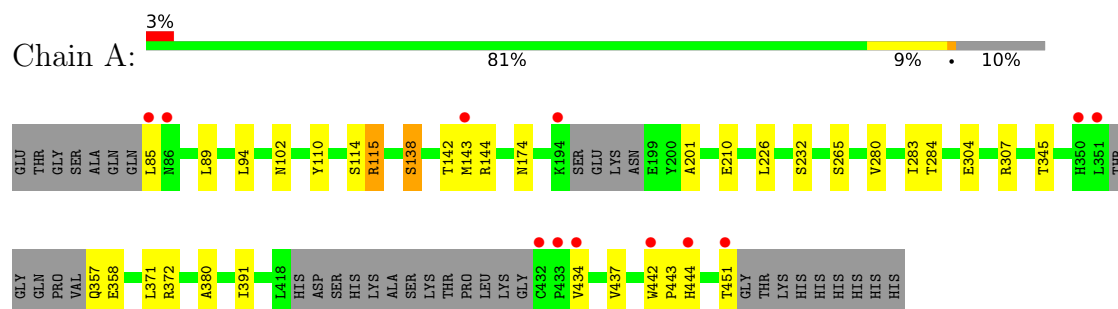
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	42	Total 42	O 42	0	0
5	B	20	Total 20	O 20	0	0

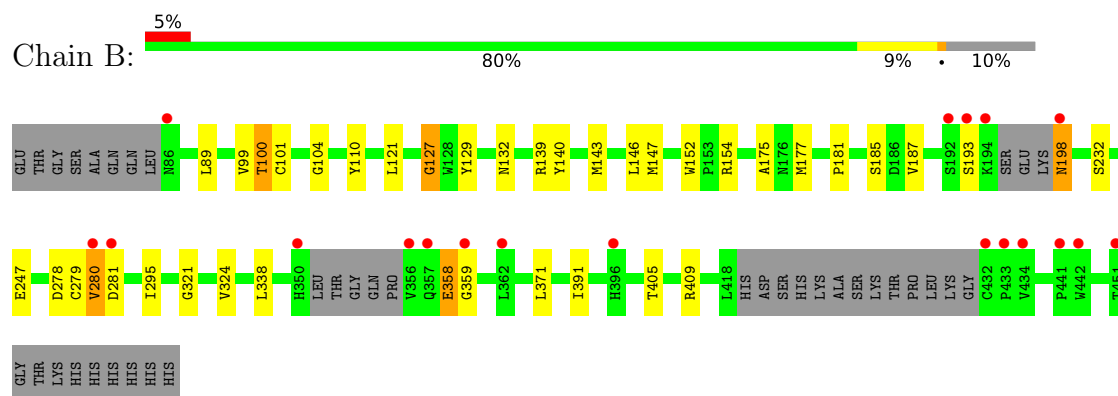
3 Residue-property plots [i](#)

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: PROTEIN NOTUM HOMOLOG



• Molecule 1: PROTEIN NOTUM HOMOLOG



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	74.22Å 177.56Å 60.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.78 – 2.30 88.78 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (88.78-2.30) 99.9 (88.78-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.208 , 0.243 (Not available) , 0.229	Depositor DCC
R_{free} test set	1088 reflections (2.97%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5644	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, IOD, CL

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	0.74	0/2844	0.85	0/3865
1	B	0.68	0/2843	0.83	1/3864 (0.0%)
All	All	0.71	0/5687	0.84	1/7729 (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	B	0	1

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	B	232	SER	CB-CA-C	-6.06	108.99	117.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	99	VAL	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	A	2771	0	2671	16	0
1	B	2770	0	2664	31	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
3	A	5	0	0	0	0
3	B	6	0	0	1	0
4	A	1	0	0	1	0
4	B	1	0	0	1	0
5	A	42	0	0	0	0
5	B	20	0	0	0	0
All	All	5644	0	5361	47	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 4.

All (47) 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:121:LEU:HD12	1:B:177:MET:HE1	1.57	0.87
1:B:139:ARG:NH1	1:B:185:SER:OG	2.12	0.83
1:B:140:TYR:N	1:B:147:MET:HE1	2.04	0.73
1:B:177:MET:HE2	1:B:177:MET:HA	1.70	0.72
1:B:121:LEU:CD1	1:B:177:MET:HE1	2.23	0.69
1:B:198:ASN:HD22	1:B:198:ASN:C	2.07	0.62
1:A:232:SER:HA	1:A:265:SER:O	2.02	0.60
1:A:304:GLU:OE2	1:A:307:ARG:NH1	2.35	0.59
1:B:100:THR:HG22	1:B:101:CYS:O	2.01	0.59
1:A:115:ARG:NH1	4:A:1456:CL:CL	2.72	0.59
1:B:278:ASP:O	1:B:280:VAL:HG22	2.04	0.57
1:B:152:TRP:CZ2	1:B:181:PRO:HB2	2.40	0.57
1:B:127:GLY:O	1:B:139:ARG:NH2	2.39	0.56
1:A:283:ILE:O	1:A:345:THR:HG22	2.07	0.54
1:B:247:GLU:OE2	3:B:1455:IOD:I	2.96	0.54
1:B:89:LEU:HB3	1:B:110:TYR:HB3	1.90	0.53
1:B:140:TYR:HA	1:B:147:MET:HE3	1.90	0.53
1:A:442:TRP:CD2	1:A:443:PRO:HD2	2.44	0.53
1:B:154:ARG:HD2	4:B:1459:CL:CL	2.45	0.52
1:B:140:TYR:N	1:B:147:MET:CE	2.73	0.51
1:B:175:ALA:HB3	1:B:177:MET:CE	2.41	0.50
1:B:175:ALA:HB3	1:B:177:MET:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:LEU:CG	1:B:177:MET:HE1	2.43	0.48
1:A:358:GLU:OE1	1:A:358:GLU:N	2.47	0.48
1:A:372:ARG:HG2	1:A:437:VAL:HG11	1.95	0.48
1:A:442:TRP:CE3	1:A:443:PRO:HD2	2.49	0.48
1:B:338:LEU:HA	1:B:371:LEU:HD23	1.96	0.48
1:B:177:MET:HE2	1:B:177:MET:CA	2.43	0.47
1:A:89:LEU:HB3	1:A:110:TYR:HB3	1.97	0.46
1:A:102:ASN:HA	1:A:201:ALA:O	2.15	0.46
1:B:321:GLY:HA2	1:B:324:VAL:HG12	1.97	0.46
1:A:138:SER:O	1:A:142:THR:HG23	2.16	0.45
1:B:100:THR:CG2	1:B:101:CYS:O	2.64	0.45
1:A:94:LEU:HD22	1:A:210:GLU:HG3	1.98	0.45
1:B:139:ARG:NH1	1:B:185:SER:CB	2.79	0.45
1:B:358:GLU:O	1:B:359:GLY:C	2.61	0.44
1:B:140:TYR:CA	1:B:147:MET:CE	2.96	0.44
1:B:100:THR:CG2	1:B:104:GLY:HA2	2.49	0.43
1:A:226:LEU:C	1:A:226:LEU:HD23	2.43	0.43
1:A:283:ILE:HG13	1:A:284:THR:HG23	2.01	0.43
1:B:405:THR:HG23	1:B:409:ARG:HG2	2.00	0.42
1:A:114:SER:OG	1:A:174:ASN:O	2.30	0.42
1:B:140:TYR:HA	1:B:147:MET:CE	2.50	0.41
1:B:139:ARG:C	1:B:147:MET:CE	2.94	0.41
1:B:143:MET:HG2	1:B:146:LEU:HD12	2.03	0.41
1:B:132:ASN:OD1	1:B:132:ASN:C	2.63	0.41
1:A:380:ALA:HA	1:A:434:VAL:HG12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	337/383 (88%)	324 (96%)	12 (4%)	1 (0%)	36	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	337/383 (88%)	319 (95%)	14 (4%)	4 (1%)	10	12
All	All	674/766 (88%)	643 (95%)	26 (4%)	5 (1%)	18	23

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	391	ILE
1	A	391	ILE
1	B	279	CYS
1	B	129	TYR
1	B	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	A	301/333 (90%)	291 (97%)	10 (3%)	33	50
1	B	301/333 (90%)	293 (97%)	8 (3%)	39	58
All	All	602/666 (90%)	584 (97%)	18 (3%)	36	53

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LEU
1	A	115	ARG
1	A	138	SER
1	A	143	MET
1	A	144	ARG
1	A	280	VAL
1	A	357	GLN
1	A	371	LEU
1	A	444	HIS
1	A	451	THR
1	B	100	THR

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Mol	Chain	Res	Type
1	B	187	VAL
1	B	193	SER
1	B	198	ASN
1	B	280	VAL
1	B	281	ASP
1	B	295	ILE
1	B	358	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	92	HIS
1	A	135	ASN
1	A	299	ASN
1	A	412	HIS
1	B	198	ASN
1	B	357	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 13 are monoatomic - leaving 2 for Mogul analysis.

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	1452	1	14,14,15	0.63	0	17,19,21	1.25	2 (11%)
2	NAG	B	1452	1	14,14,15	0.70	0	17,19,21	1.16	2 (11%)

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	1452	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1452	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($^{\circ}$)	Ideal($^{\circ}$)
2	A	1452	NAG	C4-C3-C2	-3.07	106.52	111.02
2	A	1452	NAG	C8-C7-N2	2.51	120.28	116.12
2	B	1452	NAG	C4-C3-C2	2.34	114.45	111.02
2	B	1452	NAG	C3-C4-C5	2.08	114.01	110.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1452	NAG	C8-C7-N2-C2
2	A	1452	NAG	O7-C7-N2-C2

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

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, 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	345/383 (90%)	0.09	12 (3%) 47 49	24, 38, 74, 100	0
1	B	345/383 (90%)	0.31	19 (5%) 30 32	30, 49, 76, 95	0
All	All	690/766 (90%)	0.20	31 (4%) 38 40	24, 44, 76, 100	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	434	VAL	6.1
1	A	85	LEU	5.0
1	B	432	CYS	4.9
1	B	434	VAL	4.0
1	B	356	VAL	3.7
1	A	433	PRO	3.6
1	A	432	CYS	3.6
1	B	194	LYS	3.6
1	A	86	ASN	3.4
1	A	451	THR	3.0
1	A	351	LEU	2.8
1	A	442	TRP	2.8
1	B	442	TRP	2.8
1	B	359	GLY	2.7
1	B	451	THR	2.6
1	B	350	HIS	2.6
1	B	357	GLN	2.5
1	B	280	VAL	2.4
1	A	350	HIS	2.4
1	A	194	LYS	2.4
1	B	192	SER	2.3
1	A	444	HIS	2.3
1	B	281	ASP	2.2
1	A	143	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	86	ASN	2.2
1	B	433	PRO	2.2
1	B	193	SER	2.1
1	B	362	LEU	2.1
1	B	441	PRO	2.1
1	B	396	HIS	2.1
1	B	198	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](#)

There are no oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	NAG	A	1452	14/15	0.80	0.12	59,63,70,72	0
2	NAG	B	1452	14/15	0.83	0.13	61,67,71,72	0
3	IOD	A	1455	1/1	0.92	0.21	111,111,111,111	0
3	IOD	A	1458	1/1	0.94	0.14	88,88,88,88	0
4	CL	A	1456	1/1	0.94	0.11	45,45,45,45	0
3	IOD	A	1457	1/1	0.95	0.13	96,96,96,96	0
3	IOD	B	1456	1/1	0.96	0.18	95,95,95,95	0
3	IOD	B	1458	1/1	0.96	0.14	103,103,103,103	0
3	IOD	B	1455	1/1	0.96	0.10	74,74,74,74	1
3	IOD	B	1457	1/1	0.97	0.06	70,70,70,70	1
4	CL	B	1459	1/1	0.97	0.06	41,41,41,41	0
3	IOD	A	1454	1/1	0.99	0.07	51,51,51,51	0
3	IOD	B	1453	1/1	0.99	0.07	53,53,53,53	0
3	IOD	B	1454	1/1	0.99	0.11	68,68,68,68	0
3	IOD	A	1453	1/1	1.00	0.10	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.